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(54) Title: METHODS FOR CONTROLLING PESTS USING RNAI

(57) Abstract: The present invention concerns methods for controlling insect infestation via RNAi- mediated gene silencing,
whereby the intact insect cell(s) are contacted with a double-stranded RNA from outside the insect cell(s) and whereby the
double-stranded RNA is taken up by the intact insect cell(s). In one particular embodiment, the methods of the invention are used to
alleviate plants from insect pests. Alternatively, the methods are used for treating and/or preventing insect infestation on a substrate
or a subject in need of such treatment and/or prevention. Suitable insect target genes and fragments thereof, dsRNA constructs,
recombinant constructs and compositions are disclosed.

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METHODS FOR CONTROLLING PESTS USING RNAi

Field of the invention

The present invention relates to the field of double-stranded RNA (dsRNA)-mediated gene
5   silencing in insect species. More particularly, the present invention relates to genetic constructs
     designed for the expression of dsRNA corresponding to novel target genes. These constructs are
     particularly useful in RNAi-mediated insect pest control. The invention further relates to methods for
     controlling insects, methods for preventing insect infestation and methods for down-regulating gene
     expression in insects using RNAi.

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Background to the invention

Insect and other pests can cause injury and even death by their bites or stings.
Additionally, many pests transmit bacteria and other pathogens that cause diseases. For example,
mosquitoes transmit pathogens that cause malaria, yellow fever, encephalitis, and other diseases.
15   The bubonic plague, or black death, is caused by bacteria that infect rats and other rodents.
Compositions for controlling microscopic pest infestations have been provided in the form of
antibiotic, antiviral, and antifungal compositions. Methods for controlling infestations by pests, such
as nematodes and insects, have typically been in the form of chemical compositions that are
applied to surfaces on which pests reside, or administered to infested animals in the form of pellets,
20   powders, tablets, pastes, or capsules.

Control of insect pests on agronomically important crops is an important field, for instance
insect pests which damage plants belonging to the Solanaceae family, especially potato (*Solanum
tuberosum*), but also tomato (*Solanum lycopersicum*), eggplant (*Solanum melongena*), capsicums
(*Solanum capsicum*), and nightshade (for example, *Solanum aculeastrum, S. bulbocastanum, S.
25   cardiophyllum, S. douglasii, S. dulcamara, S. lanceolatum, S. robustum,* and *S. triquetrum*),
particularly the control of coleopteran pests.

Substantial progress has been made in the last few decades towards developing more
efficient methods and compositions for controlling insect infestations in plants. Chemical pesticides
have been very effective in eradicating pest infestations.
30   Biological control using extract from neem seed has been shown to work against
coleopteran pests of vegetables. Commercially available neem-based insecticides have
azadirachtin as the primary active ingredient. These insecticides are applicable to a broad
spectrum of insects. They act as insect growth regulator; azadirachtin prevents insects from
molting by inhibiting production of an insect hormone, ecdysone.
35   Biological control using protein Cry3A from *Bacillus thuringiensis* varieties tenebrionis and
san diego, and derived insecticidal proteins are alternatives to chemical control. The Bt toxin
protein is effective in controlling Colorado potato beetle larvae either as formulations sprayed onto
the foliage or expressed in the leaves of potatoes.

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An alternative biological agent is dsRNA. Over the last few years, down-regulation of genes (also referred to as "gene silencing") in multicellular organisms by means of RNA interference or "RNAi" has become a well-established technique.

RNA interference or "RNAi" is a process of sequence-specific down-regulation of gene expression (also referred to as "gene silencing" or "RNA-mediated gene silencing") initiated by double-stranded RNA (dsRNA) that is complementary in sequence to a region of the target gene to be down-regulated (Fire, A. Trends Genet. Vol. 15, 358-363, 1999; Sharp, P.A. Genes Dev. Vol. 15, 485-490, 2001).

Over the last few years, down-regulation of target genes in multicellular organisms by means of RNA interference (RNAi) has become a well established technique. Reference may be made to International Applications WO 99/32619 (Carnegie Institution) and WO 00/01846 (by Applicant).

DsRNA gene silencing finds application in many different areas, such as for example dsRNA mediated gene silencing in clinical applications (WO2004/001013) and in plants. In plants, dsRNA constructs useful for gene silencing have also been designed to be cleaved and to be processed into short interfering RNAs (siRNAs).

Although the technique of RNAi has been generally known in the art in plants, C. elegans and mammalian cells for some years, to date little is known about the use of RNAi to down-regulate gene expression in insects. Since the filing and publication of the WO 00/01846 and WO 99/32619 applications, only few other applications have been published that relate to the use of RNAi to protect plants against insects. These include the International Applications WO 01/37654 (DNA Plant Technologies), WO 2005/019408 (Bar Ilan University), WO 2005/049841 (CSIRO, Bayer Cropscience), WO 05/047300 (University of Utah Research foundation), and the US application 2003/00150017 (Mesa et al.). The present invention provides target genes and constructs useful in the RNAi-mediated insect pest control. Accordingly, the present invention provides methods and compositions for controlling pest infestation by repressing, delaying, or otherwise reducing gene expression within a particular pest.

Description of the invention

The present invention describes a novel non-compound, non-protein based approach for the control of insect crop pests. The active ingredient is a nucleic acid, a double-stranded RNA (dsRNA), which can be used as an insecticidal formulation, for example, as a foliar spray. The sequence of the dsRNA corresponds to part or whole of an essential insect gene and causes downregulation of the insect target via RNA interference (RNAi). As a result of the downregulation of mRNA, the dsRNA prevents expression of the target insect protein and hence causes death, growth arrest or sterility of the insect.

The methods of the invention can find practical application in any area of technology where it is desirable to inhibit viability, growth, development or reproduction of the insect, or to decrease pathogenicity or infectivity of the insect. The methods of the invention further find practical application where it is desirable to specifically down-regulate expression of one or more target

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genes in an insect. Particularly useful practical applications include, but are not limited to, (1) protecting plants against insect pest infestation; (2) pharmaceutical or veterinary use in humans and animals (for example to control, treat or prevent insect infections in humans and animals); (3) protecting materials against damage caused by insects; (4) protecting perishable materials (such

5   as foodstuffs, seed, etc.) against damage caused by insects; and generally any application wherein insects need to be controlled and/or wherein damage caused by insects needs to be prevented.

In accordance with one embodiment the invention relates to a method for controlling insect growth on a cell or an organism, or for preventing insect infestation of a cell or an organism susceptible to insect infection, comprising contacting insects with a double-stranded RNA, wherein

10   the double-stranded RNA comprises annealed complementary strands, one of which has a nucleotide sequence which is complementary to at least part of the nucleotide sequence of an insect target gene, whereby the double-stranded RNA is taken up by the insect and thereby controls growth or prevents infestation.

The present invention therefore provides isolated novel nucleotide sequences of insect

15   target genes, said isolated nucleotide sequences comprising at least one nucleic acid sequence selected from the group comprising:

(i) sequences represented by any of SEQ ID NOs 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 49 to 158, 159, 160-163, 168, 173, 178, 183, 188, 193, 198, 203, 208, 215, 220, 225, 230, 240 to 247, 249, 251, 253, 255, 257, 259, 275 to 472, 473, 478, 483, 488, 493, 498, 503, 508 to 513, 515,

20   517, 519, 521, 533 to 575, 576, 581, 586, 591, 596, 601, 603, 605, 607, 609, 621 to 767, 768, 773, 778, 783, 788,.793, 795, 797, 799, 801, 813 to 862, 863, 868, 873, 878, 883, 888, 890, 892, 894, 896, 908 to 1040, 1041, 1046, 1051, 1056, 1061, 1066 to 1071, 1073, 1075, 1077, 1079, 1081, 1083, 1085, 1087, 1089, 1091, 1093, 1095, 1097, 1099, 1101, 1103, 1105, 1107, 1109, 1111, 1113, 1161 to 1571, 1572, 1577, 1582, 1587, 1592, 1597, 1602, 1607, 1612, 1617, 1622, 1627,

25   1632, 1637, 1642, 1647, 1652, 1657, 1662, 1667, 1672, 1677, 1682, 1684, 1686, 1688, 1690, 1692, 1694, 1696, 1698, 1700, 1702, 1704, 1730 to 2039, 2040, 2045, 2050, 2055, 2060, 2065, 2070, 2075, 2080, 2085, 2090, 2095, 2100, 2102, 2104, 2106, 2108, 2120 to 2338, 2339, 2344, 2349, 2354, 2359, 2364, 2366, 2368, 2370, 2372, 2384 to 2460, 2461, 2466, 2471, 2476, 2481 or 2486, or the complement thereof,

30   (ii) sequences which are at least 70 %, preferably at least 75%, 80%, 85%, 90%, more preferably at least 95%, 96%, 97%, 98% or 99% identical to a sequence represented by any of SEQ ID NOs 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 49 to 158, 159, 160-163, 168, 173, 178, 183, 188, 193, 198, 203, 208, 215, 220, 225, 230, 240 to 247, 249, 251, 253, 255, 257, 259, 275 to 472, 473, 478, 483, 488, 493, 498, 503, 508 to 513, 515, 517, 519, 521, 533 to 575, 576, 581, 586, 591,

35   596, 601, 603, 605, 607, 609, 621 to 767, 768, 773, 778, 783, 788, 793, 795, 797, 799, 801, 813 to 862, 863, 868, 873, 878, 883, 888, 890, 892, 894, 896, 908 to 1040, 1041, 1046, 1051, 1056, 1061, 1066 to 1071, 1073, 1075, 1077, 1079, 1081, 1083, 1085, 1087, 1089, 1091, 1093, 1095, 1097, 1099, 1101, 1103, 1105, 1107, 1109, 1111, 1113, 1161 to 1571, 1572, 1577, 1582, 1587, 1592, 1597, 1602, 1607, 1612, 1617, 1622, 1627, 1632, 1637, 1642, 1647, 1652, 1657, 1662, 1667,

40   1672, 1677, 1682, 1684, 1686, 1688, 1690, 1692, 1694, 1696, 1698, 1700, 1702, 1704, 1730 to

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2039, 2040, 2045, 2050, 2055, 2060, 2065, 2070, 2075, 2080, 2085, 2090, 2095, 2100, 2102, 2104, 2106, 2108, 2120 to 2338, 2339, 2344, 2349, 2354, 2359, 2364, 2366, 2368, 2370, 2372, 2384 to 2460, 2461, 2466, 2471, 2476, 2481 or 2486, or the complement thereof, and

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(iii) sequences comprising at least 17 contiguous nucleotides of any of the sequences represented by SEQ ID NOs 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 49 to 158, 159, 160-163, 168, 173, 178, 183, 188, 193, 198, 203, 208, 215, 220, 225, 230, 240 to 247, 249, 251, 253, 255, 257, 259, 275 to 472, 473, 478, 483, 488, 493, 498, 503, 508 to 513, 515, 517, 519, 521, 533 to 575, 576, 581, 586, 591, 596, 601, 603, 605, 607, 609, 621 to 767, 768, 773, 778, 783, 788, 793, 795, 797, 799, 801, 813 to 862, 863, 868, 873, 878, 883, 888, 890, 892, 894, 896, 908 to 1040, 1041,

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1046, 1051, 1056, 1061, 1066 to 1071, 1073, 1075, 1077, 1079, 1081, 1083, 1085, 1087, 1089, 1091, 1093, 1095, 1097, 1099, 1101, 1103, 1105, 1107, 1109, 1111, 1113, 1161 to 1571, 1572, 1577, 1582, 1587, 1592, 1597, 1602, 1607, 1612, 1617, 1622, 1627, 1632, 1637, 1642, 1647, 1652, 1657, 1662, 1667, 1672, 1677, 1682, 1684, 1686, 1688, 1690, 1692, 1694, 1696, 1698, 1700, 1702, 1704, 1730 to 2039, 2040, 2045, 2050, 2055, 2060, 2065, 2070, 2075, 2080, 2085,

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2090, 2095, 2100, 2102, 2104, 2106, 2108, 2120 to 2338, 2339, 2344, 2349, 2354, 2359, 2364, 2366, 2368, 2370, 2372, 2384 to 2460, 2461, 2466, 2471, 2476, 2481 or 2486, or the complement thereof, or wherein said nucleic acid sequence is an orthologue of a gene comprising at least 17 contiguous nucleotides of any of SEQ ID NOs 49 to 158, 275 to 472, 533 to 575, 621 to 767, 813 to 862, 908 to 1040, 1161 to 1571, 1730 to 2039, 2120 to 2338, 2384 to 2460, or a complement

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thereof, said nucleic acid sequences being useful for preparing the double stranded RNAs of the invention for controlling insect growth.

"Controlling pests" as used in the present invention means killing pests, or preventing pests to develop, or to grow or preventing pests to infect or infest. Controlling pests as used herein also encompasses controlling insect progeny (development of eggs). Controlling pests as used

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herein also encompasses inhibiting viability, growth, development or reproduction of the insect, or to decrease pathogenicity or infectivity of the insect. The compounds and/or compositions described herein, may be used to keep an organism healthy and may be used curatively, preventively or systematically to control pests or to avoid insect growth or development or infection or infestation.

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Particular pests envisaged by the present invention are insect pests. Controlling insects as used herein thus also encompasses controlling insect progeny (such as development of eggs, for example for insect pests). Controlling insects as used herein also encompasses inhibiting viability, growth, development or reproduction of the insect, or decreasing pathogenicity or infectivity of the insect. In the present invention, controlling insects may inhibit a biological activity in an insect,

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resulting in one or more of the following attributes: reduction in feeding by the insect, reduction in viability of the insect, death of the insect, inhibition of differentiation and development of the insect, absence of or reduced capacity for sexual reproduction by the insect, muscle formation, juvenile hormone formation, juvenile hormone regulation, ion regulation and transport, maintenance of cell membrane potential, amino acid biosynthesis, amino acid degradation, sperm formation,

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pheromone synthesis, pheromone sensing, antennae formation, wing formation, leg formation,

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development and differentiation, egg formation, larval maturation, digestive enzyme formation, haemolymph synthesis, haemolymph maintenance, neurotransmission, cell division, energy metabolism, respiration, apoptosis, and any component of a eukaryotic cells' cytoskeletal structure, such as, for example, actins and tubulins.The compounds and/or compositions described herein, may be used to keep an organism healthy and may be used curatively, preventively or systematically to control an insect or to avoid insect growth or development or infection or infestation. Thus, the invention may allow previously susceptible organisms to develop resistance against infestation by the insect organism.

The expression "complementary to at least part of" as used herein means that the nucleotide sequence is fully complementary to the nucleotide sequence of the target over more than two nucleotides, for instance over at least 15, 16, 17, 18, 19, 20, 21, 22 , 23, 24 or more contiguous nucleotides.

According to a further embodiment , the invention relates to a method method for down-regulating expression of a target gene in an insect, comprising contacting said insect with a double-stranded RNA, wherein the double-stranded RNA comprises annealed complementary strands, one of which has a nucleotide sequence which is complementary to at least part of the nucleotide sequence of the insect target gene to be down-regulated, whereby the double-stranded RNA is taken up into the insect and thereby down-regulates expression of the insect target gene.

Whenever the term "a" is used within the context of "a target gene", this means "at least one" target gene. The same applies for "a" target organism meaning "at least one" target organism, and "a" RNA molecule or host cell meaning "at least one" RNA molecule or host cell. This is also detailed further below.

According to one embodiment, the methods of the invention rely on uptake by the insect of double-stranded RNA present outside of the insect (e. g. by feeding) and does not require expression of double-stranded RNA within cells of the insect. In addition, the present invention also encompasses methods as described above wherein the insect is contacted with a composition comprising the double-stranded RNA.

Said double-stranded RNA may be expressed by a prokaryotic (for instance, but not limited to, a bacterial) or eukaryotic (for instance, but not limited to, a yeast) host cell or host organism.

The insect can be any insect, meaning any organism belonging to the Kingdom Animals, more specific to the Phylum Arthropoda, and to the Class Insecta or the Class Arachnida. The methods of the invention are applicable to all insects that are susceptible to gene silencing by RNA interference and that are capable of internalising double-stranded RNA from their immediate environment. The invention is also applicable to the insect at any stage in its development. Because insects have a non-living exoskeleton, they cannot grow at a uniform rate and rather grow in stages by periodically shedding their exoskeleton. This process is referred to as moulting or ecdysis. The stages between moults are referred to as "instars" and these stages may be targeted according to the invention. Also, insect eggs or live young may also be targeted according to the present invention. All stages in the developmental cycle, which includes metamorphosis in the

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pterygotes, may be targeted according to the present invention. Thus, individual stages such as larvae, pupae, nymph etc stages of development may all be targeted.

In one embodiment of the invention, the insect may belong to the following orders: Acari, Araneae, Anoplura, Coleoptera, Collembola, Dermaptera, Dictyoptera, Diplura, Diptera,

5   Embioptera, Ephemeroptera, Grylloblatodea, Hemiptera, Homoptera, Hymenoptera, Isoptera, Lepidoptera, Mallophaga, Mecoptera, Neuroptera, Odonata, Orthoptera, Phasmida, Plecoptera, Protura, Psocoptera, Siphonaptera, Siphunculata, Thysanura, Strepsiptera, Thysanoptera, Trichoptera, and Zoraptera.

In preferred, but non-limiting, embodiments and methods of the invention the insect is

10   chosen from the group consisting of:

(1) an insect which is a plant pest, such as but not limited to *Nilaparvata* spp. (e.g. *N. lugens (brown planthopper)); Laodelphax* spp. (e.g. *L. striatellus* (small brown planthopper)); *Nephotettix* spp. (e.g. *N. virescens* or *N. cincticeps* (green leafhopper), or *N.nigropictus* (rice leafhopper)); *Sogatella* spp. (e.g. *S. furcifera* (white-backed planthopper)); *Blissus* spp. (e.g. *B.*

15   *leucopterus leucopterus* (chinch bug)); *Scotinophora* spp. (e.g. *S. vermidulate* (rice blackbug)); *Acrosternum* spp. (e.g. *A. hilare* (green stink bug)); *Parnara* spp. (e.g. *P. guttata* (rice skipper)); *Chilo* spp. (e.g. *C. suppressalis* (rice striped stem borer), *C. auricilius* (gold-fringed stem borer), or *C. polychrysus* (dark-headed stem borer)); *Chilotraea* spp. (e.g. *C. polychrysa* (rice stalk borer)); *Sesamia* spp. (e.g. *S. inferens* (pink rice borer)); *Tryporyza* spp. (e.g. *T. innotata* (white rice borer),

20   or *T. incertulas* (yellow rice borer)); *Cnaphalocrocis* spp. (e.g. *C. medinalis* (rice leafroller)); *Agromyza* spp. (e.g. *A. oryzae* (leafminer), or *A. parvicornis* (corn blot leafminer)); *Diatraea* spp. (e.g. *D. saccharalis* (sugarcane borer), or *D. grandiosella* (southwestern corn borer)); *Narnaga* spp. (e.g. *N. aenescens* (green rice caterpillar)); *Xanthodes* spp. (e.g. *X. transversa* (green caterpillar)); *Spodoptera* spp. (e.g. *S. frugiperda* (fall armyworm), *S. exigua* (beet armyworm), *S. littoralis*

25   (climbing cutworm) or *S. praefica* (western yellowstriped armyworm)); *Mythimna* spp. (e.g. *Mythimna (Pseudaletia) seperata* (armyworm)); *Helicoverpa* spp. (e.g. *H. zea* (corn earworm)); *Colaspis* spp. (e.g. *C. brunnea* (grape colaspis)); *Lissorhoptrus* spp. (e.g. *L. oryzophilus* (rice water weevil)); *Echinocnemus* spp. (e.g. *E. squamos* (rice plant weevil)); *Diclodispa* spp. (e.g. *D. armigera* (rice hispa)); *Oulema* spp. (e.g. *O. oryzae* (leaf beetle); *Sitophilus* spp. (e.g. *S. oryzae*

30   (rice weevil)); *Pachydiplosis* spp. (e.g. *P. oryzae* (rice gall midge)); *Hydrellia* spp. (e.g. *H. griseola* (small rice leafminer), or *H. sasakii* (rice stem maggot)); *Chlorops* spp. (e.g. *C. oryzae* (stem maggot)); *Diabrotica* spp. (e.g. *D. virgifera virgifera* (western corn rootworm), *D. barberi* (northern corn rootworm), *D. undecimpunctata* howardi (southern corn rootworm), *D. virgifera zeae* (Mexican corn rootworm); *D. balteata* (banded cucumber beetle)); *Ostrinia* spp. (e.g. *O. nubilalis* (European

35   corn borer)); *Agrotis* spp. (e.g. *A.ipsilon* (black cutworm)); *Elasmopalpus* spp. (e.g. *E. lignosellus* (lesser cornstalk borer)); *Melanotus* spp. (wireworms); *Cyclocephala* spp. (e.g. *C. borealis* (northern masked chafer), or *C. immaculata* (southern masked chafer)); *Popillia* spp. (e.g. *P. japonica* (Japanese beetle)); *Chaetocnema* spp. (e.g. *C. pulicaria* (corn flea beetle)); *Sphenophorus* spp. (e.g. *S. maidis* (maize billbug)); *Rhopalosiphum* spp. (e.g. *R. maidis* (corn leaf

40   aphid)); *Anuraphis* spp. (e.g. *A. maidiradicis* (corn root aphid)); *Melanoplus* spp. (e.g. *M.*

femurrubrum (redlegged grasshopper) *M. differentialis* (differential grasshopper) or *M. sanguinipes* (migratory grasshopper)); *Hylemya* spp. (e.g. *H. platura* (seedcorn maggot)); *Anaphothrips* spp. (e.g. *A. obscrurus* (grass thrips)); *Solenopsis* spp. (e.g. *S. milesta* (thief ant)); or spp. (e.g. *T. urticae* (twospotted spider mite), *T. cinnabarinus* (carmine spider mite); *Helicoverpa* spp. (e.g. *H.*

5   *zea* (cotton bollworm), or *H. armigera* (American bollworm)); *Pectinophora* spp. (e.g. *P. gossypiella* (pink bollworm)); *Earias* spp. (e.g. *E. vittella* (spotted bollworm)); *Heliothis* spp. (e.g. *H. virescens* (tobacco budworm)); *Anthonomus* spp. (e.g. *A. grandis* (boll weevil)); *Pseudatomoscelis* spp. (e.g. *P. seriatus* (cotton fleahopper)); *Trialeurodes* spp. (e.g. *T. abutiloneus* (banded-winged whitefly) *T. vaporariorum* (greenhouse whitefly)); *Bemisia* spp. (e.g. *B. argentifoli* (silverleaf whitefly)); *Aphis*

10   spp. (e.g. *A. gossypii* (cotton aphid)); *Lygus* spp. (e.g. *L. lineolaris* (tarnished plant bug) or *L. hesperus* (western tarnished plant bug)); *Euschistus* spp. (e.g. *E. conspersus* (consperse stink bug)); *Chlorochroa* spp. (e.g. *C. sayi* (Say stinkbug)); *Nezara* spp. (e.g. *N. viridula* (southern green stinkbug)); *Thrips* spp. (e.g. *T. tabaci* (onion thrips)); *Frankliniella* spp. (e.g. *F. fusca* (tobacco thrips), or *F. occidentalis* (western flower thrips)); *Leptinotarsa* spp. (e.g. *L. decemlineata* (Colorado

15   potato beetle), *L. juncta* (false potato beetle), or *L. texana* (Texan false potato beetle)); *Lema* spp. (e.g. *L. trilineata* (three-lined potato beetle)); *Epitrix* spp. (e.g. *E. cucumeris* (potato flea beetle), *E. hirtipennis* (flea beetle), or *E. tuberis* (tuber flea beetle)); *Epicauta* spp. (e.g. *E. vittata* (striped blister beetle)); *Phaedon* spp. (e.g. *P. cochleariae* (mustard leaf beetle)); *Epilachna* spp. (e.g. *E. varivetis* (mexican bean beetle)); *Acheta* spp. (e.g. *A. domesticus* (house cricket)); *Empoasca* spp.

20   (e.g. *E. fabae* (potato leafhopper)); *Myzus* spp. (e.g. *M. persicae* (green peach aphid)); *Paratrioza* spp. (e.g. *P. cockerelli* (psyllid)); *Conoderus* spp. (e.g. *C. falli* (southern potato wireworm), or *C. vespertinus* (tobacco wireworm)); *Phthorimaea* spp. (e.g. *P. operculella* (potato tuberworm)); *Macrosiphum* spp. (e.g. *M. euphorbiae* (potato aphid)); *Thyanta* spp. (e.g. *T. pallidovirens* (redshouldered stinkbug)); *Phthorimaea* spp. (e.g. *P. operculella* (potato tuberworm)); *Helicoverpa*

25   spp. (e.g. *H. zea* (tomato fruitworm); *Keiferia* spp. (e.g. *K. lycopersicella* (tomato pinworm)); *Limonius* spp. (wireworms); *Manduca* spp. (e.g. *M. sexta* (tobacco hornworm), or *M. quinquemaculata* (tomato hornworm)); *Liriomyza* spp. (e.g. *L. sativae, L. trifolli* or *L. huidobrensis* (leafminer)); *Drosophilla* spp. (e.g. *D. melanogaster, D. yakuba, D. pseudoobscura* or *D. simulans*); *Carabus* spp. (e.g. *C. granulatus*); *Chironomus* spp. (e.g. *C. tentanus*); *Ctenocephalides* spp. (e.g.

30   *C. felis* (cat flea)); *Diaprepes* spp. (e.g. *D. abbreviatus* (root weevil)); *Ips* spp. (e.g. *I. pini* (pine engraver)); *Tribolium* spp. (e.g. *T. castaneum* (red floor beetle)); *Glossina* spp. (e.g. *G. morsitans* (tsetse fly)); *Anopheles* spp. (e.g. *A. gambiae* (malaria mosquito)); *Helicoverpa* spp. (e.g. *H. armigera* (African Bollworm)); *Acyrthosiphon* spp. (e.g. *A. pisum* (pea aphid)); *Apis* spp. (e.g. *A. melifera* (honey bee)); *Homalodisca* spp. (e.g. *H. coagulate* (glassy-winged sharpshooter)); Aedes

35   spp. (e.g. Ae. aegypti *(yellow fever mosquito))*; *Bombyx* spp. *(e.g. B. mori (silkworm))*; *Locusta* spp. *(e.g. L. migratoria* (migratory locust)); *Boophilus* spp. (e.g. *B. microplus* (cattle tick)); *Acanthoscurria* spp. (e.g. *A. gomesiana* (red-haired chololate bird eater)); *Diploptera* spp. (e.g. *D. punctata* (pacific beetle cockroach)); *Heliconius* spp. (e.g. *H. erato* (red passion flower butterfly) or *H. melpomene* (postman butterfly)); *Curculio* spp. (e.g. *C. glandium* (acorn weevil)); *Plutella* spp.

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(e.g. *P. xylostella* (diamondback moth)); *Amblyomma* spp. (e.g. *A. variegatum* (cattle tick)); *Anteraea* spp. (e.g. *A. yamamai* (silkmoth)); and *Armigeres* spp. (e.g. *A. subalbatus);*

(2) an insect capable of infesting or injuring humans and/or animals such as, but not limited to those with piercing-sucking mouthparts, as found in Hemiptera and some Hymenoptera and Diptera such as mosquitos, bees, wasps, lice, fleas and ants, as well as members of the Arachnidae such as ticks and mitesorder, class or familiy of Acarina (ticks and mites) e.g. representatives of the families *Argasidae, Dermanyssidae, Ixodidae, Psoroptidae* or *Sarcoptidae* and representatives of the species *Amblyomma* spp., *Anocentor* spp., *Argas* spp., *Boophilus* spp., *Cheyletiella* spp., *Chorioptes* spp., *Demodex* spp., *Dermacentor* spp., *Dermanyssus* spp., *Haemophysalis* spp., *Hyalomma* spp., *Ixodes* spp., *Lynxacarus* spp., *Mesostigmata* spp., *Notoedres* spp., *Ornithodoros* spp., *Ornithonyssus* spp., *Otobius* spp., *otodectes* spp., *Pneumonyssus* spp., *Psoroptes* spp., *Rhipicephalus* spp., *Sarcoptes* spp., or *Trombicula* spp. ; Anoplura (sucking and biting lice) e.g. representatives of the species *Bovicola* spp., *Haematopinus* spp., *Linognathus* spp., *Menopon* spp., *Pediculus* spp., *Pemphigus* spp., *Phylloxera* spp., or *Solenopotes* spp. ; Diptera (flies) e.g. representatives of the species *Aedes* spp., *Anopheles* spp., *Calliphora* spp., *Chrysomyia* spp., *Chrysops* spp., *Cochliomyia* spp., *Culex* spp., *Culicoides* spp., *Cuterebra* spp., *Dermatobia* spp., *Gastrophilus* spp., *Glossina* spp., *Haematobia* spp. , *Haematopota* spp., *Hippobosca* spp., *Hypoderma* spp., *Lucilia* spp., *Lyperosia* spp., *Melophagus* spp., *Oestrus* spp., *Phaenicia* spp., *Phlebotomus* spp., *Phormia* spp., *Sarcophaga* spp., *Simulium* spp., *Stomoxys* spp., *Tabanus* spp., *Tannia* spp. or *Tipula* spp.; Mallophaga (biting lice) e.g. representatives of the species *Damalina* spp., *Felicola* spp., *Heterodoxus* spp. or *Trichodectes* spp.; or Siphonaptera (wingless insects) e.g. representatives of the species *Ceratophyllus* spp., spp., *Pulex* spp., or *Xenopsylla* spp; Cimicidae (true bugs) e.g. representatives of the species *Cimex* spp., *Tritominae* spp., *Rhodinius* spp., or *Triatoma* spp.

and

(3) an insect that causes unwanted damage to substrates or materials, such as insects that attack foodstuffs, seeds, wood, paint, plastic, clothing etc.

(4) an insect or arachnid relevant for public health and hygiene, including household insects and ecto-parasites such as, by way of example and not limitation, flies, spider mites, thrips, ticks, red poultry mite, ants, cockroaches, termites, crickets including house-crickets, silverfish, booklice, beetles, earwigs, mosquitos and fleas. More preferred targets are cockroaches (Blattodea) such as but not limited to *Blatella* spp. (e.g. *Blatella germanica* (german cockroach)), *Periplaneta* spp. (e.g. *Periplaneta americana* (American cockroach) and *Periplaneta australiasiae* (Australian cockroach)), *Blatta* spp. (e.g. *Blatta orientalis* (Oriental cockroach)) and Supella spp. (e.g. *Supella longipalpa (*brown-banded cockroach); ants (Formicoidea), such as but not limited to *Solenopsis* spp. (e.g. *Solenopsis invicta* (Red Fire Ant)), *Monomorium* spp. *(e.g. Monomorium pharaonis* (Pharaoh Ant)), *Camponotus* spp. *(e.g. Camponotus* spp (Carpenter Ants*)), lasius* spp. *(e.g. lasius niger* (Small Black Ant)), *Tetramorium* spp. (e.g. *Tetramorium caespitum* (Pavement Ant)), *Myrmica* spp. *(e.g. Myrmica rubra* (Red Ant)), *Formica* spp (wood ants), *Crematogaster* spp. *(e.g. Crematogaster lineolata* (Acrobat Ant)), *Iridomyrmex* spp. *(e.g. Iridomyrmex humilis*

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(Argentine Ant)), *Pheidole* spp. (Big Headed Ants), and *Dasymutilla* spp. *(e.g. Dasymutilla occidentalis* (Velvet Ant)); termites (Isoptera and/or Termitidae) such as but not limited to *Amitermes* spp. *(e.g. Amitermes floridensis* (Florida dark-winged subterranean termite)), *Reticulitermes* spp. *(e.g. Reticulitermes flavipes* (the eastern subterranean termile),*Reticulitermes*

5   *hesperus* (Western Subterranean Termite)), *Coptotermes* spp. *(e.g. Coptotermes formosanus* (Formosan Subterranean Termite)), *Incisitermes* spp. *(e.g. Incisitermes minor* (Western Drywood Termite)), *Neotermes spp. (e.g. Neotermes connexus* (Forest Tree Termite)).

In terms of "susceptible organisms", which benefit from the present invention, any organism which is susceptible to pest infestation is included. Pests of many different organisms,

10   for example animals such as humans, domestic animals (such as pets like cats, dogs etc) and livestock (including sheep, cows, pigs, chickens etc.).

In this context, preferred, but non-limiting, embodiments of the invention the insect or arachnid is chosen from the group consisting of:

(1)   Acari: mites including Ixodida (ticks)

15   (2)   Arachnida: Araneae (spiders) and Opiliones (harvestman), examples include: *Latrodectus mactans* (black widow) and *Loxosceles recluse* (Brown Recluse Spider)

(3)   Anoplura: lice, such as *Pediculus humanus* (human body louse)

(4)   Blattodea: cockroaches including German cockroach (*Blatella germanica*), of the genus Periplaneta, including American cockroach (*Periplaneta americana*) and Australian

20   cockroach (*Periplaneta australiasiae*), of the genus Blatta, including Oriental cockroach (*Blatta orientalis*) and of the genus Supella, including brown-banded cockroach (*Supella longipalpa*). A most preferred target is German cockroach (*Blatella germanica*).

(5)   Coleoptera: beetles, examples include: the family of Powderpost beetle (family of Bostrichoidea); *Dendroctonus spp.* (Black Turpentine Beetle, Southern Pine Beetle, IPS

25   Engraver Beetle); Carpet Beetles (*Anthrenus spp, Attagenus spp*); Old House Borer (family of Cerambycidae: *Hylotrupes bajulus*); *Anobium punctatum; Tribolium spp* (flour beetle); *Trogoderma granarium* (Khapra Beetle); *Oryzaephilus sarinamensis* (Toothed Grain Beetle) etc. (Bookworm)

(6)   Dermaptera: family of earwigs

30   (7)   Diptera: mosquitoes (Culicidae) and flies (Brachycera), examples are: Anophelinae such as *Anopheles* spp. and Culicinae such as *Aedes fulvus*; Tabanidae such as *Tabanus punctifer* (Horse Fly), *Glossina morsitans morsitans* (tsetse fly), drain flies (Psychodidae) and Calyptratae such as *Musca domestica (House fly), flesh flies* (family of Sarcophagidae) etc.

35   (8)   Heteroptera: bugs, such as *Cimex lectularius* (bed bug)

(9)   Hymenoptera: wasps (Apocrita), including ants (Formicoidea), bees (Apoidea): *Solenopsis invicta* (Red Fire Ant), *Monomorium pharaonis* (Pharaoh Ant), *Camponotus*

spp (Carpenter Ants), *lasius niger* (Small Black Ant), *tetramorium caespitum* (Pavement Ant), *Myrmica rubra* (Red Ant), *Formica spp* (wood ants), *Crematogaster lineolata* (Acrobat Ant), *Iridomyrmex humilis* (Argentine Ant), *Pheidole spp.* (Big Headed Ants, *Dasymutilla occidentalis* (Velvet Ant) etc.

5   (10) Isoptera: termites, examples include: *Amitermes floridensis* (Florida dark-winged subterranean termite), the eastern subterranean termite (*Reticulitermes flavipes*), the *R. hesperus* (Western Subterranean Termite), *Coptotermes formosanus* (Formosan Subterranean Termite), *Incisitermes minor* (Western Drywood Termite), *Neotermes connexus* (Forest Tree Termite) and Termitidae

10   (11) Lepidoptera: moths, examples include: Tineidae & Oecophoridae such as *Tineola bisselliella* (Common Clothes Moth), and Pyralidae such as *Pyralis farinalis* (Meal Moth) etc

     (12) Psocoptera: booklice (Psocids)

     (13) Siphonaptera: fleas such as *Pulex irritans*

15   (14) Sternorrhyncha: aphids (Aphididae)

     (15) Zygentoma: silverfish, examples are: *Thermobia domestica* and *Lepisma saccharina*

     Preferred plant pathogenic insects according to the invention are plant pest and are selected from the group consisting of *Leptinotarsa* spp. (e.g. *L. decemlineata* (Colorado potato beetle), *L. juncta* (false potato beetle), or *L. texana* (Texan false potato beetle)); *Nilaparvata* spp.
20   (e.g. *N. lugens (brown planthopper))*; *Laodelphax* spp. (e.g. *L. striatellus* (small brown planthopper)); *Nephotettix* spp. (e.g. *N. virescens* or *N. cincticeps* (green leafhopper), or *N.nigropictus* (rice leafhopper)); *Sogatella* spp. (e.g. *S. furcifera* (white-backed planthopper)); *Chilo* spp. (e.g. *C. suppressalis* (rice striped stem borer), *C. auricilius* (gold-fringed stem borer), or *C. polychrysus* (dark-headed stem borer)); *Sesamia* spp. (e.g. *S. inferens* (pink rice borer));
25   *Tryporyza* spp. (e.g. *T. innotata* (white rice borer), or *T. incertulas* (yellow rice borer)); *Diabrotica* spp. (e.g. *D. virgifera virgifera* (western corn rootworm), *D. barberi* (northern corn rootworm), *D. undecimpunctata* howardi (southern corn rootworm), *D. virgifera zeae* (Mexican corn rootworm); *Ostrinia* spp. (e.g. *O. nubilalis* (European corn borer)); *Anaphothrips* spp. (e.g. *A. obscrurus* (grass thrips)); *Pectinophora* spp. (e.g. *P. gossypiella* (pink bollworm)); *Heliothis* spp. (e.g. *H. virescens*
30   (tobacco budworm)); *Trialeurodes* spp. (e.g. *T. abutiloneus* (banded-winged whitefly) *T. vaporariorum* (greenhouse whitefly)); *Bemisia* spp. (e.g. *B. argentifoli* (silverleaf whitefly)); *Aphis* spp. (e.g. *A. gossypii* (cotton aphid)); *Lygus* spp. (e.g. *L. lineolaris* (tarnished plant bug) or *L. hesperus* (western tarnished plant bug)); *Euschistus* spp. (e.g. *E. conspersus* (conperse stink bug)); *Chlorochroa* spp. (e.g. *C. sayi* (Say stinkbug)); *Nezara* spp. (e.g. *N. viridula* (southern green
35   stinkbug)); *Thrips* spp. (e.g. *T. tabaci* (onion thrips)); *Frankliniella* spp. (e.g. *F. fusca* (tobacco thrips), or *F. occidentalis* (western flower thrips)); *Myzus* spp. (e.g. *M. persicae* (green peach aphid)); *Macrosiphum spp. (e.g. M. euphorbiae* (potato aphid)); *Blissus* spp. (e.g. *B. leucopterus*

leucopterus (chinch bug)); *Acrosternum* spp. (e.g. *A. hilare* (green stink bug)); *Chilotraea* spp. (e.g. *C. polychrysa* (rice stalk borer)); *Lissorhoptrus* spp. (e.g. *L. oryzophilus* (rice water weevil)); *Rhopalosiphum* spp. (e.g. *R. maidis* (corn leaf aphid)); and *Anuraphis* spp. (e.g. *A. maidiradicis* (corn root aphid)).

According to a more specific embodiment, the methods of the invention are applicable for Leptinotarsa species. Leptinotarsa belong to the family of Chrysomelidae or leaf beatles. Chrysomelid beetles such as Flea Beetles and Corn Rootworms and Curculionids such as Alfalfa Weevils are particularly important pests. Flea Beetles include a large number of small leaf feeding beetles that feed on the leaves of a number of grasses, cereals and herbs. Flea Beetles include a large number of genera (e.g., Attica, Apphthona, Argopistes, Disonycha, Epitrix, Longitarsus, Prodagricomela, Systena, and Phyllotreta). The Flea Beetle, Phyllotreta cruciferae, also known as the Rape Flea Beetle, is a particularly important pest. Corn rootworms include species found in the genus Diabrotica (e.g., D. undecimpunctata undecimpunctata, D. undecimpunctata howardii, D. longicornis, D. virgifera and D. balteata). Corn rootworms cause extensive damage to corn and curcubits. The Western Spotted Cucumber Beetle, D. undecimpunctata undecimpunctata, is a pest of curcubits in the western U.S. Alfalfa weevils (also known as clover weevils) belong to the genus, Hypera (H. postica, H. brunneipennis, H. nigrirostris, H. punctata and H. meles), and are considered an important pest of legumes. The Egyptian alfalfa weevil, H. brunneipennis, is an important pest of alfalfa in the western U.S.

There are more than 30 Leptinotarsa species. The present invention thus encompasses methods for controlling Leptinotarsa species, more specific methods for killing insects, or preventing Leptinotarsa insects to develop or to grow, or preventing insects to infect or infest. Specific Leptinotarsa species to control according to the invention include Colorado Potato Beetle (Leptinotarsa decemlineata (Say) and False Potato Beetle (Leptinotarsa juncta (Say).

CPB is a (serious) pest on our domestic potato (Solanum tuberosum), other cultivated and wild tuber bearing and non-tuber bearing potato species (e.g. S. demissum, S.phureja a.o.) and other Solanaceous (nightshades) plant species incuding:

(a) the crop species tomato (several Lycopersicon species), eggplant (Solanum melongena), peppers (several Capsicum species), tobacco (several Nicotiana species including ornamentals) and ground cherry (Physalis species);

(b) the weed/herb species, horse nettle (S. carolinense), common nightshade (S. dulcamara), belladonna (Atropa species), thorn apple (datura species), henbane (Hyoscyamus species) and buffalo burr (S. rostratum).

FPB is primarily found on horse nettle, but also occurs on common nightshade, ground cherry, and husk tomato (Physalis species).

The term "insect" encompasses insects of all types and at all stages of development, including egg, larval or nymphal, pupal and adult stages.

The present invention extends to methods as described herein, wherein the insect is *Leptinotarsa decemlineata* (Colorado potato beetle) and the plant is potato, eggplant, tomato, pepper, tobacco, ground cherry or rice, corn or cotton.

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The present invention extends to methods as described herein, wherein the insect is *Phaedon cochleariae* (mustard leaf beetle) and the plant is mustard, chinese cabbage, turnip greens, collard greens or bok choy.

The present invention extends to methods as described herein, wherein the insect is *Epilachna varivetis* (Mexican bean beetle) and the plant is bean, field bean, garden bean, snap bean, lima bean, mung bean, string bean, black-eyed bean, velvet bean, soybean, cowpea, pigeon pea, clover or alfalfa.

The present invention extends to methods as described herein, wherein the insect is *Anthonomus grandis* (cotton boll weevil) and the plant is cotton.

The present invention extends to methods as described herein, wherein the insect is *Tribolium castaneum* (red flour beetle) and the plant is in the form of stored grain products such as flour, cereals, meal, crackers, beans, spices, pasta, cake mix, dried pet food, dried flowers, chocolate, nuts, seeds, and even dried museum specimens.

The present invention extends to methods as described herein, wherein the insect is *Myzus persicae* (green peach aphid) and the plant is a tree such as *Prunus*, particularly peach, apricot and plum; a vegetable crop of the families *Solanaceae, Chenopodiaceae, Compositae, Cruciferae, and Cucurbitaceae*, including but not limited to, artichoke, asparagus, bean, beets, broccoli, Brussels sprouts, cabbage, carrot, cauliflower, cantaloupe, celery, corn, cucumber, fennel, kale, kohlrabi, turnip, eggplant, lettuce, mustard, okra, parsley, parsnip, pea, pepper, potato, radish, spinach, squash, tomato, turnip, watercress, and watermelon; a field crops such as, but not limited to, tobacco, sugar beet, and sunflower; a flower crop or other ornamental plant.

The present invention extends to methods as described herein, wherein the insect is *Nilaparvata lugens* and the plant is a rice plant.

The present invention extends to methods as described herein, wherein the insect is *Chilo suppressalis* (rice striped stem borer) and the plant is a rice plant, bareley, sorghum, maize, wheat or a grass.

The present invention extends to methods as described herein, wherein the insect is *Plutella xylostella* (Diamondback moth) and the plant is a *Brassica* species such as, but not limited to cabbage, chinese cabbage, Brussels sprouts, kale, rapeseed, broccoli, cauliflower, turnip, mustard or radish.

The present invention extends to methods as described herein, wherein the insect is *Acheta domesticus* (house cricket) and the plant is any plant as described herein or any organic matter.

In this context the term "plant" encompasses any plant material that it is desired to treat to prevent or reduce insect growth and/or insect infestation. This includes, *inter alia*, whole plants, seedlings, propagation or reproductive material such as seeds, cuttings, grafts, explants, etc. and also plant cell and tissue cultures. The plant material should express, or have the capability to express, the RNA molecule comprising at least one nucleotide sequence that is the RNA complement of or that represents the RNA equivalent of at least part of the nucleotide sequence of the sense strand of at least one target gene of the pest organism, such that the RNA molecule is

taken up by a pest upon plant-pest interaction, said RNA molecule being capable of inhibiting the target gene or down-regulating expression of the target gene by RNA interference.

The target gene may be any of the target genes herein described, for instance a target gene that is essential for the viability, growth, development or reproduction of the pest. The present invention relates to any gene of interest in the insect (which may be referred to herein as the "target gene") that can be down-regulated.

The terms "down-regulation of gene expression" and "inhibition of gene expression" are used interchangeably and refer to a measurable or observable reduction in gene expression or a complete abolition of detectable gene expression, at the level of protein product and/or mRNA product from the target gene. Preferably the down-regulation does not substantially directly inhibit the expression of other genes of the insect.The down-regulation effect of the dsRNA on gene expression may be calculated as being at least 30%, 40%, 50%, 60%, preferably 70%, 80% or even more preferably 90% or 95% when compared with normal gene expression.Depending on the nature of the target gene, down-regulation or inhibition of gene expression in cells of an insect can be confirmed by phenotypic analysis of the cell or the whole insect or by measurement of mRNA or protein expression using molecular techniques such as RNA solution hybridization, PCR, nuclease protection, Northern hybridization, reverse transcription, gene expression monitoring with a microarray, antibody binding, enzyme-linked immunosorbent assay (ELISA), Western blotting, radioimmunoassay (RIA), other immunoassays, or fluorescence-activated cell analysis (FACS).

The "target gene" may be essentially any gene that is desirable to be inhibited because it interferes with growth or pathogenicity or infectivity of the insect. For instance, if the method of the invention is to be used to prevent insect growth and/or infestation then it is preferred to select a target gene which is essential for viability, growth, development or reproduction of the insect, or any gene that is involved with pathogenicity or infectivity of the insect, such that specific inhibition of the target gene leads to a lethal phenotype or decreases or stops insect infestation.

According to one non-limiting embodiment, the target gene is such that when its expression is down-regulated or inhibited using the method of the invention, the insect is killed, or the reproduction or growth of the insect is stopped or retarded. This type of target genes is considered to be essential for the viability of the insect and is referred to as essential genes. Therefore, the present invention encompasses a method as described herein, wherein the target gene is an essential gene.

According to a further non-limiting embodiment, the target gene is such that when it is down-regulated using the method of the invention, the infestation or infection by the insect, the damage caused by the insect, and/or the ability of the insect to infest or infect host organisms and/or cause such damage, is reduced. The terms "infest" and "infect" or "infestation" and "infection" are generally used interchangeably throughout. This type of target genes is considered to be involved in the pathogenicity or infectivity of the insect. Therefore, the present invention extends to methods as described herein, wherein the target gene is involved in the pathogenicity or infectivity of the insect. The advantage of choosing the latter type of target gene is that the insect is blocked to infect further plants or plant parts and is inhibited to form further generations.

According to one embodiment, target genes are conserved genes or insect-specific genes.

In addition, any suitable double-stranded RNA fragment capable of directing RNAi or RNA-mediated gene silencing or inhibition of an insect target gene may be used in the methods of the invention.

5   In another embodiment, a gene is selected that is essentially involved in the growth, development, and reproduction of a pest, (such as an insect). Exemplary genes include but are not limited to the structural subunits of ribosomal proteins and a beta-coatamer gene, such as the CHD3 gene. Ribosomal proteins such as S4 (RpS4) and S9(RpS9) are structural constituents of the ribosome involved in protein biosynthesis and which are components of the cytosolic small

10   ribosomal subunit, the ribosomal proteins such as L9 and L19 are structural constituent of ribosome involved in protein biosynthesis which is localised to the ribosome. The beta coatamer gene in C. elegans encodes a protein which is a subunit of a multimeric complex that forms a membrane vesicle coat. Similar sequences have been found in diverse organisms such as Arabidopsis thaliana, Drosophila melanogaster, and Saccharomyces cerevisiae. Related

15   sequences are found in diverse organisms such as *Leptinotarsa decemlineata, Phaedon cochleariae, Epilachna varivestis, Anthonomus grandis, Tribolium castaneum, Myzus persicae, Nilaparvata lugens, Chilo suppressalis, Plutella xylostella* and *Acheta domesticus*.

Other target genes for use in the present invention may include, for example, those that play important roles in viability, growth, development, reproduction, and infectivity. These target

20   genes include, for example, house keeping genes, transcription factors, and pest specific genes or lethal knockout mutations in Caenorhabditis or Drosophila. The target genes for use in the present invention may also be those that are from other organisms, e.g., from insects or arachnidae (e.g. *Leptinotarsa* spp., *Phaedon* spp., *Epilachna* spp., *Anthonomus* spp., *Tribolium* spp., *Myzus* spp., *Nilaparvata* spp., *Chilo* spp., *Plutella* spp., or *Acheta* spp.).

25   Preferred target genes include those specified in **Table 1A** and orthologous genes from other target organisms, such as from other pest organisms.

In the methods of the present invention, dsRNA is used to inhibit growth or to interfere with the pathogenicity or infectivity of the insect.

The invention thus relates to isolated double-stranded RNA comprising annealed

30   complementary strands, one of which has a nucleotide sequence which is complementary to at least part of a target nucleotide sequence of a target gene of an insect. The target gene may be any of the target genes described herein, or a part thereof that exerts the same function.

According to one embodiment of the present invention, an isolated double-stranded RNA is provided comprising annealed complementary strands, one of which has a nucleotide sequence

35   which is complementary to at least part of a nucleotide sequence of an insect target gene, wherein said target gene comprises a sequence which is selected from the group comprising:

(i) sequences which are at least 75% identical to a sequence represented by any of SEQ ID NOs 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 49 to 158, 159, 160-163, 168, 173, 178, 183, 188, 193, 198, 203, 208, 215, 220, 225, 230, 247, 249, 251, 253, 255, 257, 259, 275 to 472, 473,

40   478, 483, 488, 493, 498, 503, 513, 515, 517, 519, 521, 533 to 575, 576, 581, 586, 591, 596,

601, 603, 605, 607, 609, 621 to 767, 768, 773, 778, 783, 788, 793, 795, 797, 799, 801, 813 to
862, 863, 868, 873, 878, 883, 888, 890, 892, 894, 896, 908 to 1040, 1041, 1046, 1051, 1056,
1061, 1071, 1073, 1075, 1077, 1079, 1081, 1083, 1085, 1087, 1089, 1091, 1093, 1095, 1097,
1099, 1101, 1103, 1105, 1107, 1109, 1111, 1113, 1161 to 1571, 1572, 1577, 1582, 1587,
1592, 1597, 1602, 1607, 1612, 1617, 1622, 1627, 1632, 1637, 1642, 1647, 1652, 1657, 1662,
1667, 1672, 1677, 1682, 1684, 1686, 1688, 1690, 1692, 1694, 1696, 1698, 1700, 1702, 1704,
1730 to 2039, 2040, 2045, 2050, 2055, 2060, 2065, 2070, 2075, 2080, 2085, 2090, 2095,
2100, 2102, 2104, 2106, 2108, 2120 to 2338, 2339, 2344, 2349, 2354, 2359, 2364, 2366,
2368, 2370, 2372, 2384 to 2460, 2461, 2466, 2471, 2476 or 2481, or the complement thereof,
and

(ii) sequences comprising at least 17 contiguous nucleotides of any of SEQ ID NOs 1, 3, 5, 7,
9, 11, 13, 15, 17, 19, 21, 23, 49 to 158, 159, 160-163, 168, 173, 178, 183, 188, 193, 198, 203,
208, 215, 220, 225, 230, 247, 249, 251, 253, 255, 257, 259, 275 to 472, 473, 478, 483, 488,
493, 498, 503, 513, 515, 517, 519, 521, 533 to 575, 576, 581, 586, 591, 596, 601, 603, 605,
607, 609, 621 to 767, 768, 773, 778, 783, 788, 793, 795, 797, 799, 801, 813 to 862, 863, 868,
873, 878, 883, 888, 890, 892, 894, 896, 908 to 1040, 1041, 1046, 1051, 1056, 1061, 1071,
1073, 1075, 1077, 1079, 1081, 1083, 1085, 1087, 1089, 1091, 1093, 1095, 1097, 1099, 1101,
1103, 1105, 1107, 1109, 1111, 1113, 1161 to 1571, 1572, 1577, 1582, 1587, 1592, 1597,
1602, 1607, 1612, 1617, 1622, 1627, 1632, 1637, 1642, 1647, 1652, 1657, 1662, 1667, 1672,
1677, 1682, 1684, 1686, 1688, 1690, 1692, 1694, 1696, 1698, 1700, 1702, 1704, 1730 to
2039, 2040, 2045, 2050, 2055, 2060, 2065, 2070, 2075, 2080, 2085, 2090, 2095, 2100, 2102,
2104, 2106, 2108, 2120 to 2338, 2339, 2344, 2349, 2354, 2359, 2364, 2366, 2368, 2370,
2372, 2384 to 2460, 2461, 2466, 2471, 2476 or 2481, or the complement thereof,

or wherein said insect target gene is an insect orthologue of a gene comprising at least 17
contiguous nucleotides of any of SEQ ID NOs 49 to 158, 275 to 472, 533 to 575, 621 to 767, 813 to
862, 908 to 1040, 1161 to 1571, 1730 to 2039, 2120 to 2338, 2384 to 2460, or the complement
thereof.

Depending on the assay used to measure gene silencing, the growth inhibition can be
quantified as being greater than about 5%, 10%, more preferably about 20%, 25%, 33%, 50%,
60%, 75%, 80%, most preferably about 90%, 95%, or about 99% as compared to a pest organism
that has been treated with control dsRNA.

According to another embodiment of the present invention, an isolated double-stranded
RNA is provided, wherein at least one of said annealed complementary strands comprises the RNA
equivalent of at least one of the nucleotide sequences represented by any of SEQ ID NOs 1, 3, 5,
7, 9, 11, 13, 15, 17, 19, 21, 23, 49 to 158, 159, 160-163, 168, 173, 178, 183, 188, 193, 198, 203,
208, 215, 220, 225, 230, 247, 249, 251, 253, 255, 257, 259, 275 to 472, 473, 478, 483, 488, 493,
498, 503, 513, 515, 517, 519, 521, 533 to 575, 576, 581, 586, 591, 596, 601, 603, 605, 607, 609,
621 to 767, 768, 773, 778, 783, 788, 793, 795, 797, 799, 801, 813 to 862, 863, 868, 873, 878, 883,
888, 890, 892, 894, 896, 908 to 1040, 1041, 1046, 1051, 1056, 1061, 1071, 1073, 1075, 1077,
1079, 1081, 1083, 1085, 1087, 1089, 1091, 1093, 1095, 1097, 1099, 1101, 1103, 1105, 1107,

1109, 1111, 1113, 1161 to 1571, 1572, 1577, 1582, 1587, 1592, 1597, 1602, 1607, 1612, 1617, 1622, 1627, 1632, 1637, 1642, 1647, 1652, 1657, 1662, 1667, 1672, 1677, 1682, 1684, 1686, 1688, 1690, 1692, 1694, 1696, 1698, 1700, 1702, 1704, 1730 to 2039, 2040, 2045, 2050, 2055, 2060, 2065, 2070, 2075, 2080, 2085, 2090, 2095, 2100, 2102, 2104, 2106, 2108, 2120 to 2338,

5   2339, 2344, 2349, 2354, 2359, 2364, 2366, 2368, 2370, 2372, 2384 to 2460, 2461, 2466, 2471, 2476 or 2481, or wherein at least one of said annealed complementary strands comprises the RNA equivalent of a fragment of at least 17 basepairs in length thereof, preferably at least 18, 19, 20 or 21, more preferably at least 22, 23 or 24 basepairs in length thereof.

        If the method of the invention is used for specifically controlling growth or infestation of a

10   specific insect in or on a host cell or host organism, it is preferred that the double-stranded RNA does not share any significant homology with any host gene, or at least not with any essential gene of the host. In this context, it is preferred that the double-stranded RNA shows less than 30%, more preferably less that 20%, more preferably less than 10%, and even more preferably less than 5% nucleic acid sequence identity with any gene of the host cell. % sequence identity should be

15   calculated across the full length of the double-stranded RNA region. If genomic sequence data is available for the host organism one may cross-check sequence identity with the double-stranded RNA using standard bioinformatics tools. In one embodiment, there is no sequence identity between the dsRNA and a host sequences over 21 contiguous nucleotides, meaning that in this context, it is preferred that 21 contiguous base pairs of the dsRNA do not occur in the genome of

20   the host organism. In another embodiment, there is less than about 10% or less than about 12.5 % sequence identity over 24 contiguous nucleotides of the dsRNA with any nucleotide sequence from a host species.

        The double-stranded RNA comprises annealed complementary strands, one of which has a nucleotide sequence which corresponds to a target nucleotide sequence of the target gene to be

25   down-regulated. The other strand of the double-stranded RNA is able to base-pair with the first strand.

        The expression "target region" or "target nucleotide sequence" of the target insect gene may be any suitable region or nucleotide sequence of the gene. The target region should comprise at least 17, at least 18 or at least 19 consecutive nucleotides of the target gene, more preferably at

30   least 20 or at least 21 nucleotide and still more preferably at least 22, 23 or 24 nucleotides of the target gene.

        It is preferred that (at least part of) the double-stranded RNA will share 100% sequence identity with the target region of the insect target gene. However, it will be appreciated that 100% sequence identity over the whole length of the double stranded region is not essential for functional

35   RNA inhibition. RNA sequences with insertions, deletions, and single point mutations relative to the target sequence have also been found to be effective for RNA inhibition. The terms "corresponding to" or "complementary to" are used herein interchangeable, and when these terms are used to refer to sequence correspondence between the double-stranded RNA and the target region of the target gene, they are to be interpreted accordingly, i.e. as not absolutely requiring 100% sequence

40   identity. However, the % sequence identity between the double-stranded RNA and the target

region will generally be at least 80% or 85% identical, preferably at least 90%, 95%, 96%, or more preferably at least 97%, 98% and still more preferably at least 99%. Two nucleic acid strands are "substantially complementary" when at least 85% of their bases pair.

5   The term "complementary" as used herein relates to both DNA-DNA complementarity as to DNA-RNA complementarity. In analogy herewith, the term "RNA equivalent" substantially means that in the DNA sequence(s), the base "T" may be replaced by the corresponding base "U" normally present in ribonucleic acids.

The dsRNA contains a sequence which corresponds to the target region of the target gene it is not absolutely essential for the whole of the dsRNA to correspond to the sequence

10   of the target region. For example, the dsRNA may contain short non-target regions flanking the target-specific sequence, provided that such sequences do not affect performance of the dsRNA in RNA inhibition to a material extent.

The dsRNA may contain one or more substitute bases in order to optimise performance in RNAi. It will be apparent to the skilled reader how to vary each of the bases of the dsRNA in turn

15   and test the activity of the resulting dsRNAs (e.g. in a suitable *in vitro* test system) in order to optimise the performance of a given dsRNA.

The dsRNA may further contain DNA bases, non-natural bases or non-natural backbone linkages or modifications of the sugar-phosphate backbone, for example to enhance stability during storage or enhance resistance to degradation by nucleases.

20   It has been previously reported that the formation of short interfering RNAs (siRNAs) of about 21 bp is desirable for effective gene silencing. However, in applications of applicant it has been shown that the minimum length of dsRNA preferably is at least about 80-100 bp in order to be efficiently taken up by certain pest organisms. There are indications that in invertebrates such as the free living nematode *C. elegans* or the plant parasitic nematode *Meloidogyne incognita*, these

25   longer fragments are more effective in gene silencing, possibly due to a more efficient uptake of these long dsRNA by the invertebrate.

It has also recently been suggested that synthetic RNA duplexes consisting of either 27-mer blunt or short hairpin (sh) RNAs with 29 bp stems and 2-nt 3' overhangs are more potent inducers of RNA interference than conventional 21-mer siRNAs. Thus, molecules based upon the

30   targets identified above and being either 27-mer blunt or short hairpin (sh) RNA's with 29-bp stems and 2-nt 3'overhangs are also included within the scope of the invention.

Therefore, in one embodiment, the double-stranded RNA fragment (or region) will itself preferably be at least 17 bp in length, preferably 18 or 19bp in length, more preferably at least 20bp, more preferably at least 21 bp, or at least 22 bp, or at least 23 bp, or at least 24 bp, 25 bp,

35   26 bp or at least 27 bp in length. The expressions "double-stranded RNA fragment" or "double-stranded RNA region" refer to a small entity of the double-stranded RNA corresponding with (part of) the target gene.

Generally, the double stranded RNA is preferably between about 17-1500 bp, even more preferably between about 80 - 1000 bp and most preferably between about 17-27 bp or between

40   about 80-250 bp; such as double stranded RNA regions of about 17 bp, 18 bp, 19 bp, 20 bp, 21 bp,

22 bp, 23 bp, 24 bp, 25 bp, 27 bp, 50 bp, 80 bp, 100 bp, 150 bp, 200 bp, 250 bp, 300 bp, 350 bp, 400 bp, 450 bp, 500 bp, 550 bp, 600 bp, 650 bp, 700 bp, 900 bp, 100 bp, 1100 bp, 1200 bp, 1300 bp, 1400 bp or 1500 bp.

The upper limit on the length of the double-stranded RNA may be dependent on i) the requirement for the dsRNA to be taken up by the insect and ii) the requirement for the dsRNA to be processed within the cell into fragments that direct RNAi. The chosen length may also be influenced by the method of synthesis of the RNA and the mode of delivery of the RNA to the cell. Preferably the double-stranded RNA to be used in the methods of the invention will be less than 10,000 bp in length, more preferably 1000 bp or less, more preferably 500 bp or less, more preferably 300 bp or less, more preferably 100 bp or less. For any given target gene and insect, the optimum length of the dsRNA for effective inhibition may be determined by experiment.

The double-stranded RNA may be fully or partially double-stranded. Partially double-stranded RNAs may include short single-stranded overhangs at one or both ends of the double-stranded portion, provided that the RNA is still capable of being taken up by insects and directing RNAi. The double-stranded RNA may also contain internal non-complementary regions.

The methods of the invention encompass the simultaneous or sequential provision of two or more different double-stranded RNAs or RNA constructs to the same insect, so as to achieve down-regulation or inhibition of multiple target genes or to achieve a more potent inhibition of a single target gene.

Alternatively, multiple targets are hit by the provision of one double-stranded RNA that hits multiple target sequences, and a single target is more efficiently inhibited by the presence of more than one copy of the double stranded RNA fragment corresponding to the target gene. Thus, in one embodiment of the invention, the double-stranded RNA construct comprises multiple dsRNA regions, at least one strand of each dsRNA region comprising a nucleotide sequence that is complementary to at least part of a target nucleotide sequence of an insect target gene. According to the invention, the dsRNA regions in the RNA construct may be complementary to the same or to different target genes and/or the dsRNA regions may be complementary to targets from the same or from different insect species.

The terms "hit", "hits" and "hitting" are alternative wordings to indicate that at least one of the strands of the dsRNA is complementary to, and as such may bind to, the target gene or nucleotide sequence.

In one embodiment, the double stranded RNA region comprises multiple copies of the nucleotide sequence that is complementary to the target gene. Alternatively, the dsRNA hits more than one target sequence of the same target gene. The invention thus encompasses isolated double stranded RNA constructs comprising at least two copies of said nucleotide sequence complementary to at least part of a nucleotide sequence of an insect target.

The term "multiple" in the context of the present invention means at least two, at least three, at least four, at least five, at least six, etc.

The expressions "a further target gene" or "at least one other target gene" mean for instance a second, a third or a fourth, etc. target gene.

DsRNA that hits more than one of the above-mentioned targets, or a combination of different dsRNA against different of the above mentioned targets are developed and used in the methods of the present invention.

Accordingly the invention relates to an isolated double stranded RNA construct comprising at least two copies of the RNA equivalent of at least one of the nucleotide sequences represented by any of SEQ ID NOs 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 49 to 158, 159, 160-163, 168, 173, 178, 183, 188, 193, 198, 203, 208, 215, 220, 225, 230, 247, 249, 251, 253, 255, 257, 259, 275 to 472, 473, 478, 483, 488, 493, 498, 503, 513, 515, 517, 519, 521, 533 to 575, 576, 581, 586, 591, 596, 601, 603, 605, 607, 609, 621 to 767, 768, 773, 778, 783, 788, 793, 795, 797, 799, 801, 813 to 862, 863, 868, 873, 878, 883, 888, 890, 892, 894, 896, 908 to 1040, 1041, 1046, 1051, 1056, 1061, 1071, 1073, 1075, 1077, 1079, 1081, 1083, 1085, 1087, 1089, 1091, 1093, 1095, 1097, 1099, 1101, 1103, 1105, 1107, 1109, 1111, 1113, 1161 to 1571, 1572, 1577, 1582, 1587, 1592, 1597, 1602, 1607, 1612, 1617, 1622, 1627, 1632, 1637, 1642, 1647, 1652, 1657, 1662, 1667, 1672, 1677, 1682, 1684, 1686, 1688, 1690, 1692, 1694, 1696, 1698, 1700, 1702, 1704, 1730 to 2039, 2040, 2045, 2050, 2055, 2060, 2065, 2070, 2075, 2080, 2085, 2090, 2095, 2100, 2102, 2104, 2106, 2108, 2120 to 2338, 2339, 2344, 2349, 2354, 2359, 2364, 2366, 2368, 2370, 2372, 2384 to 2460, 2461, 2466, 2471, 2476 or 2481, or at least two copies of the RNA equivalent of a fragment of at least 17 basepairs in length thereof, preferably at least 18, 19, 20 or 21, more preferably at least 22, 23 or 24 basepairs in length thereof. Preferably, said double-stranded RNA comprises the RNA equivalent of the nucleotide sequence as represented in SEQ ID NO 159 or 160, or a fragment of at least 17, preferably at least 18, 19, 20 or 21, more preferably at least 22, 23 or 24 basepairs in length thereof. In a further embodiment, the invention relates to an an isolated double stranded RNA construct comprising at least two copies of the RNA equivalent of the nucleotide sequence as represented by SEQ ID NO 159 or 160.

Accordingly, the present invention extends to methods as described herein, wherein the dsRNA comprises annealed complementary strands, one of which has a nucleotide sequence which is complementary to at least part of a target nucleotide sequence of an insect target gene, and which comprises the RNA equivalents of at least wo nucleotide sequences independently chosen from each other. In one embodiment, the dsRNA comprises the RNA equivalents of at least two, preferably at least three, four or five, nucleotide sequences indepently chosen from the sequences represented by any of SEQ ID NOs 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 49 to 158, 159, 160-163, 168, 173, 178, 183, 188, 193, 198, 203, 208, 215, 220, 225, 230, 247, 249, 251, 253, 255, 257, 259, 275 to 472, 473, 478, 483, 488, 493, 498, 503, 513, 515, 517, 519, 521, 533 to 575, 576, 581, 586, 591, 596, 601, 603, 605, 607, 609, 621 to 767, 768, 773, 778, 783, 788, 793, 795, 797, 799, 801, 813 to 862, 863, 868, 873, 878, 883, 888, 890, 892, 894, 896, 908 to 1040, 1041, 1046, 1051, 1056, 1061, 1071, 1073, 1075, 1077, 1079, 1081, 1083, 1085, 1087, 1089, 1091, 1093, 1095, 1097, 1099, 1101, 1103, 1105, 1107, 1109, 1111, 1113, 1161 to 1571, 1572, 1577, 1582, 1587, 1592, 1597, 1602, 1607, 1612, 1617, 1622, 1627, 1632, 1637, 1642, 1647, 1652, 1657, 1662, 1667, 1672, 1677, 1682, 1684, 1686, 1688, 1690, 1692, 1694, 1696, 1698, 1700, 1702, 1704, 1730 to 2039, 2040, 2045, 2050, 2055, 2060, 2065, 2070, 2075, 2080, 2085,

2090, 2095, 2100, 2102, 2104, 2106, 2108, 2120 to 2338, 2339, 2344, 2349, 2354, 2359, 2364, 2366, 2368, 2370, 2372, 2384 to 2460, 2461, 2466, 2471, 2476 or 2481, or fragments thereof of at least 17 basepairs in length, preferably at least 18, 19, 20 or 21, more preferably at least 22, 23 or 24 basepairs in length thereof.

The at least two nucleotide sequences may be derived from the target genes herein described. According to one preferred embodiment the dsRNA hits at least one target gene that is essential for viability, growth, development or reproduction of the insect and hits at least one gene involved in pathogenicity or infectivity as described hereinabove. Alternatively, the dsRNA hits multiple genes of the same category, for example, the dsRNA hits at least 2 essential genes or at least 2 genes involved in the same cellular function. According to a further embodiment, the dsRNA hits at least 2 target genes, which target genes are involved in a different cellular function. For example the dsRNA hits two or more genes involved in protein synthesis (e.g. ribosome subunits), intracellular protein transport, nuclear mRNA splicing, or involved in one of the functions described in Table 1A.

Preferably, the present invention extends to methods as described herein, wherein said insect target gene comprises a sequence which is which is selected from the group comprising:

(i) sequences which are at least 75% identical to a sequence represented by any of SEQ ID NOs 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 49 to 158, 159, 160-163, 168, 173, 178, 183, 188, 193, 198, 203, 208, 215, 220, 225, 230, 247, 249, 251, 253, 255, 257, 259, 275 to 472, 473, 478, 483, 488, 493, 498, 503, 513, 515, 517, 519, 521, 533 to 575, 576, 581, 586, 591, 596, 601, 603, 605, 607, 609, 621 to 767, 768, 773, 778, 783, 788, 793, 795, 797, 799, 801, 813 to 862, 863, 868, 873, 878, 883, 888, 890, 892, 894, 896, 908 to 1040, 1041, 1046, 1051, 1056, 1061, 1071, 1073, 1075, 1077, 1079, 1081, 1083, 1085, 1087, 1089, 1091, 1093, 1095, 1097, 1099, 1101, 1103, 1105, 1107, 1109, 1111, 1113, 1161 to 1571, 1572, 1577, 1582, 1587, 1592, 1597, 1602, 1607, 1612, 1617, 1622, 1627, 1632, 1637, 1642, 1647, 1652, 1657, 1662, 1667, 1672, 1677, 1682, 1684, 1686, 1688, 1690, 1692, 1694, 1696, 1698, 1700, 1702, 1704, 1730 to 2039, 2040, 2045, 2050, 2055, 2060, 2065, 2070, 2075, 2080, 2085, 2090, 2095, 2100, 2102, 2104, 2106, 2108, 2120 to 2338, 2339, 2344, 2349, 2354, 2359, 2364, 2366, 2368, 2370, 2372, 2384 to 2460, 2461, 2466, 2471, 2476 or 2481, or the complement thereof, and

(ii) sequences comprising at least 17 contiguous nucleotides of any of SEQ ID NOs 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 49 to 158, 159, 160-163, 168, 173, 178, 183, 188, 193, 198, 203, 208, 215, 220, 225, 230, 247, 249, 251, 253, 255, 257, 259, 275 to 472, 473, 478, 483, 488, 493, 498, 503, 513, 515, 517, 519, 521, 533 to 575, 576, 581, 586, 591, 596, 601, 603, 605, 607, 609, 621 to 767, 768, 773, 778, 783, 788, 793, 795, 797, 799, 801, 813 to 862, 863, 868, 873, 878, 883, 888, 890, 892, 894, 896, 908 to 1040, 1041, 1046, 1051, 1056, 1061, 1071, 1073, 1075, 1077, 1079, 1081, 1083, 1085, 1087, 1089, 1091, 1093, 1095, 1097, 1099, 1101, 1103, 1105, 1107, 1109, 1111, 1113, 1161 to 1571, 1572, 1577, 1582, 1587, 1592, 1597, 1602, 1607, 1612, 1617, 1622, 1627, 1632, 1637, 1642, 1647, 1652, 1657, 1662, 1667, 1672, 1677, 1682, 1684, 1686, 1688, 1690, 1692, 1694, 1696, 1698, 1700, 1702, 1704, 1730 to

2039, 2040, 2045, 2050, 2055, 2060, 2065, 2070, 2075, 2080, 2085, 2090, 2095, 2100, 2102, 2104, 2106, 2108, 2120 to 2338, 2339, 2344, 2349, 2354, 2359, 2364, 2366, 2368, 2370, 2372, 2384 to 2460, 2461, 2466, 2471, 2476 or 2481, or the complement thereof,

or wherein said insect target gene is an insect orthologue of a gene comprising at least 17 contiguous nucleotides of any of SEQ ID NOs 49 to 158, 275 to 472, 533 to 575, 621 to 767, 813 to 862, 908 to 1040, 1161 to 1571, 1730 to 2039, 2120 to 2338, 2384 to 2460, or the complement thereof.

The dsRNA regions (or fragments) in the double stranded RNA may be combined as follows:

a) when multiple dsRNA regions targeting a single target gene are combined, they may be combined in the original order (ie the order in which the regions appear in the target gene) in the RNA construct,

b) alternatively, the original order of the fragments may be ignored so that they are scrambled and combined randomly or deliberately in any order into the double stranded RNA construct,

c) alternatively, one single fragment may be repeated several times, for example from 1 to 10 times, e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10 times, in the ds RNA construct, or

d) the dsRNA regions (targeting a single or different target genes) may be combined in the sense or antisense orientation.

In addition, the target gene(s) to be combined may be chosen from one or more of the following categories of genes:

e) "essential" genes or "pathogenicity genes" as described above encompass genes that are vital for one or more target insects and result in a lethal or severe (e.g. feeding, reproduction, growth) phenotype when silenced. The choice of a strong lethal target gene results in a potent RNAi effect. In the RNA constructs of the invention, multiple dsRNA regions targeting the same or different (very effective) lethal genes can be combined to further increase the potency, efficacy or speed of the RNAi effect in insect control.

f) "weak" genes encompass target genes with a particularly interesting function in one of the cellular pathways described herein, but which result in a weak phenotypic effect when silenced. In the RNA constructs of the invention, multiple dsRNA regions targeting a single or different weak gene(s) may be combined to obtain a stronger RNAi effect.

g) "insect specific" genes encompass genes that have no substantial homologous counterpart in non-insect organisms as can be determined by bioinformatics homology searches, for example by BLAST searches. The choice of an insect specific target gene results in a species specific RNAi effect, with no effect or no substantial (adverse) effect in non-target organisms.

h) "conserved genes" encompass genes that are conserved (at the amino acid level) between the target organism and non-target organism(s). To reduce possible effects on non-target species, such effective but conserved genes are analysed and target sequences from the

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variable regions of these conserved genes are chosen to be targeted by the dsRNA regions in the RNA construct. Here, conservation is assessed at the level of the nucleic acid sequence. Such variable regions thus encompass the least conserved sections, at the level of the nucleic acid sequence, of the conserved target gene(s).

5   i) "conserved pathway" genes encompass genes that are involved in the same biological pathway or cellular process, or encompass genes that have the same functionality in different insect species resulting in a specific and potent RNAi effect and more efficient insect control;

j) alternatively, the RNA constructs according to the present invention target multiple genes
10   from different biological pathways, resulting in a broad cellular RNAi effect and more efficient insect control.

According to the invention, all double stranded RNA regions comprise at least one strand that is complementary to at least part or a portion of the nucleotide sequence of any of the target genes herein described. However, provided one of the double stranded RNA regions comprises at
15   least one strand that is complementary to a portion of the nucleotide sequence of any one of the target genes herein described, the other double stranded RNA regions may comprise at least one strand that is complementary to a portion of any other insect target gene (including known target genes).

According to yet another embodiment of the present invention there is provided an isolated
20   double stranded RNA or RNA construct as herein described, further comprising at least one additional sequence and optionally a linker. In one embodiment, the additional sequence is chosen from the group comprising (i) a sequence facilitating large-scale production of the dsRNA construct; (ii) a sequence effecting an increase or decrease in the stability of the dsRNA; (iii) a sequence allowing the binding of proteins or other molecules to facilitate uptake of the RNA construct by
25   insects; (iv) a sequence which is an aptamer that binds to a receptor or to a molecule on the surface or in the cytoplasm of an insect to facilitate uptake, endocytosis and/or transcytosis by the insect; or (v) additional sequences to catalyze processing of dsRNA regions. In one embodiment, the linker is a conditionally self-cleaving RNA sequence, preferably a pH sensitive linker or a hydrophobic sensitive linker. In one embodiment, the linker is an intron.

30   In one embodiment, the multiple dsRNA regions of the double-stranded RNA construct are connected by one or more linkers. In another embodiment, the linker is present at a site in the RNA construct, separating the dsRNA regions from another region of interest. Different linker types for the dsRNA constructs are provided by the present invention.

In another embodiment, the multiple dsRNA regions of the double-stranded RNA construct
35   are connected without linkers.

In a particular embodiment of the invention, the linkers may be used to disconnect smaller dsRNA regions in the pest organism. Advantageously, in this situation the linker sequence may promote division of a long dsRNA into smaller dsRNA regions under particular circumstances, resulting in the release of separate dsRNA regions under these circumstances and leading to more
40   efficient gene silencing by these smaller dsRNA regions. Examples of suitable conditionally self-

cleaving linkers are RNA sequences that are self-cleaving at high pH conditions. Suitable examples of such RNA sequences are described by Borda et al. (Nucleic Acids Res. 2003 May 15;31(10):2595-600), which document is incorporated herein by reference. This sequence originates from the catalytic core of the hammerhead ribozyme HH16.

In another aspect of the invention, a linker is located at a site in the RNA construct, separating the dsRNA regions from another, e.g. the additional, sequence of interest, which preferably provides some additional function to the RNA construct.

In one particular embodiment of the invention, the dsRNA constructs of the present invention are provided with an aptamer to facilitate uptake of the dsRNA by the insect. The aptamer is designed to bind a substance which is taken up by the insect. Such substances may be from an insect or plant origin. One specific example of an aptamer, is an aptamer that binds to a transmembrane protein, for example a transmembrane protein of an insect. Alternatively, the aptamer may bind a (plant) metabolite or nutrient which is taken up by the insect.

Alternatively, the linkers are self-cleaving in the endosomes. This may be advantageous when the constructs of the present invention are taken up by the insect via endocytosis or transcytosis, and are therefore compartmentalized in the endosomes of the insect species. The endosomes may have a low pH environment, leading to cleavage of the linker.

The above mentioned linkers that are self-cleaving in hydrophobic conditions are particularly useful in dsRNA constructs of the present invention when used to be transferred from one cell to another via the transit in a cell wall, for example when crossing the cell wall of an insect pest organism.

An intron may also be used as a linker. An "intron" as used herein may be any non-coding RNA sequence of a messenger RNA. Particular suitable intron sequences for the constructs of the present invention are (1) U-rich (35-45%); (2) have an average length of 100 bp (varying between about 50 and about 500 bp) which base pairs may be randomly chosen or may be based on known intron sequences; (3) start at the 5' end with -AG:GT- or -CG:GT- and/or (4) have at their 3' end -AG:GC- or -AG:AA.

A non-complementary RNA sequence, ranging from about 1 base pair to about 10,000 base pairs, may also be used as a linker.

Without wishing to be bound by any particular theory or mechanism, it is thought that long double-stranded RNAs are taken up by the insect from their immediate environment. Double-stranded RNAs taken up into the gut and transferred to the gut epithelial cells are then processed within the cell into short double-stranded RNAs, called small interfering RNAs (siRNAs), by the action of an endogenous endonuclease. The resulting siRNAs then mediate RNAi via formation of a multi-component RNase complex termed the RISC or RNA interfering silencing complex.

In order to achieve down-regulation of a target gene within an insect cell the double-stranded RNA added to the exterior of the cell wall may be any dsRNA or dsRNA construct that can be taken up into the cell and then processed within the cell into siRNAs, which then mediate RNAi, or the RNA added to the exterior of the cell could itself be an siRNA that can be taken up into the cell and thereby direct RNAi.

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siRNAs are generally short double-stranded RNAs having a length in the range of from 19 to 25 base pairs, or from 20 to 24 base pairs. In preferred embodiments siRNAs having 19, 20, 21, 22, 23, 24 or 25 base pairs, and in particular 21 or 22 base pairs, corresponding to the target gene to be down-regulated may be used. However, the invention is not intended to be limited to the use
5   of such siRNAs.

siRNAs may include single-stranded overhangs at one or both ends, flanking the double-stranded portion. In a particularly preferred embodiment the siRNA may contain 3' overhanging nucleotides, preferably two 3' overhanging thymidines (dTdT) or uridines (UU). 3' TT or UU overhangs may be included in the siRNA if the sequence of the target gene immediately upstream
10   of the sequence included in double-stranded part of the dsRNA is AA. This allows the TT or UU overhang in the siRNA to hybridise to the target gene. Although a 3' TT or UU overhang may also be included at the other end of the siRNA it is not essential for the target sequence downstream of the sequence included in double-stranded part of the siRNA to have AA. In this context, siRNAs which are RNA/DNA chimeras are also contemplated. These chimeras include, for example, the
15   siRNAs comprising a double-stranded RNA with 3' overhangs of DNA bases (e.g. dTdT), as discussed above, and also double-stranded RNAs which are polynucleotides in which one or more of the RNA bases or ribonucleotides, or even all of the ribonucleotides on an entire strand, are replaced with DNA bases or deoxynucleotides.

The dsRNA may be formed from two separate (sense and antisense) RNA strands that are
20   annealed together by (non-covalent) basepairing. Alternatively, the dsRNA may have a foldback stem-loop or hairpin structure, wherein the two annealed strands of the dsRNA are covalently linked. In this embodiment the sense and antisense stands of the dsRNA are formed from different regions of single polynucleotide molecule that is partially self-complementary. RNAs having this structure are convenient if the dsRNA is to be synthesised by expression *in vivo*, for example in a
25   host cell or organism as discussed below, or by *in vitro* transcription. The precise nature and sequence of the "loop" linking the two RNA strands is generally not material to the invention, except that it should not impair the ability of the double-stranded part of the molecule to mediate RNAi. The features of "hairpin" or "stem-loop" RNAs for use in RNAi are generally known in the art (see for example WO 99/53050, in the name of CSIRO, the contents of which are incorporated herein by
30   reference). In other embodiments of the invention, the loop structure may comprise linker sequences or additional sequences as described above.

The double-stranded RNA or construct may be prepared in a manner known *per se*. For example, double-stranded RNAs may be synthesised *in vitro* using chemical or enzymatic RNA synthesis techniques well known in the art. In one approach the two separate RNA strands may be
35   synthesised separately and then annealed to form double-strands.In a further embodiment, double-stranded RNAs or constructs may be synthesised by intracellular expression in a host cell or organism from a suitable expression vector. This approach is discussed in further detail below.

The amount of double-stranded RNA with which the insect is contacted is such that specific down-regulation of the one or more target genes is achieved. The RNA may be introduced
40   in an amount which allows delivery of at least one copy per cell. However, in certain embodiments

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higher doses (e.g., at least 5, 10, 100, 500 or 1000 copies per cell) of double-stranded RNA may yield more effective inhibition. For any given insect gene target the optimum amount of dsRNA for effective inhibition may be determined by routine experimentation.

The insect can be contacted with the double-stranded RNA in any suitable manner, permitting direct uptake of the double-stranded RNA by the insect. For example, the insect can be contacted with the double-stranded RNA in pure or substantially pure form, for example an aqueous solution containing the dsRNA. In this embodiment, the insect may be simply "soaked" with an aqueous solution comprising the double-stranded RNA. In a further embodiment the insect can be contacted with the double-stranded RNA by spraying the insect with a liquid composition comprising the double-stranded RNA.

Alternatively, the double-stranded RNA may be linked to a food component of the insects, such as a food component for a mammalian pathogenic insect, in order to increase uptake of the dsRNA by the insect.

The double-stranded RNA may also be incorporated in the medium in which the insect grows or in or on a material or substrate that is infested by the insect or impregnated in a substrate or material susceptible to infestation by insect.

According to another embodiment, the dsRNA is expressed in a bacterial or fungal cell and the bacterial or fungal cell is taken up or eaten by the insect species.

As illustrated in the examples, bacteria can be engineered to produce any of the dsRNA or dsRNA constructs of the invention. These bacteria can be eaten by the insect species. When taken up, the dsRNA can initiate an RNAi response, leading to the degradation of the target mRNA and weakening or killing of the feeding insect.

Therefore, in a more specific embodiment, said double-stranded RNA or RNA construct is expressed by a prokaryotic, such as a bacterial, or eukaryotic, such as a yeast, host cell or host organism. According to this embodiment, any bacterium or yeast cell that is capable of expressing dsRNA or dsRNA constructs can be used. The bacterium is chosen from the group comprising Gram-negative and Gram-positive bacteria, such as, but not limited to, Escherichia spp. (e.g. E. coli), Bacillus spp. (e.g. B. thuringiensis), Rhizobium spp., Lactobacilllus spp., Lactococcus spp., etc.. The yeast may be chosen from the group comprising Saccharomyces spp., etc.

Some bacteria have a very close interaction with the host plant, such as, but not limited to, symbiotic Rhizobium with the Legminosea (for example Soy). Such recombinant bacteria could be mixed with the seeds (for instance as a coating) and used as soil improvers.

Accordingly, the present invention also encompasses a cell comprising any of the nucleotide sequences or recombinant DNA constructs described herein. The invention further encompasses prokaryotic cells (such as, but not limited to, gram-positive and gram-negative bacterial cells) and eukaryotic cells (such as, but not limited to, yeast cells or plant cells). Preferably said cell is a bacterial cell or a yeast cell or an algal cell.

In other embodiments the insect may be contacted with a composition as described further herein. The composition may, in addition to the dsRNA or DNA contain further excipients, diluents or carriers. Preferred features of such compositions are discussed in more detail below.

26

Alternatively, dsRNA producing bacteria or yeast cells can be sprayed directly onto the crops.

Thus, as described above, the invention provides a host cell comprising an RNA construct and/or a DNA construct and/or an expression construct of the invention. Preferably, the host cell is a bacterial or yeast cell, but may be a virus for example. A virus such as a baculovirus may be utilised which specifically infects insects. This ensures safety for mammals, especially humans, since the virus will not infect the mammal, so no unwanted RNAi effect will occur.

The bacterial cell or yeast cell preferably should be inactivated before being utilised as a biological pesticide, for instance when the agent is to be used in an environment where contact with humans or other mammals is likely (such as a kitchen). Inactivation may be achieved by any means, such as by heat treatment, phenol or formaldehyde treatment for example, or by mechanical treatment.

In a still alternative embodiment, an inactivated virus, such as a suitably modified baculovirus may be utilised in order to deliver the dsRNA regions of the invention for mediating RNAi to the insect pest.

Possible applications include intensive greenhouse cultures, for instance crops that are less interesting from a GMO point of view, as well as broader field crops such as soy.

This approach has several advantages, eg: since the problem of possible dicing by a plant host is not present, it allows the delivery of large dsRNA fragments into the gut lumen of the feeding pest; the use of bacteria as insecticides does not involve the generation of transgenic crops, especially for certain crops where transgenic variants are difficult to obtain; there is a broad and flexible application in that different crops can be simultaneously treated on the same field and/or different pests can be simultaneously targeted, for instance by combining different bacteria producing distinct dsRNAs.

Another aspect of the present invention are target nucleotide sequences of the insect target genes herein disclosed. Such target nucleotide sequences are particularly important to design the dsRNA constructs according to the present invention. Such target nucleotide sequences are preferably at least 17, preferably at least 18, 19, 20 or 21, more preferably at least 22, 23 or 24 nucleotides in length. Non-limiting examples of preferred target nucleotide sequences are given in the examples.

According to one embodiment, the present invention provides an isolated nucleotide sequence encoding a double stranded RNA or double stranded RNA construct as described herein.

According to a more specific embodiment, the present invention relates to an isolated nucleic acid sequence consisting of a sequence represented by any of SEQ ID NOs 49 to 158, 275 to 472, 533 to 575, 621 to 767, 813 to 862, 908 to 1040, 1161 to 1571, 1730 to 2039, 2120 to 2338, 2384 to 2460, or a fragment of at least 17 preferably at least 18, 19, 20 or 21, more preferably at least 22, 23 or 24 nucleotides thereof.

A person skilled in the art will recognize that homologues of these target genes can be found and that these homologues are also useful in the methods of the present invention.

Protein, or nucleotide sequences are likely to be homologous if they show a "significant" level of sequence similarity or more preferably sequence identity. Truely homologous sequences are related by divergence from a common ancestor gene. Sequence homologues can be of two types:(i) where homologues exist in different species they are known as orthologues. e.g. the α-

5   globin genes in mouse and human are orthologues.(ii) paralogues are homologous genes in within a single species. e.g. the α- and β- globin genes in mouse are paralogues

Preferred homologues are genes comprising a sequence which is at least about 85% or 87.5%, still more preferably about 90%, still more preferably at least about 95% and most preferably at least about 99% identical to a sequence selected from the group of sequences

10   represented by SEQ ID NOs 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 49 to 158, 159, 160-163, 168, 173, 178, 183, 188, 193, 198, 203, 208, 215, 220, 225, 230, 247, 249, 251, 253, 255, 257, 259, 275 to 472, 473, 478, 483, 488, 493, 498, 503, 513, 515, 517, 519, 521, 533 to 575, 576, 581, 586, 591, 596, 601, 603, 605, 607, 609, 621 to 767, 768, 773, 778, 783, 788, 793, 795, 797, 799, 801, 813 to 862, 863, 868, 873, 878, 883, 888, 890, 892, 894, 896, 908 to 1040, 1041, 1046, 1051, 1056, 1061,

15   1071, 1073, 1075, 1077, 1079, 1081, 1083, 1085, 1087, 1089, 1091, 1093, 1095, 1097, 1099, 1101, 1103, 1105, 1107, 1109, 1111, 1113, 1161 to 1571, 1572, 1577, 1582, 1587, 1592, 1597, 1602, 1607, 1612, 1617, 1622, 1627, 1632, 1637, 1642, 1647, 1652, 1657, 1662, 1667, 1672, 1677, 1682, 1684, 1686, 1688, 1690, 1692, 1694, 1696, 1698, 1700, 1702, 1704, 1730 to 2039, 2040, 2045, 2050, 2055, 2060, 2065, 2070, 2075, 2080, 2085, 2090, 2095, 2100, 2102, 2104,

20   2106, 2108, 2120 to 2338, 2339, 2344, 2349, 2354, 2359, 2364, 2366, 2368, 2370, 2372, 2384 to 2460, 2461, 2466, 2471, 2476 or 2481, or the complement thereof. Methods for determining sequence identity are routine in the art and include use of the Blast software and *EMBOSS software (The European Molecular Biology Open Software Suite* (2000), Rice,P. Longden, I. and Bleasby, A. Trends in Genetics 16, (6) pp276—277). The term "identity" as used herein refers to

25   the relationship between sequences at the nucleotide level. The expression "% identical" is determined by comparing optimally aligned sequences, e.g. two or more, over a comparison window wherein the portion of the sequence in the comparison window may comprise insertions or deletions as compared to the reference sequence for optimal alignment of the sequences. The reference sequence does not comprise insertions or deletions. The reference window is chosen

30   from between at least 10 contiguous nucleotides to about 50, about 100 or to about 150 nucleotides, preferably between about 50 and 150 nucleotides. "% identity" is then calculated by determining the number of nucleotides that are identical between the sequences in the window, dividing the number of identical nucleotides by the number of nucleotides in the window and multiplying by 100.

35   Other homologues are genes which are alleles of a gene comprising a sequence as represented by any of SEQ ID NOs 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 49 to 158, 159, 160-163, 168, 173, 178, 183, 188, 193, 198, 203, 208, 215, 220, 225, 230, 247, 249, 251, 253, 255, 257, 259, 275 to 472, 473, 478, 483, 488, 493, 498, 503, 513, 515, 517, 519, 521, 533 to 575, 576, 581, 586, 591, 596, 601, 603, 605, 607, 609, 621 to 767, 768, 773, 778, 783, 788, 793, 795, 797,

40   799, 801, 813 to 862, 863, 868, 873, 878, 883, 888, 890, 892, 894, 896, 908 to 1040, 1041, 1046,

1051, 1056, 1061, 1071, 1073, 1075, 1077, 1079, 1081, 1083, 1085, 1087, 1089, 1091, 1093, 1095, 1097, 1099, 1101, 1103, 1105, 1107, 1109, 1111, 1113, 1161 to 1571, 1572, 1577, 1582, 1587, 1592, 1597, 1602, 1607, 1612, 1617, 1622, 1627, 1632, 1637, 1642, 1647, 1652, 1657, 1662, 1667, 1672, 1677, 1682, 1684, 1686, 1688, 1690, 1692, 1694, 1696, 1698, 1700, 1702, 1704, 1730 to 2039, 2040, 2045, 2050, 2055, 2060, 2065, 2070, 2075, 2080, 2085, 2090, 2095, 2100, 2102, 2104, 2106, 2108, 2120 to 2338, 2339, 2344, 2349, 2354, 2359, 2364, 2366, 2368, 2370, 2372, 2384 to 2460, 2461, 2466, 2471, 2476 or 2481. Further preferred homologues are genes comprising at least one single nucleotide polymorphism (SNIP) compared to a gene comprising a sequence as represented by any of SEQ ID NO 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 49 to 158, 159, 160-163, 168, 173, 178, 183, 188, 193, 198, 203, 208, 215, 220, 225, 230, 247, 249, 251, 253, 255, 257, 259, 275 to 472, 473, 478, 483, 488, 493, 498, 503, 513, 515, 517, 519, 521, 533 to 575, 576, 581, 586, 591, 596, 601, 603, 605, 607, 609, 621 to 767, 768, 773, 778, 783, 788, 793, 795, 797, 799, 801, 813 to 862, 863, 868, 873, 878, 883, 888, 890, 892, 894, 896, 908 to 1040, 1041, 1046, 1051, 1056, 1061, 1071, 1073, 1075, 1077, 1079, 1081, 1083, 1085, 1087, 1089, 1091, 1093, 1095, 1097, 1099, 1101, 1103, 1105, 1107, 1109, 1111, 1113, 1161 to 1571, 1572, 1577, 1582, 1587, 1592, 1597, 1602, 1607, 1612, 1617, 1622, 1627, 1632, 1637, 1642, 1647, 1652, 1657, 1662, 1667, 1672, 1677, 1682, 1684, 1686, 1688, 1690, 1692, 1694, 1696, 1698, 1700, 1702, 1704, 1730 to 2039, 2040, 2045, 2050, 2055, 2060, 2065, 2070, 2075, 2080, 2085, 2090, 2095, 2100, 2102, 2104, 2106, 2108, 2120 to 2338, 2339, 2344, 2349, 2354, 2359, 2364, 2366, 2368, 2370, 2372, 2384 to 2460, 2461, 2466, 2471, 2476 or 2481.

According to another embodiment, the invention encompasses target genes which are insect orthologues of a gene comprising a nucleotide sequence as represented in any of SEQ ID NOs 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 49 to 158, 159, 160-163, 168, 173, 178, 183, 188, 193, 198, 203, 208, 215, 220, 225, 230, 247, 249, 251, 253, 255, 257, 259, 275 to 472, 473, 478, 483, 488, 493, 498, 503, 513, 515, 517, 519, 521, 533 to 575, 576, 581, 586, 591, 596, 601, 603, 605, 607, 609, 621 to 767, 768, 773, 778, 783, 788, 793, 795, 797, 799, 801, 813 to 862, 863, 868, 873, 878, 883, 888, 890, 892, 894, 896, 908 to 1040, 1041, 1046, 1051, 1056, 1061, 1071, 1073, 1075, 1077, 1079, 1081, 1083, 1085, 1087, 1089, 1091, 1093, 1095, 1097, 1099, 1101, 1103, 1105, 1107, 1109, 1111, 1113, 1161 to 1571, 1572, 1577, 1582, 1587, 1592, 1597, 1602, 1607, 1612, 1617, 1622, 1627, 1632, 1637, 1642, 1647, 1652, 1657, 1662, 1667, 1672, 1677, 1682, 1684, 1686, 1688, 1690, 1692, 1694, 1696, 1698, 1700, 1702, 1704, 1730 to 2039, 2040, 2045, 2050, 2055, 2060, 2065, 2070, 2075, 2080, 2085, 2090, 2095, 2100, 2102, 2104, 2106, 2108, 2120 to 2338, 2339, 2344, 2349, 2354, 2359, 2364, 2366, 2368, 2370, 2372, 2384 to 2460, 2461, 2466, 2471, 2476 or 2481. By way of example, orthologues may comprise a nucleotide sequence as represented in any of SEQ ID NOs 49 to 123, 275 to 434, 533 to 562, 621 to 738, 813 to 852, 908 to 1010, 1161 to 1437, 1730 to 1987, 2120 to 2290, and 2384 to 2438, or a fragment thereof of at least 17, 18, 19, 20, 21, 22, 23, 24, 25, 26 or 27 nucleotides. A non-limiting list of insect or arachnida orthologues genes or sequences comprising at least a fragment of 17 bp of one of the sequences of the invention, is given in **Tables 4**.

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According to another embodiment, the invention encompasses target genes which are nematode orthologues of a gene comprising a nucleotide sequence as represented in any of 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 49 to 158, 159, 160-163, 168, 173, 178, 183, 188, 193, 198, 203, 208, 215, 220, 225, 230, 247, 249, 251, 253, 255, 257, 259, 275 to 472, 473, 478, 483, 488, 493,

5   498, 503, 513, 515, 517, 519, 521, 533 to 575, 576, 581, 586, 591, 596, 601, 603, 605, 607, 609, 621 to 767, 768, 773, 778, 783, 788, 793, 795, 797, 799, 801, 813 to 862, 863, 868, 873, 878, 883, 888, 890, 892, 894, 896, 908 to 1040, 1041, 1046, 1051, 1056, 1061, 1071, 1073, 1075, 1077, 1079, 1081, 1083, 1085, 1087, 1089, 1091, 1093, 1095, 1097, 1099, 1101, 1103, 1105, 1107, 1109, 1111, 1113, 1161 to 1571, 1572, 1577, 1582, 1587, 1592, 1597, 1602, 1607, 1612, 1617,

10   1622, 1627, 1632, 1637, 1642, 1647, 1652, 1657, 1662, 1667, 1672, 1677, 1682, 1684, 1686, 1688, 1690, 1692, 1694, 1696, 1698, 1700, 1702, 1704, 1730 to 2039, 2040, 2045, 2050, 2055, 2060, 2065, 2070, 2075, 2080, 2085, 2090, 2095, 2100, 2102, 2104, 2106, 2108, 2120 to 2338, 2339, 2344, 2349, 2354, 2359, 2364, 2366, 2368, 2370, 2372, 2384 to 2460, 2461, 2466, 2471, 2476 or 248. By way of example, nematode orthologues may comprise a nucleotide sequence as

15   represented in any of SEQ ID NOs 124 to 135, 435 to 446, 563 to 564, 739 to 751, 853, 854, 1011 to 1025, 1438 to 1473, 1988 to 2001, 2291 to 2298, 2439 or 2440, or a fragment of at least 17, 18, 19, 20 or 21 nucleotides thereof. According to another aspect, the invention thus encompasses any of the methods described herein for controlling nematode growth in an organism, or for preventing nematode infestation of an organism susceptible to nematode infection, comprising contacting

20   nematode cells with a double-stranded RNA, wherein the double-stranded RNA comprises annealed complementary strands, one of which has a nucleotide sequence which is complementary to at least part of the nucleotide sequence of a target gene comprising a fragment of at least 17, 18, 19, 20 or 21 nucleotides of any of the sequences as represented in SEQ ID NOs 124 to 135, 435 to 446, 563 to 564, 739 to 751, 853, 854, 1011 to 1025, 1438 to 1473, 1988 to

25   2001, 2291 to 2298, 2439 or 2440, whereby the double-stranded RNA is taken up by the nematode and thereby controls growth or prevents infestation. A non-limiting list of nematode orthologues genes or sequences comprising at least a fragment of 17 bp of one of the sequences of the invention, is given in **Tables 5**.

According to another embodiment, the invention encompasses target genes which are

30   fungal orthologues of a gene comprising a nucleotide sequence as represented in any of 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 49 to 158, 159, 160-163, 168, 173, 178, 183, 188, 193, 198, 203, 208, 215, 220, 225, 230, 247, 249, 251, 253, 255, 257, 259, 275 to 472, 473, 478, 483, 488, 493, 498, 503, 513, 515, 517, 519, 521, 533 to 575, 576, 581, 586, 591, 596, 601, 603, 605, 607, 609, 621 to 767, 768, 773, 778, 783, 788, 793, 795, 797, 799, 801, 813 to 862, 863, 868, 873, 878, 883, 888,

35   890, 892, 894, 896, 908 to 1040, 1041, 1046, 1051, 1056, 1061, 1071, 1073, 1075, 1077, 1079, 1081, 1083, 1085, 1087, 1089, 1091, 1093, 1095, 1097, 1099, 1101, 1103, 1105, 1107, 1109, 1111, 1113, 1161 to 1571, 1572, 1577, 1582, 1587, 1592, 1597, 1602, 1607, 1612, 1617, 1622, 1627, 1632, 1637, 1642, 1647, 1652, 1657, 1662, 1667, 1672, 1677, 1682, 1684, 1686, 1688, 1690, 1692, 1694, 1696, 1698, 1700, 1702, 1704, 1730 to 2039, 2040, 2045, 2050, 2055, 2060,

40   2065, 2070, 2075, 2080, 2085, 2090, 2095, 2100, 2102, 2104, 2106, 2108, 2120 to 2338, 2339,

2344, 2349, 2354, 2359, 2364, 2366, 2368, 2370, 2372, 2384 to 2460, 2461, 2466, 2471, 2476 or 2481. By way of example, fungal orthologues may comprise a nucleotide sequence as represented in any of SEQ ID NOs 136 to 158, 447 to 472, 565 to 575, 752 to 767, 855 to 862, 1026 to 1040, 1475 to 1571, 2002 to 2039, 2299 to 2338, 2441 to 2460, or a fragment of at least 17, 18, 19, 20,

5   21, 22, 23, 24, 25, 26 or 27 nucleotides thereof. According to another aspect, the invention thus encompasses any of the methods described herein for controlling fungal growth on a cell or an organism, or for preventing fungal infestation of a cell or an organism susceptible to fungal infection, comprising contacting fungal cells with a double-stranded RNA, wherein the double-stranded RNA comprises annealed complementary strands, one of which has a nucleotide

10 sequence which is complementary to at least part of the nucleotide sequence of a target gene comprising a fragment of at least 17, 18, 19, 20 or 21 nucleotides of any of the sequences as represented in SEQ ID NOs 136 to 158, 447 to 472, 565 to 575, 752 to 767, 855 to 862, 1026 to 1040, 1475 to 1571, 2002 to 2039, 2299 to 2338, 2441 to 2460, whereby the double-stranded RNA is taken up by the fungus and thereby controls growth or prevents infestation. A non-limiting list of

15 fungal orthologues genes or sequences comprising at least a fragment of 17 bp of one of the sequences of the invention, is given in **Tables 6**.

In an alternative embodiment, the regulatory sequence comprises a promoter selected

The term "regulatory sequence" is to be taken in a broad context and refers to a regulatory nucleic acid capable of effecting expression of the sequences to which it is operably linked.

Encompassed by the aforementioned term are promoters and nucleic acids or synthetic

20 fusion molecules or derivatives thereof which activate or enhance expression of a nucleic acid, so called activators or enhancers. The term "operably linked" as used herein refers to a functional linkage between the "promoter" sequence and the nucleic acid molecule of interest, such that the "promoter" sequence is able to initiate transcription of the nucleic acid molecule to produce the appropriate dsRNA.

25 A preferred regulatory sequence is a promoter, which may be a constitutive or an inducible promoter. Preferred promoters are inducible promoters to allow tight control of expression of the RNA molecules. Promoters inducible through use of an appropriate chemical, such as IPTG are preferred. Alternatively, the transgene encoding the RNA molecule is placed under the control of a strong constitutive promoter. Preferably, any promoter which is used will direct strong expression of

30 the RNA. The nature of the promoter utilised may, in part, be determined by the specific host cell utilised to produce the RNA. In one embodiment, the regulatory sequence comprises a bacteriophage promoter, such as a T7, T3, SV40 or SP6 promoter, most preferably a T7 promoter. In yet other embodiments of the present invention, other promoters useful for the expression of RNA are used and include, but are not limited to, promoters from an RNA Pol I, an RNA Pol II or an

35 RNA Pol III polymerase. Other promoters derived from yeast or viral genes may also be utilised as appropriate.

In an alternative embodiment, the regulatory sequence comprises a promoter selected from the well known tac, trc and lac promoters. Inducible promoters suitable for use with bacterial hosts include β-lactamase promoter, E. coli λ phage PL and PR promoters, and E. coli galactose

40 promoter, arabinose promoter and alkaline phosphatase promoter.Therefore, the present invention

also encompasses a method for generating any of the RNA molecules or RNA constructs of the invention. This method comprises the steps of introducing (e.g. by transformation, transfection or injection) an isolated nucleic acid or a recombinant (DNA) construct of the invention in a host cell of the invention under conditions that allow transcription of said nucleic acid or recombinant (DNA)
5   construct to produce the RNA which acts to down regulate a target gene of interest (when the host cell is ingested by the target organism or when a host cell or extract derived therefrom is taken up by the target organism).

Optionally, one or more transcription termination sequences or "terminators" may also be incorporated in the recombinant construct of the invention. The term "transcription termination
10   sequence" encompasses a control sequence at the end of a transcriptional unit, which signals 3' processing and poly-adenylation of a primary transcript and termination of transcription. The transcription termination sequence is useful to prevent read through transcription such that the RNA molecule is accurately produced in or by the host cell. In one embodiment, the terminator comprises a T7, T3, SV40 or SP6 terminator, preferably a T7 terminator. Other terminators derived
15   from yeast or viral genes may also be utilised as appropriate.

Additional regulatory elements, such as transcriptional or translational enhancers, may be incorporated in the expression construct.

The recombinant constructs of the invention may further include an origin of replication which is required for maintenance and/or replication in a specific cell type. One example is when an
20   expression construct is required to be maintained in a bacterial cell as an episomal genetic element (e.g. plasmid or cosmid molecule) in a cell. Preferred origins of replication include, but are not limited to, f1-ori and colE1 ori.

The recombinant construct may optionally comprise a selectable marker gene. As used herein, the term "selectable marker gene" includes any gene, which confers a phenotype on a cell
25   in which it is expressed to facilitate the identification and/or selection of cells, which are transfected or transformed, with a recombinant (expression) construct of the invention. Examples of suitable selectable markers include resistance genes against ampicillin (Ampr), tetracycline (Tcr), kanamycin (Kanr), phosphinothricin, and chloramphenicol (CAT) gene. Other suitable marker genes provide a metabolic trait, for example manA. Visual marker genes may also be used and
30   include for example beta-glucuronidase (GUS), luciferase and green fluorescent protein (GFP).

In yet other embodiments of the present invention, other promoters useful for the expression of dsRNA are used and include, but are not limited to, promoters from an RNA PolI, an RNA PolII, an RNA PolIII, T7 RNA polymerase or SP6 RNA polymerase. These promoters are typically used for *in vitro*-production of dsRNA, which dsRNA is then included in an antiinsecticidal
35   agent, for example, in an anti-insecticidal liquid, spray or powder.

Therefore, the present invention also encompasses a method for generating any of the double-stranded RNA or RNA constructs of the invention. This method comprises the steps of

      a.   contacting an isolated nucleic acid or a recombinant DNA construct of the invention with cell-free components; or

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b. introducing (e.g. by transformation, transfection or injection) an isolated nucleic acid or a recombinant DNA construct of the invention in a cell,

under conditions that allow transcription of said nucleic acid or recombinant DNA construct to produce the dsRNA or RNA construct.

Optionally, one or more transcription termination sequences may also be incorporated in the recombinant construct of the invention. The term "transcription termination sequence" encompasses a control sequence at the end of a transcriptional unit, which signals 3' processing and poly-adenylation of a primary transcript and termination of transcription. Additional regulatory elements, such as transcriptional or translational enhancers, may be incorporated in the expression construct.

The recombinant constructs of the invention may further include an origin of replication which is required for maintenance and/or replication in a specific cell type. One example is when an expression construct is required to be maintained in a bacterial cell as an episomal genetic element (e.g. plasmid or cosmid molecule) in a cell. Preferred origins of replication include, but are not limited to, f1-ori and colE1 ori.

The recombinant construct may optionally comprise a selectable marker gene. As used herein, the term "selectable marker gene" includes any gene, which confers a phenotype on a cell in which it is expressed to facilitate the identification and/or selection of cells, which are transfected or transformed, with an expression construct of the invention. Examples of suitable selectable markers include resistance genes against ampicillin (Ampr), tetracycline (Tcr), kanamycin (Kanr), phosphinothricin, and chloramphenicol (CAT) gene. Other suitable marker genes provide a metabolic trait, for example manA. Visual marker genes may also be used and include for example beta-glucuronidase (GUS), luciferase and Green Fluorescent Protein (GFP).

The present invention relates to methods for preventing insect growth on a plant or for preventing insect infestation of a plant. The plants to be treated according to the methods of the invention encompasses plants selected from the group comprising: alfalfa, ,apple, apricot, artichoke, asparagus, avocado, banana, barley, beans, beet, blackberry, blueberry, broccoli, brussel sprouts, cabbage, canola, carrot, cassava, cauliflower, a cereal, celery, cherry, citrus, clemintine, coffee, corn, cotton, cucumber, eggplant, endive, eucalyptus, figes, grape, grapefruit, groundnuts, ground cherry, kiwifruit, lettuce, leek, lemon, lime, pine, maize, mango, melon, millet, mushroom, nut aot, okra, onion, orange, an ornamental plant or flower or tree, papaya,, parsley, pea, peach, peanut, peat, pepper, persimmon, pineapple, plantain, plum, pomegranate, potato, pumpkin, radicchio, radish, rapeseed, raspberry, rice, rye, sorghum, soy, soybean, spinach, strawberry, sugarbeet, sugargcane, sunflower, sweet poatao, tangerine, tea, tobacco, tomato, a vine; waetermelon, wheat, yams or zucchiniplant; preferably a potato, eggplant, tomato, pepper, tobacco, ground cherry, rice corn or cotton plant), or a seed or tuber (e.g. an alfalfa, apple, apricot, artichoke, asparagus, avocado, banana, barley, beans, beet, blackberry, blueberry, broccoli, brussel sprouts, cabbage, canola, carrot, cassava, cauliflower, a cereal, celery, cherry, citrus, clemintine, coffee, corn, cotton, cucumber, eggplant, endive, eucalyptus, figes, grape, grapefruit, groundnuts, ground cherry, kiwifruit, lettuce, leek, lemon, lime, pine, maize, mango, melon, millet,

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mushroom, nut aot, okra, onion, orange, an ornamental plant or flower or tree, papaya,, parsley,
pea, peach, peanut, peat, pepper, persimmon, pineapple, plantain, plum, pomegranate, potato,
pumpkin, radicchio, radish, rapeseed, raspberry, rice, rye, sorghum, soy, soybean, spinach,
strawberry, sugarbeet, sugargcane, sunflower, sweet poatao, tangerine, tea, tobacco, tomato, a

5   vine, waetermelon, wheat, yams and zucchini.

The amount of targeted RNA which is taken up, preferably by ingestion, by the target
organism is such that specific down-regulation of the one or more target genes is achieved. The
RNA may be expressed by the host cell in an amount which allows delivery of at least one copy per
cell. However, in certain embodiments higher doses (e.g., at least 5, 10, 100, 500 or 1000 copies

10   per cell of the target organism) of RNA may yield more effective inhibition. For any given target
gene and target organism the optimum amount of the targeted RNA molecules for effective
inhibition may be determined by routine experimentation.

The target organism can be contacted with the host cell expressing the RNA molecule in
any suitable manner, to permit ingestion by the target organism. Preferably, the host cells

15   expressing the dsRNA may be linked to a food component of the target organisms in order to
increase uptake of the dsRNA by the target organism. The host cells expressing the dsRNA may
also be incorporated in the medium in which the target organism grows or in or on a material or
substrate that is infested by a pest organism or impregnated in a substrate or material susceptible
to infestation by a pest organism.

20   In alternative embodiments, a suitable extract derived from the host cells expressing the
RNA molecule may be utilised in order to achieve down regulation of a target gene in a target
organism. Here, the extracts may be derived by any suitable means of lysis of the host cells
expressing the RNA molecules. For example, techniques such as sonication, French press,
freeze-thaw and lysozyme treatment (see Sambrook and Russell - Molecular Cloning: A laboratory

25   manual - third edition and the references provided therein in table 15-4) may be utilised in order to
prepare a crude host cell extract (lysate). Further purification of the extract may be carried out as
appropriate provided the ability of the extract to mediate targeted down regulation of target gene
expression is not adversely affected. Affinity purification may be utilised for example. It may also
be appropriate to add certain components to the extract, to prevent degradation of the RNA

30   molecules. For example, RNase inhibitors may be added to the extracts derived from the host cells
expressing the RNA. In one example, the target organism can be contacted with the host cell
expressing the RNA in pure or substantially pure form, for example an aqueous solution containing
the cell extract. In this embodiment, the target organism, especially pest organisms such as
insects may be simply "soaked" with an aqueous solution comprising the host cell extract. In a

35   further embodiment the target organism can be contacted with the host cells expressing the RNA
molecule by spraying the target organism with a liquid composition comprising the cell extract.

If the method of the invention is used for specifically controlling growth or infestation of a
specific pest, it is preferred that the RNA expressed in the host cell does not share any significant
homology with a gene or genes from a non-pest organism, in particular that it does not share any

40   significant homology with any essential gene of the non-pest organism. Thus, the non-pest

organism is typically the organism susceptible to infestation by the pest and which is therefore protected from the pest according to the methods of the invention. So, for example, non-pest species may comprise a plant or a mammalian species. Preferably, the mammalian species is Homo sapiens. The non-target species may also include animals other than humans which may be

5   exposed to the organism or substrate protected against infestation. Examples include birds which may feed on protected plants, and livestock and domestic animals such as cats, dogs, horses, cattle, chickens, pigs, sheep etc. In this context, it is preferred that the dsRNA shows less than 30%, more preferably less that 20%, more preferably less than 10%, and even more preferably less than 5% nucleic acid sequence identity with any gene of the susceptible or non-target

10   organism. Percentage sequence identity should be calculated across the full length of the targetted RNA region. If genomic sequence data is available for the organism to be protected according to the invention or for any non-target organism, one may cross-check sequence identity with the targetted RNA using standard bioinformatics tools. In one embodiment, there is no sequence identity between the RNA molecule and a non-pest organism's genes over 21 contiguous

15   nucleotides, meaning that in this context, it is preferred that 21 contiguous nucleotides of the RNA do not occur in the genome of the non-pest organism. In another embodiment, there is less than about 10% or less than about 12.5 % sequence identity over 24 contiguous nucleotides of the RNA with any nucleotide sequence from a non-pest (susceptible) species. In particular, orthologous genes from a non-pest species may be of particular note, since essential genes from the pest

20   organism may often be targeted in the methods of the invention. Thus, in one embodiment, the RNA molecule has less than 12.5% sequence identity with the corresponding nucleotide sequence of an orthologous gene from a non-pest species.

In a further embodiment, the invention relates to a composition for controlling insect growth and/or preventing or reducing insect infestation, comprising comprising at least one double-

25   stranded RNA, wherein said double-stranded RNA comprises annealed complementary strands, one of which has a nucleotide sequence which is complementary to at least part of a nucleotide sequence of an insect target gene.. The invention also relates to a composition comprising at least one of the nucleotide sequence or at least one recombinant DNA construct as described herein. The invention also relates to a composition comprising at least one bacterial cell or yeast cell

30   expressing at least one double stranded RNA or a double stranded RNA construct as described herein; or expressing at least one nucleotide sequence or a recombinant DNA construct as described herein. Optionally, the composition further comprises at least one suitable carrier, excipient or diluent. The target gene may be any target gene described herein. Preferably the insect target gene is essential for the viability, growth, development or reproduction of the insect.

35   In another aspect the invention relates to a composition as described above, wherein the insect target gene comprises a sequence which is at least 75%, preferably at least 80%, 85%, 90%, more preferably at least 95%, 98% or 99% identical to a sequence selected from the group of sequences represented by any of SEQ ID NOs 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 49 to 158, 159, 160-163, 168, 173, 178, 183, 188, 193, 198, 203, 208, 215, 220, 225, 230, 240 to 247, 249,

40   251, 253, 255, 257, 259, 275 to 472, 473, 478, 483, 488, 493, 498, 503, 508 to 513, 515, 517, 519,

521, 533 to 575, 576, 581, 586, 591, 596, 601, 603, 605, 607, 609, 621 to 767, 768, 773, 778, 783,

788, 793, 795, 797, 799, 801, 813 to 862, 863, 868, 873, 878, 883, 888, 890, 892, 894, 896, 908 to

1040, 1041, 1046, 1051, 1056, 1061, 1066 to 1071, 1073, 1075, 1077, 1079, 1081, 1083, 1085,

1087, 1089, 1091, 1093, 1095, 1097, 1099, 1101, 1103, 1105, 1107, 1109, 1111, 1113, 1161 to

1571, 1572, 1577, 1582, 1587, 1592, 1597, 1602, 1607, 1612, 1617, 1622, 1627, 1632, 1637,

1642, 1647, 1652, 1657, 1662, 1667, 1672, 1677, 1682, 1684, 1686, 1688, 1690, 1692, 1694,

1696, 1698, 1700, 1702, 1704, 1730 to 2039, 2040, 2045, 2050, 2055, 2060, 2065, 2070, 2075,

2080, 2085, 2090, 2095, 2100, 2102, 2104, 2106, 2108, 2120 to 2338, 2339, 2344, 2349, 2354,

2359, 2364, 2366, 2368, 2370, 2372, 2384 to 2460, 2461, 2466, 2471, 2476, 2481 or 2486, or the

complement thereof, or wherein said insect target gene is an insect orthologue of a gene

comprising at least 17 contiguous nucleotides of any of SEQ ID NOs 1, 3, 5, 7, 9, 11, 13, 15, 17,

19, 21, 23, 49 to 158, 159, 160-163, 168, 173, 178, 183, 188, 193, 198, 203, 208, 215, 220, 225,

230, 240 to 247, 249, 251, 253, 255, 257, 259, 275 to 472, 473, 478, 483, 488, 493, 498, 503, 508

to 513, 515, 517, 519, 521, 533 to 575, 576, 581, 586, 591, 596, 601, 603, 605, 607, 609, 621 to

767, 768, 773, 778, 783, 788, 793, 795, 797, 799, 801, 813 to 862, 863, 868, 873, 878, 883, 888,

890, 892, 894, 896, 908 to 1040, 1041, 1046, 1051, 1056, 1061, 1066 to 1071, 1073, 1075, 1077,

1079, 1081, 1083, 1085, 1087, 1089, 1091, 1093, 1095, 1097, 1099, 1101, 1103, 1105, 1107,

1109, 1111, 1113, 1161 to 1571, 1572, 1577, 1582, 1587, 1592, 1597, 1602, 1607, 1612, 1617,

1622, 1627, 1632, 1637, 1642, 1647, 1652, 1657, 1662, 1667, 1672, 1677, 1682, 1684, 1686,

1688, 1690, 1692, 1694, 1696, 1698, 1700, 1702, 1704, 1730 to 2039, 2040, 2045, 2050, 2055,

2060, 2065, 2070, 2075, 2080, 2085, 2090, 2095, 2100, 2102, 2104, 2106, 2108, 2120 to 2338,

2339, 2344, 2349, 2354, 2359, 2364, 2366, 2368, 2370, 2372, 2384 to 2460, 2461, 2466, 2471,

2476, 2481 or 2486, or the complement thereof.

The present invention further relates to a composition comprising at least one double-stranded RNA, at least one double-stranded RNA construct, at least one nucleotide sequence, at least one recombinant DNA construct and/or at least one host cell (e.g. a bacterial or a yeast) expressing a dsRNA of the invention, or a virus encoding a dsRNA of the invention, optionally further comprising at least one suitable carrier, excipient or diluent.

The composition may be in any suitable physical form for application to insects. The composition may be in solid form (such as a powder, pellet or a bait), liquid form (such as a spray) or gel form for example.

According to a most preferred embodiment, the composition is in a form suitable for ingestion by an insect.

The composition may contain further components which serve to stabilise the dsRNA and/or prevent degradation of the dsRNA during prolonged storage of the composition.

The composition may still further contain components which enhance or promote uptake of the dsRNA by the insect. These may include, for example, chemical agents which generally promote the uptake of RNA into cells e.g. lipofectamin etc.

The composition may still further contain components which serve to preserve the viability of the host cell during prolonged storage.

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The composition may be in any suitable physical form for application to insects, to substrates, to cells (e.g. plant cells), or to organisms infected by or susceptible to infestation by insects.

In one embodiment, the composition may be provided in the form of a spray. Thus, a human user can spray the insect or the substrate directly with the composition.

The present invention thus relates to a spray comprising a composition comprising at least one bacterial cell or yeast cell expressing at least one double stranded RNA or a double stranded RNA construct as described herein; or expressing at least one nucleotide sequence or a recombinant DNA construct as described herein. More specific, the invention relates to a spray as defined above wherein said bacterial cell comprises at least one of the sequences represented by any of SEQ ID NOs 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 49 to 158, 159, 160-163, 168, 173, 178, 183, 188, 193, 198, 203, 208, 215, 220, 225, 230, 240 to 247, 249, 251, 253, 255, 257, 259, 275 to 472, 473, 478, 483, 488, 493, 498, 503, 508 to 513, 515, 517, 519, 521, 533 to 575, 576, 581, 586, 591, 596, 601, 603, 605, 607, 609, 621 to 767, 768, 773, 778, 783, 788, 793, 795, 797, 799, 801, 813 to 862, 863, 868, 873, 878, 883, 888, 890, 892, 894, 896, 908 to 1040, 1041, 1046, 1051, 1056, 1061, 1066 to 1071, 1073, 1075, 1077, 1079, 1081, 1083, 1085, 1087, 1089, 1091, 1093, 1095, 1097, 1099, 1101, 1103, 1105, 1107, 1109, 1111, 1113, 1161 to 1571, 1572, 1577, 1582, 1587, 1592, 1597, 1602, 1607, 1612, 1617, 1622, 1627, 1632, 1637, 1642, 1647, 1652, 1657, 1662, 1667, 1672, 1677, 1682, 1684, 1686, 1688, 1690, 1692, 1694, 1696, 1698, 1700, 1702, 1704, 1730 to 2039, 2040, 2045, 2050, 2055, 2060, 2065, 2070, 2075, 2080, 2085, 2090, 2095, 2100, 2102, 2104, 2106, 2108, 2120 to 2338, 2339, 2344, 2349, 2354, 2359, 2364, 2366, 2368, 2370, 2372, 2384 to 2460, 2461, 2466, 2471, 2476, 2481 or 2486, or a fragment thereof of at least 17 contiguous nucleotides. Preferably, said spray comprises at least one of the sequences represented by any of SEQ ID NOs 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 49 to 158, 159, 160-163, 168, 173, 178, 183, 188, 193, 198, 203, 208, 215, 220, 225, 230, 240 to 247, 249, 251, 253, 255, 257, 259, 275 to 472, 473, 478, 483, 488, 493, 498, 503, 508 to 513, 515, 517, 519, 521, 533 to 575, 576, 581, 586, 591, 596, 601, 603, 605, 607, 609, 621 to 767, 768, 773, 778, 783, 788, 793, 795, 797, 799, 801, 813 to 862, 863, 868, 873, 878, 883, 888, 890, 892, 894, 896, 908 to 1040, 1041, 1046, 1051, 1056, 1061, 1066 to 1071, 1073, 1075, 1077, 1079, 1081, 1083, 1085, 1087, 1089, 1091, 1093, 1095, 1097, 1099, 1101, 1103, 1105, 1107, 1109, 1111, 1113, 1161 to 1571, 1572, 1577, 1582, 1587, 1592, 1597, 1602, 1607, 1612, 1617, 1622, 1627, 1632, 1637, 1642, 1647, 1652, 1657, 1662, 1667, 1672, 1677, 1682, 1684, 1686, 1688, 1690, 1692, 1694, 1696, 1698, 1700, 1702, 1704, 1730 to 2039, 2040, 2045, 2050, 2055, 2060, 2065, 2070, 2075, 2080, 2085, 2090, 2095, 2100, 2102, 2104, 2106, 2108, 2120 to 2338, 2339, 2344, 2349, 2354, 2359, 2364, 2366, 2368, 2370, 2372, 2384 to 2460, 2461, 2466, 2471, 2476, 2481 or 2486, or a fragment thereof of at least 17 contiguous nucleotides.

The invention also relates to a spray comprising at least one composition or comprising at least one host cell as described herein, and further at least one adjuvant and optionally at least one surfactant

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The effectiveness of a pesticide may depend on the effectiveness of the spray application. Adjuvants can minimize or eliminate many spray application problems associated with pesticide stability, solubility, incompatibility, suspension, foaming, drift, evaporation, volatilization, degradation, adherence, penetration, surface tension, and coverage. Adjuvants are designed to
5   perform specific functions, including wetting, spreading, sticking, reducing evaporation, reducing volatilization, buffering, emulsifying, dispersing, reducing spray drift, and reducing foaming. No single adjuvant can perform all these functions, but different compatible adjuvants often can be combined to perform multiple functions simultaneously. These chemicals, also called wetting agents and spreaders, physically alter the surface tension of a spray droplet. For a pesticide to
10   perform its function properly, a spray droplet must be able to wet the foliage and spread out evenly over a leaf. Surfactants enlarge the area of pesticide coverage, thereby increasing the pest's exposure to the chemical. Surfactants are particularly important when applying a pesticide to waxy or hairy leaves. Without proper wetting and spreading, spray droplets often run off or fail to adequately cover these surfaces. Too much surfactant, however, can cause excessive runoff or
15   deposit loss, thus reducing pesticide efficacy. Pesticide formulations often contain surfactants to improve the suspension of the pesticide's active ingredient. This is especially true for emulsifiable concentrate (EC) formulations.

As used herein the term "adjuvant" means any nonpesticide material added to a pesticide product or pesticide spray mixture to improve the mixing and stability of the products in the spray
20   tank and the application. As further used herein the term "surfactant"means a chemical that modifies surface tension. Surfactants can influence the wetting and spreading of liquids, and can modify the dispersion, suspension, or precipitation of a pesticide in water. There are nonionic surfactants (no electrical charge), anionic surfactants (negative charge), and cationic surfactants (positive charge)

25   In particular embodiments the host cells comprised in the spray are inactivated, for instance by heat inactiviation or mechanical disruption (as discussed in greater detail herein).

The nature of the excipients and the physical form of the composition may vary depending upon the nature of the substrate that it is desired to treat. For example, the composition may be a liquid that is brushed or sprayed onto or imprinted into the material or substrate to be treated, or a
30   coating or powder that is applied to the material or substrate to be treated. Thus, in one embodiment, the composition is in the form of a coating on a suitable surface which adheres to, and is eventually ingested by an insect which comes into contact with the coating.

According to a preferred embodiment, the substrate is a plant or crop to be treated against insect pest infestation. The composition is then internalized or eaten by the insect, from where it
35   can mediate RNA interference, thus controlling the insect The spray is preferably a pressurized/aerosolized spray or a pump spray. The particles may be of suitable size such that they adhere to the substrate to be treated or to the insect, for example to the exoskeleton, of the insect and/or arachnid and may be absorbed therefrom.

In one embodiment, the composition is in the form of a bait. The bait is designed to lure
40   the insect to come into contact with the composition. Upon coming into contact therewith, the

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composition is then internalised by the insect, by ingestion for example and mediates RNAi to thus kill the insect. Said bait may comprise a food substance, such as a protein based food, for example fish meal. Boric acid may also be used as a bait. The bait may depend on the species being targeted. An attractant may also be used. The attractant may be a pheromone, such as a male or

5   female pheremone for example. As an example, the pheromones referred to in the book "Insect Pheremones and their use in Pest Management" (Howse et al, Chapman and Hall, 1998) may be used in the invention. The attractant acts to lure the insect to the bait, and may be targeted for a particular insect or may attract a whole range of insects. The bait may be in any suitable form, such as a solid, paste, pellet or powdered form.

10   .   The bait may also be carried away by the insect back to the colony. The bait may then act as a food source for other members of the colony, thus providing an effective control of a large number of insects and potentially an entire insect pest colony. This is an advantage associated with use of the double stranded RNA or bacteria expressing the dsRNA of the invention, because the delayed action of the RNAi mediated effects on the pests allows the bait to be carried back to the

15   colony, thus delivering maximal impact in terms of exposure to the insects.

Additionally, compositions which come into contact with the insects may remain on the cuticle of the insect. When cleaning, either an individual insect cleaning itself or insects cleaning one another, the compositions may be ingested and can thus mediate their effects in the insect. This requires that the composition is sufficiently stable such that the dsRNA or host cells

20   expressing dsRNA remain intact and capable of mediating RNAi even when exposed to external environmental conditions for a length of time, which may be a period of days for example.

The baits may be provided in a suitable "housing" or "trap". Such housings and traps are commercially available and existing traps may be adapted to include the compositions of the invention. Any housing or trap which may attract an insect to enter it is included within the scope of

25   the invention. The housing or trap may be box-shaped for example, and may be provided in pre-formed condition or may be formed of foldable cardboard for example. Suitable materials for a housing or trap include plastics and cardboard, particularly corrugated cardboard. Suitable dimensions for such a housing or trap are, for example, 7-15 cm wide, 15-20 cm long and 1-5 cm high. The inside surfaces of the traps may be lined with a sticky substance in order to restrict

30   movement of the insect once inside the trap. The housing or trap may contain a suitable trough inside which can hold the bait in place. A trap is distinguished from a housing because the insect can not readily leave a trap following entry, whereas a housing acts as a "feeding station" which provides the insect arachnid with a preferred environment in which they can feed and feel safe from predators.

35   Accordingly, in a further aspect the invention provides a housing or trap for insects which contains a composition of the invention, which may incorporate any of the features of the composition described herein.

It is contemplated that the "composition" of the invention may be supplied as a "kit-of-parts" comprising the double-stranded RNA in one container and a suitable diluent, excipient or carrier for

40   the RNA containing entity (such as a ds RNA or ds RNA construct, DNA construct, expression

construct) in a separate container; or comprising the host cell(s) in one container and a suitable diluent, excipient, carrier or preservative for the host cell in a separate container. The invention also relates to supply of the double-stranded RNA or host cells alone without any further components. In these embodiments the dsRNA or host cells may be supplied in a concentrated form, such as a concentrated aqueous solution. It may even be supplied in frozen form or in freeze-dried or lyophilised form. The latter may be more stable for long term storage and may be de-frosted and/or reconstituted with a suitable diluent immediately prior to use.

The present invention further encompasses a method for controlling growth of a pest organism and/or for preventing infestation of a susceptible organism by the pest organism on a substrate comprising applying an effective amount of any of the compositions and/or sprays as described herein to said substrate.

The invention further encompasses a method for treating and/or preventing a disease or condition caused by a target organism, comprising administering to a subject in need of such treatment and/or prevention, a composition or a spray as described herein, wherein down-regulation of expression of the target gene in the target organism caused by the composition or spray is effective to treat and/or prevent the disease caused by the target organism. A preferred target organism is a pest, in particular an insect as described in more detail herein.

The present invention further relates to the medical use of any of the double-stranded RNAs, double-stranded RNA constructs, nucleotide sequences, recombinant DNA constructs or compositions described herein.

Insects and other Arthropods can cause injury and even death by their bites or stings. More people die each year in the United States from bee and wasp stings than from snake bites. Many insects can transmit bacteria and other pathogens that cause diseases. During every major war between countries, more people have been injured or killed by diseases transmitted by insects than have been injured or killed by bullets and bombs. Insects that bite man and domestic animals are mostly those with piercing-sucking mouthparts, as found in Hemiptera and some Diptera. Much of the discomfort from a bite is a result of enzymes that the insect pumps into the victim. Ticks and chiggers are different kinds of mites (Class Arachnida) that feed on blood of animals. Ticks can also transmit viruses and other pathogens that cause diseases, including Lyme disease and Rocky Mountain spotted fever. Other kinds of mites can cause mange on humans, dogs, cats, and other animals. Order Hemiptera includes bed bugs, kissing bugs, and assassin bugs, all of which have beaks for piercing their hosts. The most painful bites among all insects are those of assassin bugs. Kissing bugs are involved in causing Chagas disease in Central and South America. The caterpillars of some moths can "sting." The Diptera are the most important order of insects that affect people. Biting flies include many species of mosquitoes, black flies, biting gnats, horse flies, and others. Many of these biting flies are transmitters of diseases, such as the tse-tse fly that transmits African sleeping sickness. Flies with sponging mouthparts, such as the house fly, also transmit bacteria and other pathogens that cause typhoid fever and other diseases. Screwworms and maggots of both flies are fly larvae that invade living tissue of animals. Mosquitoes transmit pathogens that cause malaria, yellow fever, encephalitis, and other diseases. Malaria is caused by

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a protozoan parasite that lives part of its life cycle in the *Anopheles* mosquitoes and part of its cycle in humans. Plague, also known as bubonic plague or black death, is caused by bacteria that infect rats and other rodents. The main transmitter of this disease to humans is the Oriental rat flea (Order Siphonaptera). Many bees, wasps, and ants (Order Hymenoptera) can cause pain and even death by their stinging. Deaths usually are a result of allergic reactions to the venom. Other major stingers include hornets, yellow jackets, and paper wasps. The Africanized honey bee, or "killer" bee is a strain of our domesticated honey bee. The two strains are almost identical in appearance. However, the Africanized strain is much more aggressive and will attack in larger numbers.

In one specific embodiment, the composition is a pharmaceutical or veterinary composition for treating or preventing insect disease or infections of humans or animals, respectively. Such compositions will comprise at least one double-stranded RNA or RNA construct, or nucleotide sequence or recombinant DNA construct encoding the double-stranded RNA or RNA construct, wherein the double-stranded RNA comprises annealed complementary strands, one of which has a nucleotide sequence which corresponds to a target nucleotide sequence of an insect target gene that causes the disease or infection, and at least one carrier, excipient or diluent suitable for pharmaceutical use.

The composition may be a composition suitable for topical use, such as application on the skin of an animal or human, for example as liquid composition to be applied to the skin as drops, gel, aerosol, or by brushing, or a spray, cream, ointment, etc. for topical application or as transdermal patches.

Alternatively, the insect dsRNA is produced by bacteria (e.g. lactobacillus) or fungi (e.g. Sacharomyces spp.) which can be included in food and which functions as an oral vaccine against the insect infection.

Other conventional pharmaceutical dosage forms may also be produced, including tablets, capsules, pessaries, transdermal patches, suppositories, etc. The chosen form will depend upon the nature of the target insect and hence the nature of the disease it is desired to treat.

In one specific embodiment, the composition may be a coating, paste or powder that can be applied to a substrate in order to protect said substrate from infestation by insects and/or arachnids. In this embodiment, the composition can be used to protect any substrate or material that is susceptible to infestation by or damage caused by the insect, for example foodstuffs and other perishable materials, and substrates such as wood. Houses and other wood products can be destroyed by termites, powder post beetles, and carpenter ants. The subterranean termite and Formosan termite are the most serious pests of houses in the southern United States and tropical regions. Any harvested plant or animal product can be attacked by insects. Flour beetles, grain weevils, meal moths and other stored product pests will feed on stored grain, cereals, pet food, powdered chocolate, and almost everything else in the kitchen pantry that is not protected. Larvae of clothes moths eat clothes made from animal products, such as fur, silk and wool. Larvae of carpet beetles eat both animal and plant products, including leather, fur, cotton, stored grain, and even museum specimens. Book lice and silverfish are pests of libraries. These insects eat the starchy glue in the bindings of books. Other insects that have invaded houses include cockroaches

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which eat almost anything. Cockroaches are not known to be a specific transmitter of disease, but they contaminate food and have an unpleasant odor. They are very annoying, and many pest control companies are kept busy in attempts to control them. The most common cockroaches in houses, grocery stores, and restaurants include the German cockroach, American cockroach,
5   Oriental cockroach, and brown banded cockroach.

The nature of the excipients and the physical form of the composition may vary depending upon the nature of the substrate that is desired to treat. For example, the composition may be a liquid that is brushed or sprayed onto or imprinted into the material or substrate to be treated, or a coating that is applied to the material or substrate to be treated.
10   The present invention further encompasses a method for treating and/or preventing insect infestation on a substrate comprising applying an effective amount of any of the compositions or sprays as described herein to said substrate.

The invention further encompasses a method for treating and/or preventing an insect disease or condition, comprising administering to a subject in need of such treatment and/or
15   prevention, any of the compositions or sprays as herein described comprising at least one double-stranded RNA or double stranded RNA construct comprising annealed complementary strands, one of which has a nucleotide sequence which is complementary to at least part of a nucleotide sequence of an insect target gene of the insect that causes the insect disease or condition. According to a more specific embodiment, said composition or spray to be administered comprises
20   and/or expressing at least one bacterial cell or yeast cell expressing at least one double stranded RNA or double stranded RNA construct as described herein; or comprising and/or expressing at least one nucleotide sequence or recombinant DNA construct as described herein, said RNA or nucleotide sequence being complementary to at least part of a nucleotide sequence of an insect target gene of the insect that causes the insect disease or condition.
25   In another embodiment of the invention the compositions are used as a insecticide for a plant or for propagation or reproductive material of a plant, such as on seeds. As an example, the composition can be used as an insecticide by spraying or applying it on plant tissue or spraying or mixing it on the soil before or after emergence of the plantlets.

In yet another embodiment, the present invention provides a method for treating and/or
30   preventing insect growth and/or insect infestation of a plant or propagation or reproductive material of a plant, comprising applying an effective amount of any of the compositions or sprays herein described to a plant or to propagation or reproductive material of a plant.

In another embodiment the invention relates to the use of any double-stranded RNA or RNA construct, or nucleotide sequence or recombinant DNA construct encoding the double-
35   stranded RNA or RNA construct, or at least one host cell (e.g. a bacterial or a yeast) expressing a dsRNA of the invention, or a virus encoding a dsRNA described herein, or to any of the compositions or sprays comprising the same, used for controlling insect growth; for preventing insect infestation of plants susceptible to insect infection; or for treating insect infection of plants. Specific plants to be treated for insect infections caused by specific insect species are as described
40   earlier and are encompassed by the said use

In a more specific embodiment, the invention relates to the use of a spray comprising at least one host cell or at least one host cell (e.g. a bacterial or a yeast) expressing a dsRNA of the invention, or a virus encoding a dsRNA described herein, or to any of the compositions comprising the same, for controlling insect growth; for preventing insect infestation of plants susceptible to
5   insect infection; or for treating insect infection of plants. Preferably said host cell comprises at least one of the sequences represented by any of SEQ ID NOs 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 49 to 158, 159, 160-163, 168, 173, 178, 183, 188, 193, 198, 203, 208, 215, 220, 225, 230, 240 to 247, 249, 251, 253, 255, 257, 259, 275 to 472, 473, 478, 483, 488, 493, 498, 503, 508 to 513, 515, 517, 519, 521, 533 to 575, 576, 581, 586, 591, 596, 601, 603, 605, 607, 609, 621 to 767, 768, 773,
10   778, 783, 788, 793, 795, 797, 799, 801, 813 to 862, 863, 868, 873, 878, 883, 888, 890, 892, 894, 896, 908 to 1040, 1041, 1046, 1051, 1056, 1061, 1066 to 1071, 1073, 1075, 1077, 1079, 1081, 1083, 1085, 1087, 1089, 1091, 1093, 1095, 1097, 1099, 1101, 1103, 1105, 1107, 1109, 1111, 1113, 1161 to 1571, 1572, 1577, 1582, 1587, 1592, 1597, 1602, 1607, 1612, 1617, 1622, 1627, 1632, 1637, 1642, 1647, 1652, 1657, 1662, 1667, 1672, 1677, 1682, 1684, 1686, 1688, 1690,
15   1692, 1694, 1696, 1698, 1700, 1702, 1704, 1730 to 2039, 2040, 2045, 2050, 2055, 2060, 2065, 2070, 2075, 2080, 2085, 2090, 2095, 2100, 2102, 2104, 2106, 2108, 2120 to 2338, 2339, 2344, 2349, 2354, 2359, 2364, 2366, 2368, 2370, 2372, 2384 to 2460, 2461, 2466, 2471, 2476, 2481 or 2486, or a fragment thereof of at least 17 contiguous nucleotides.

In a further aspect, the invention also provides combinations of methods and compositions
20   for preventing or protecting plants from pest infestation. For instance, one means provides using a combination of the transgenic approach with methods using double stranded RNA molecules and compositions with one or more Bt insecticidal proteins or chemical (organic) compounds that are toxic to the target pest. Another means provides using the transgenic approach combining methods using expression of double stranded RNA molecules in bacteria or yeast and expression of such Bt
25   insecticidal proteins in the same or in distinct bacteria or yeast. According to these approaches, for instance, one insect can be targeted or killed using the RNAi-based method or technology, while the other insect can be targeted or killed using the Bt insecticide or the chemical (organic) insecticide.

Therefore the invention also relates to any of the compositions, sprays or methods for
30   treating plants described herein, wherein said composition comprises a bacterial cell or yeast expressing said RNA molecule and further comprises a pesticidal agent or comprises a bacterial cell or yeast cell comprising or expressing a pesticidal agent (the bacterial or yeast cell can be the same or different from the first ones mentioned), said pesticidal agent selected from the group consisting of a chemical (organic) insecticide, a patatin, a *Bacillus thuringiensis* insecticidal protein,
35   a *Xenorhabdus* insecticidal protein, a *Photorhabdus* insecticidal protein, a *Bacillus laterosporous* insecticidal protein, and a *Bacillus sphearicus* insecticidal protein. Preferably said *Bacillus thuringiensis* insecticidal protein is selected from the group consisting of a Cry1, a Cry3, a TIC851, a CryET170, a Cry22, a binary insecticidal protein CryET33 and CryET34, a binary insecticidal protein CryET80 and CryET76, a binary insecticidal protein TIC100 and TIC101, and a binary
40   insecticidal protein PS149B1.

The spray can be used in a greenhouse or on the field. Typical application rates for bacteria-containing biopestides (e.g. as an emulsifiable suspension) amount to 25-100 liters/ha (10-40 liters/acre) for water based sprays: comprising about 2.5-5 liter of formulated product (emulsifiable suspension) per hectare with the formulated product including about 25% (v/v) of 'bacterial cells' plus 75% (v/v) 'other ingredients'. The amount of bacterial cells are measured in units, e.g. one unit is defined as 10^9 bacterial cells in 1ml. Depending on the crop density per hectare and the leaf surface per plant, one liter of formulated product comprises between 0.001 and 10000 units of bacteria, preferably at least 0.001, 0.003, 0.005, 0.007, 0.01, 0.03, 0.05, 0.07, 0.1, 0.3, 0.5, 0.7, more preferably at least 1, 3, 5, 7, 10, 30, 50, 70, 100, 300, 500, 700, or more preferably at least 1000, 3000, 5000, 7000 or 10000 units of bacteria.

For instance, typical plant density for potato crop plants is approximately 4.5 plants per square meter or 45.000 plants per hectare (planting in rows with spacing between rows at 75 cm and spacing between plants within rows at 30 cm). The present invention thus relates to a spray comprising at least 0.001, 0.003, 0.005, 0.007, 0.01, 0.03, 0.05, 0.07, 0.1, 0.3, 0.5, 0.7, more preferably at least 1, 3, 5, 7, 10, 30, 50, 70, 100, 300, 500, 700, or more preferably at least 1000, 3000, 5000, 7000 or 10000 units of bacteria expressing at least one of the dsRNA molecules or dsRNA constructs described herein.

The invention further relates to a kit comprising at least one double stranded RNA, or double stranded RNA construct, or nucleotide sequence, or recombinant DNA construct, or host cell, or composition or spray as described earlier for treating insect infection in plants. The kit may be supplied with suitable instructions for use. The instructions may be printed on suitable packaging in which the other components are supplied or may be provided as a separate entity, which may be in the form of a sheet or leaflet for example. The instructions may be rolled or folded for example when in a stored state and may then be unrolled and unfolded to direct use of the remaining components of the kit.

The invention will be further understood with reference to the following non-limiting examples.

Brief Description of Figures and Tables

Figure 1-LD: Survival of *L. decemlineata* on artificial diet treated with dsRNA. Insects of the second larval stage were fed diet treated with 50 μl of topically-applied solution of dsRNA (targets or gfp control). Diet was replaced with fresh diet containing topically-applied dsRNA after 7 days. The number of surviving insects were assessed at days 2, 5, 7, 8, 9, & 13. The percentage of surviving larvae was calculated relative to day 0 (start of assay). Target LD006: (SEQ ID NO 178); Target LD007 (SEQ ID NO 183); Target LD010 (SEQ ID NO 188); Target LD011 (SEQ ID NO 193); Target LD014 (SEQ ID NO 198); gfp dsRNA (SEQ ID NO 235).

Figure 2-LD: Survival of *L. decemlineata* on artificial diet treated with dsRNA. Insects of the second larval stage were fed diet treated with 50 μl of topically-applied solution of dsRNA (targets or gfp control). Diet was replaced with fresh diet only after 7 days. The number of surviving

insects was assessed at days 2, 5, 6, 7, 8, 9, 12, & 14. The percentage of surviving larvae was calculated relative to day 0 (start of assay). Target LD001 (SEQ ID NO 163); Target LD002 (SEQ ID NO 168); Target LD003 (SEQ ID NO 173); Target LD015 (SEQ ID NO 215); Target LD016 (SEQ ID NO 220); gfp dsRNA (SEQ ID NO 235).

5   **Figure 3-LD**: Average weight of *L. decemlineata* larvae on potato leaf discs treated with dsRNA. Insects of the second larval stage were fed leaf discs treated with 20 µl of a topically-applied solution (10 ng/µl) of dsRNA (target LD002 or gfp). After two days the insects were transferred on to untreated leaves every day.

         Figure 4-LD: Survival of *L. decemlineata* on artificial diet treated with shorter versions of
10   target LD014 dsRNA and concatemer dsRNA. Insects of the second larval stage were fed diet treated with 50 µl of topically-applied solution of dsRNA (gfp or targets). The number of surviving insects were assessed at days 3, 4, 5, 6, & 7. The percentage of surviving larvae were calculated relative to day 0 (start of assay).

         Figure 5-LD: Survival of *L. decemlineata* larvae on artificial diet treated with different
15   concentrations of dsRNA of target LD002 **(a)**, target LD007 **(b)**, target LD010 **(c)**, target LD011 **(d)**, target LD014 **(e)**, target LD015 **(f)**, LD016 **(g)** and target LD027 **(h)**. Insects of the second larval stage were fed diet treated with 50 µl of topically-applied solution of dsRNA. Diet was replaced with fresh diet containing topically-applied dsRNA after 7 days. The number of surviving insects were assessed at regular intervals. The percentage of surviving larvae were calculated relative to day 0
20   (start of assay).

         Figure 6-LD. Effects of *E. coli* strains expressing dsRNA target LD010 on survival of larvae of the Colorado potato beetle, *Leptinotarsa decemlineata*, over time. The two bacterial strains were tested in separate artificial diet-based bioassays: **(a)** AB301-105(DE3); data points for pGBNJ003 and pGN29 represent average mortality values from 5 different bacterial clones; **(b)** BL21(DE3);
25   data points for pGBNJ003 and pGN29 represent average mortality values from 5 different and one single bacterial clones, respectively. Error bars represent standard deviations.

         Figure 7-LD. Effects of different clones of *E. coli* strains **(a)** AB301-105(DE3) and **(b)** BL21(DE3) expressing dsRNA target LD010 on survival of larvae of the Colorado potato beetle, *Leptinotarsa decemlineata*, 12 days post infestation. Data points are average mortality values for
30   each clone for pGN29 and pGBNJ003. Clone 1 of AB301-105(DE3) harboring plasmid pGBNJ003 showed 100% mortality towards CPB at this timepoint. Error bars represent standard deviations.

         Figure 8-LD. Effects of different clones of *E. coli* strains **(a)** AB301-105(DE3) and **(b)** BL21(DE3) expressing dsRNA target LD010 on growth and development of larval survivors of the Colorado potato beetle, *Leptinotarsa decemlineata*, 7 days post infestation. Data points are %
35   average larval weight values for each clone (one clone for pGN29 and five clones for pGBNJ003) based on the data of **Table 10**. Diet only treatment represents 100% normal larval weight.

Figure 9-LD. Survival of larvae of the Colorado potato beetle, *Leptinotarsa decemlineata*, on potato plants sprayed by double-stranded RNA-producing bacteria 7 days post infestation. Number of larval survivors were counted and expressed in terms of % mortality. The bacterial host strain used was the RNaseIII-deficient strain AB301-105(DE3). Insect gene target was LD010.

5   Figure 10-LD. Growth/developmental delay of larval survivors of the Colorado potato beetle, *Leptinotarsa decemlineata*, fed on potato plants sprayed with dsRNA-producing bacteria 11 days post infestation. The bacterial host strain used was the RNaseIII-deficient strain AB301-105(DE3). Data figures represented as percentage of normal larval weight; 100 % of normal larval weight given for diet only treatment. Insect gene target was LD010. Error bars represent standard

10   deviations.

Figure 11-LD. Resistance to potato damage caused by larvae of the Colorado potato beetle, *Leptinotarsa* decemlineata, by double-stranded RNA-producing bacteria 7 days post infestation. Left, plant sprayed with 7 units of bacteria AB301-105(DE3) containing the pGN29 plasmid; right, plant sprayed with 7 units of bacteria AB301-105(DE3) containing the pGBNJ003

15   plasmid. One unit is defined as the equivalent of 1 ml of a bacterial suspension at OD value of 1 at 600 nm. Insect gene target was LD010.

Figure 12-LD. Survival of *L. decemlineata* adults on potato leaf discs treated with dsRNA. Young adult insects were fed double-stranded-RNA-treated leaf discs for the first two days and were then placed on untreated potato foliage. The number of surviving insects were assessed

20   regularly; mobile insects were recorded as insects which were alive and appeared to move normally; moribund insects were recorded as insects which were alive but appeared sick and slow moving – these insects were not able to right themselves once placed on their backs. Target LD002 (SEQ ID NO 168); Target LD010 (SEQ ID NO 188); Target LD014 (SEQ ID NO 198); Target LD016 (SEQ ID NO 220); gfp dsRNA (SEQ ID NO 235).

25   Figure 13-LD. Effects of bacterial produced target double-stranded RNA against larvae of *L. decemlineata*. Fifty µl of an OD 1 suspension of heat-treated bacteria AB301-105 (DE3) expressing dsRNA (SEQ ID NO 188) was applied topically onto the solid artificial diet in each well of a 48-well plate. CPB larvae at L2 stage were placed in each well. At day 7, a picture was taken of the CPB larvae in a plate containing (a) diet with bacteria expressing target 10 double-stranded

30   RNA, (b) diet with bacteria harboring the empty vector pGN29, and, (c) diet only.

Figure 14-LD Effects on CPB larval survival and growth of different amounts of inactivated *E. coli* AB301-105(DE3) strain harboring plasmid pGBNJ003 topically applied to potato foliage prior to insect infestation. Ten L1 larvae were fed treated potato for 7 days. Amount of bacterial suspension sprayed on plants: 0.25 U, 0.08 U, 0.025 U, 0.008 U of target 10 and 0.25 U of pGN29

35   (negative control; also included is Milli-Q water). One unit (U) is defined as the equivalent bacterial amount present in 1 ml of culture with an optical density value of 1 at 600nm. A total volume of 1.6 ml was sprayed on to each plant. Insect gene target was LD010.

Figure 15-LD Resistance to potato damage caused by CPB larvae by inactivated *E. coli* AB301-105(DE3) strain harboring plasmid pGBNJ003 seven days post infestation. (a) water, (b) 0.25 U *E. coli* AB301-105(DE3) harboring pGN29, (c) 0.025 U *E. coli* AB301-105(DE3) harboring pGBNJ003, (d) 0.008 U *E. coli* AB301-105(DE3) harboring pGBNJ003. One unit (U) is defined as the equivalent bacterial amount present in 1 ml of culture with an optical density value of 1 at 600nm. A total volume of 1.6 ml was sprayed on to each plant. Insect gene target was LD010.

Figure 1-PC: Effects of ingested target dsRNAs on survival and growth of *P. cochleariae* larvae. Neonate larvae were fed oilseed rape leaf discs treated with 25 µl of topically-applied solution of 0.1 µg/µl dsRNA (targets or gfp control). Afer 2 days, the insects were transferred onto fresh dsRNA-treated leaf discs. At day 4, larvae from one replicate for every treatment were collected and placed in a Petri dish containing fresh untreated oilseed rape foliage. The insects were assessed at days 2, 4, 7, 9 & 11. (a) Survival of *E. varivestis* larvae on oilseed rape leaf discs treated with dsRNA. The percentage of surviving larvae was calculated relative to day 0 (start of assay). (b) Average weights of *P. cochleariae* larvae on oilseed rape leaf discs treated with dsRNA. Insects from each replicate were weighed together and the average weight per larva determined. Error bars represent standard deviations. Target 1: SEQ ID NO 473; target 3: SEQ ID NO 478; target 5: SEQ ID NO 483 –; target 10: SEQ ID NO 488; target 14: SEQ ID NO 493; target 16: SEQ ID NO 498; target 27: SEQ ID NO 503; gfp dsRNA: SEQ ID NO 235.

Figure 2-PC: Survival of *P. cochleariae* on oilseed rape leaf discs treated with different concentrations of dsRNA of (a) target PC010 and (b) target PC027. Neonate larvae were placed on leaf discs treated with 25 µl of topically-applied solution of dsRNA. Insects were transferred to fresh treated leaf discs at day 2. At day 4 for target PC010 and day 5 for target PC027, the insects were transferred to untreated leaves. The number of surviving insects were assessed at days 2, 4, 7, 8, 9 & 11 for PC010 and 2, 5, 8, 9 & 12 for PC027. The percentage of surviving larvae was calculated relative to day 0 (start of assay).

Figure 3-PC: Effects of *E. coli* strain AB301-105(DE3) expressing dsRNA target PC010 on survival of larvae of the mustard leaf beetle, *P. cochleariae*, over time. Data points for each treatment represent average mortality values from 3 different replicates. Error bars represent standard deviations. Target 10: SEQ ID NO 488

Figure 1-EV: Survival of *E. varivestis* larvae on bean leaf discs treated with dsRNA. Neonate larvae were fed bean leaf discs treated with 25 µl of topically-applied solution of 1 µg/µl dsRNA (targets or gfp control). Afer 2 days, the insects were transferred onto fresh dsRNA-treated leaf discs. At day 4, larvae from one treatment were collected and placed in a plastic box containing fresh untreated bean foliage. The insects were assessed for mortality at days 2, 4, 6, 8 & 10. The percentage of surviving larvae was calculated relative to day 0 (start of assay). Target 5: SEQ ID NO 576; target 10: SEQ ID NO 586; target 15: SEQ ID NO 591; target 16: SEQ ID NO 596; gfp dsRNA: SEQ ID NO 235.

Figure 2-EV: Effects of ingested target dsRNAs on surival of *E. varivestis* adults and resistance to snap bean foliar insect damage. (a) Surivival of *E. varivestis* adults on bean leaf treated with dsRNA. Adults were fed bean leaf discs treated with 75 µl of topically-applied solution of 0.1 µg/µl dsRNA (targets or gfp control). After 24 hours, the insects were transferred onto fresh dsRNA-treated leaf discs. After a further 24 hours, adults from one treatment were collected and placed in a plastic box containing potted fresh untreated whole bean plants. The insects were assessed for mortality at days 4, 5, 6, 7, 8, & 11. The percentage of surviving adults was calculated relative to day 0 (start of assay). Target 10: SEQ ID NO 586; target 15: SEQ ID NO 591; target 16: SEQ ID NO 596; gfp dsRNA: SEQ ID NO 235. (b) Resistance to bean foliar damage caused by adults of the *E. varivestis* by dsRNA. Whole plants containing insects from one treatment (see (a)) were checked visually for foliar damage on day 9. (i) target 10; (ii) target 15; (iii) target 16; (iv) gfp dsRNA; (v) untreated.

Figure 1-TC: Survival of *T. castaneum* larvae on artificial diet treated with dsRNA of target 14. Neonate larvae were fed diet based on a flour/milk mix with 1 mg dsRNA target 14. Control was water (without dsRNA) in diet. Four replicates of 10 first instar larvae per replicate were performed for each treatment. The insects were assessed for survival as average percentage means at days 6, 17, 31, 45 and 60. The percentage of surviving larvae was calculated relative to day 0 (start of assay). Error bars represent standard deviations. Target TC014: SEQ ID NO 878.

Figure 1-MP: Effect of ingested target 27 dsRNA on the survival of *Myzus persicae* nymphs. First instars were placed in feeding chambers containing 50 µl of liquid diet with 2 µg/µl dsRNA (target 27 or gfp dsRNA control). Per treatment, 5 feeding chambers were set up with 10 instars in each feeding chamber. Number of survivors were assessed at 8 days post start of bioassay. Error bars represent standard deviations. Target MP027: SEQ ID NO 1061; gfp dsRNA: SEQ ID NO 235.

Figure 1-NL: Survival of *Nilaparvata lugens* on liquid artificial diet treated with dsRNA. Nymphs of the first to second larval stage were fed diet supplemented with 2 mg/ml solution of dsRNA targets in separate bioassays: (a) NL002, NL003, NL005, NL010; (b) NL009, NL016; (c) NL014, NL018; (d) NL013, NL015, NL021. Insect survival on targets were compared to diet only and diet with gfp dsRNA control at same concentration. Diet was replaced with fresh diet containing dsRNA every two days. The number of surviving insects were assessed every day

Figure 2-NL: Survival of *Nilaparvata lugens* on liquid artificial diet treated with different concentrations of target dsRNA NL002. Nymphs of the first to second larval stage were fed diet supplemented with 1, 0.2, 0.08, and 0.04 mg/ml (final concentration) of NL002. Diet was replaced with fresh diet containing dsRNA every two days. The numbers of surviving insects were assessed every day.

Examples

Example 1: Silencing *C.elegans* target genes in *C. elegans* in High Throughput Screening

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A *C. elegans* genome wide library was prepared in the pGN9A vector (WO 01/88121) between two identical T7-promoters and terminators, driving its expression in the sense and antisense direction upon expression of the T7 polymerase, which was induced by IPTG.

This library was transformed into the bacterial strain AB301-105 (DE3) in 96 well plate
5. format. For the genome wide screening, these bacterial cells were fed to the nuclease deficient *C. elegans nuc-1(e1392)* strain.

Feeding the dsRNA produced in the bacterial strain AB301-105 (DE3), to *C. elegans nuc-1 (e1392)* worms, was performed in a 96 well plate format as follows: *nuc-1* eggs were transferred to a separate plate and allowed to hatch simultaneously at 20 °C for synchronization of the L1
10 generation. 96 well plates were filled with 100 μL liquid growth medium comprising IPTG and with 10 μL bacterial cell culture of $OD_{600}1$ AB301-105 (DE3) of the C. elegans dsRNA library carrying each a vector with a C. elegans genomic fragment for expression of the dsRNA. To each well, 4 of the synchronized L1 worms were added and were incubated at 25 °C for at least 4 to 5 days. These experiments were performed in quadruplicate. In the screen 6 controls were used:

15   -   pGN29 = negative control, wild type

            -   pGZ1 = *unc-22* = twitcher phenotype

            -   pGZ18 = chitin synthase = embryonic lethal

            -   pGZ25 = *pos-1* = embryonic lethal

            -   pGZ59 = *bli-4D* = acute lethal

20   -   ACC = acetyl co-enzym A carboxylase = acute lethal

After 5 days, the phenotype of the *C. elegans nuc-1 (e1392)* worms fed with the bacteria producing dsRNA were compared to the phenotype of worms fed with the empty vector (pGN29) and the other controls. The worms that were fed with the dsRNA were screened for lethality (acute or larval) lethality for the parent (Po) generation, (embryonic) lethality for the first filial (F1)
25 generation, or for growth retardation of Po as follows: (i) Acute lethality of Po: L1's have not developed and are dead, this phenotype never gives progeny and the well looks quite empty; (ii) (Larval) lethality of Po: Po died in a later stage than L1, this phenotype also never gives progeny. Dead larvae or dead adult worms are found in the wells; (iii) Lethality for F1: L1's have developed until adult stage and are still alive. This phenotype has no progeny. This can be due to sterility, embryonic lethality (dead eggs on the bottom of well), embryonic arrest or larval arrest (eventually
30 ends up being lethal): (iv) Arrested in growth and growth retardation/delay: Compared to a well with normal development and normal # of progeny.

For the target sequences presented in **Table 1A**, it was concluded that dsRNA mediated silencing of the *C. elegans* target gene in nematodes, such as *C. elegans*, had a fatal effect on the
35 growth and viability of the worm.

Subsequent to the above dsRNA silencing experiment, a more detailed phenotyping experiment was conducted in *C. elegans* in a high throughput format on 24 well plates. The dsRNA library produced in bacterial strain AB301-105 (DE3), as described above, was fed to *C. elegans nuc-1 (e1392)* worms on 24 well plates as follows: *nuc-1* eggs were transferred to a
40 separate plate and allowed to hatch simultaneously at 20 C for synchronization of the L1

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generation. Subsequently 100 of the synchronized L1 worms were soaked in a mixture of 500 μL S-complete fed medium, comprising 5 μg/mL cholesterol, 4 μL/mL PEG and 1mM IPTG, and 500 μL of bacterial cell culture of OD_{600}1 AB301-105 (DE3) of the *C. elegans* dsRNA library carrying each a vector with a *C. elegans* genomic fragment for expression of the dsRNA. The soaked L1 worms were rolled for 2 hours at 25 C.

After centrifugation and removal of 950 μL of the supernatant, 5 μL of the remaining and resuspended pellet (comprising about 10 to 15 worms) was transferred in the middle of each well of a 24 well plate, filled with a layer of agar LB broth. The inoculated plate was incubated at 25°C for 2 days. At the adult stage, 1 adult worm was singled and incubated at 25°C for 2 days for inspection of its progeny. The other adult worms are inspected *in situ* on the original 24 well plate. These experiments were performed in quadruplicate.

This detailed phenotypic screen was repeated with a second batch of worms, the only difference being that the worms of the second batch were incubated at 20 C for 3 days.

The phenotype of the worms fed with *C. elegans* dsRNA was compared to the phenotype of *C. elegans nuc-1 (e1392)* worms fed with the empty vector.

Based on this experiment, it was concluded that silencing the *C. elegans* target genes as represented in **Table 1A** had a fatal effect on the growth and viability of the worm and that the target gene is essential to the viability of nematodes. Therefore these genes are good target genes to control (kill or prevent from growing) nematodes via dsRNA mediated gene silencing. Accordingly, the present invention encompasses the use of nematode orthologues of the above *C. elegans* target gene, to control nematode infestation, such as nematode infestation of plants.

Example 2: Identification of *D. melanogaster* orthologues

As described above in Example 1, numerous *C. elegans* lethal sequenes were identified and can be used for identifying orthologues in other species and genera. For example, the *C. elegans* lethal sequences can be used to identify orthologous *D. melanogasters* sequences. That is, each *C. elegans* sequence can be querried against a public database, such as GenBank, for orthologous sequences in *D. melanogaster*. Potential *D. melanogaster* orthologues were selected that share a high degree of sequence homology (E value preferably less than or equal to 1E-30) and the sequences are blast reciprocal best hits, the latter means that the sequences from different organisms (e.g. *C. elegans* and *D. melanogaster*) are each other's top blast hits. For example, sequence C from *C. elegans* is compared against sequences in *D. melanogaster* using BLAST. If sequence C has the *D. melanogaster* sequence D as best hit and when D is compared to all the sequences of *C. elegans*, also turns out to be sequence C, then D and C are reciprocal best hits. This criterium is often used to define orthology, meaning similar sequences of different species, having similar function. The *D. melanogaster* sequence identifiers are represented in **Table 1A**.

Example 3: *Leptinotarsa decemlineata* (Colorado potato beetle)

A. Cloning partial gene sequences from *Leptinotarsa decemlineata*

High quality, intact RNA was isolated from 4 different larval stages of *Leptinotarsa decemlineata* (Colorado potato beetle; source: Jeroen van Schaik, Entocare CV Biologische Gewasbescherming, Postbus 162, 6700 AD Wageningen, the Netherlands) using TRIzol Reagent (Cat. Nr. 15596-026/15596-018, Invitrogen, Rockville, Maryland, USA) following the manufacturer's

5   instructions. Genomic DNA present in the RNA preparation was removed by DNase treatment following the manufacturer's instructions (Cat. Nr. 1700, Promega). cDNA was generated using a commercially available kit (SuperScript ™ III Reverse Transcriptase, Cat. Nr. 18080044, Invitrogen, Rockville, Maryland, USA) following the manufacturer's instructions.

To isolate cDNA sequences comprising a portion of the LD001, LD002, LD003, LD006,

10   LD007, LD010, LD011, LD014, LD015, LD016, LC018 and LD027 genes, a series of PCR reactions with degenerate primers were performed using Amplitaq Gold (Cat. Nr. N8080240, Applied Biosystems) following the manufacturer's instructions.

The sequences of the degenerate primers used for amplification of each of the genes are given in **Table 2-LD**, which displays *Leptintarsa decemlineata* target genes including primer

15   sequences and cDNA sequences obtained. These primers were used in respective PCR reactions with the following conditions: 10 minutes at 95°C, followed by 40 cycles of 30 seconds at 95°C, 1 minute at 55°C and 1 minute at 72°C, followed by 10 minutes at 72°C. The resulting PCR fragments were analyzed on agarose gel, purified (QIAquick Gel Extraction kit, Cat. Nr. 28706, Qiagen), cloned into the pCR8/GW/topo vector (Cat. Nr. K2500 20, Invitrogen), and sequenced.

20   The sequences of the resulting PCR products are represented by the respective SEQ ID NOs as given in **Table 2-LD** and are referred to as the partial sequences. The corresponding partial amino acid sequence are represented by the respective SEQ ID NOs as given in **Table 3-LD**, where the start of the reading frame is indicated in brackets.

B. dsRNA production of the *Leptinotarsa decemlineata* genes

25   dsRNA was synthesized in milligram amounts using the commercially available kit T7 Ribomax™ Express RNAi System (Cat. Nr. P1700, Promega). First two separate single 5' T7 RNA polymerase promoter templates were generated in two separate PCR reactions, each reaction containing the target sequence in a different orientation relative to the T7 promoter.

For each of the target genes, the sense T7 template was generated using specific T7

30   forward and specific reverse primers. The sequences of the respective primers for amplifying the sense template for each of the target genes are given in **Table 8-LD**. The conditions in the PCR reactions were as follows: 4 minutes at 95°C, followed by 35 cycles of 30 seconds at 95°C, 30 seconds at 55°C and 1 minute at 72°C, followed by 10 minutes at 72°C. The anti-sense T7 template was generated using specific forward and specific T7 reverse primers in a PCR reaction

35   with the same conditions as described above. The sequences of the respective primers for amplifying the anti-sense template for each of the target genes are given in **Table 8-LD**. The resulting PCR products were analyzed on agarose gel and purified by PCR purification kit (Qiaquick PCR Purification Kit, Cat. Nr. 28106, Qiagen) and NaClO₄ precipitation. The generated T7 forward and reverse templates were mixed to be transcribed and the resulting RNA strands

were annealed, DNase and RNase treated, and purified by sodium acetate, following the manufacturer's instructions. The sense strand of the resulting dsRNA for each of the target genes is given in **Table 8-LD**. Table 8-LD displays sequences for preparing ds RNA fragments of *Leptinotarsa decemlineata* target sequences and concatemer sequences, including primer sequences.

C. Screening dsRNA targets using artificial diet for activity against *Leptinotarsa decemlineata*

Artificial diet for the Colorado potato beetle was prepared as follows (adapted from Gelman *et al.*, 2001, J. Ins. Sc., vol. 1, no. 7, 1-10): water and agar were autoclaved, and the remaining ingredients (shown in **Table A** below) were added when the temperature dropped to 55 °C. At this temperature, the ingredients were mixed well before the diet was aliquoted into 24-well plates (Nunc) with a quantity of 1ml of diet per well. The artificial diet was allowed to solidify by cooling at room temperature. Diet was stored at 4 °C for up to three weeks.

Table A: Ingredients for Artificial diet

Ingredients	Volume for 1 L
water	768ml
agar	14g
rolled oats	40g
Torula yeast	60g
lactalbumin hydrolysate	30g
casein	10g
fructose	20g
Wesson salt mixture	4g
tomato fruit powder	12.5g
potato leaf powder	25g
b-sitosterol	1g
sorbic acid	0.8g
methyl paraben	0.8g
Vanderzant vitamin mix	12g
neomycin sulfate	0.2g
aureomycin	0.130g
rifampicin	0.130g
chloramphenicol	0.130g
nystatin	0.050g
soybean oil	2ml
wheat germ oil	2ml

Fifty μl of a solution of dsRNA at a concentration of 1 mg/ml was applied topically onto the solid artificial diet in the wells of the multiwell plate. The diet was dried in a laminair flow cabin. Per treatment, twenty-four Colorado potato beetle larvae (2nd stage), with two insects per well, were tested. The plates were stored in the insect rearing chamber at 25 ± 2 °C, 60 % relative humidity,
5   with a 16:8 hours light:dark photoperiod. The beetles were assessed as live or dead every 1, 2 or 3 days. After seven days, for targets LD006, LD007, LD010, LD011, and LD014, the diet was replaced with fresh diet with topically applied dsRNA at the same concentration (1 mg/ml); for targets LD001, LD002, LD003, LD015, and LD016, the diet was replaced with fresh diet only. The dsRNA targets were compared to diet only or diet with topically applied dsRNA corresponding to a
10   fragment of the GFP (green fluorescent protein) coding sequence (SEQ ID NO 235).

Feeding artificial diet containing intact naked dsRNAs to *L. decemlineata* larvae resulted in significant increases in larval mortalities as indicated in two separate bioassays (**Figures 1LD-2LD**).

All dsRNAs tested resulted ultimately in 100 % mortality after 7 to 14 days. Diet with or
15   without GFP dsRNA sustained the insects throughout the bioassays with very little or no mortality.

Typically, in all assays observed, CPB second-stage larvae fed normally on diet with or without dsRNA for 2 days and molted to the third larval stage. At this new larval stage the CPB were observed to reduce significantly or stop altogether their feeding, with an increase in mortality as a result.

20   **D. Bioassay of dsRNA targets using potato leaf discs for activity against the** *Leptinotarsa decemlineata*

An alternative bioassay method was employed using potato leaf material rather than artificial diet as food source for CPB. Discs of approximately 1.1 cm in diameter (or 0.95 cm²) were cut out off leaves of 2 to 3-week old potato plants using a suitably-sized cork borer. Treated leaf
25   discs were prepared by applying 20 μl of a 10 ng/μl solution of target LD002 dsRNA or control gfp dsRNA on the adaxial leaf surface. The leaf discs were allowed to dry and placed individually in 24 wells of a 24-well multiplate (Nunc). A single second-larval stage CPB was placed into each well, which was then covered with tissue paper and a multiwell plastic lid. The plate containing the insects and leaf discs were kept in an insect chamber at 28°C with a photoperiod of 16h light/8h
30   dark. The insects were allowed to feed on the leaf discs for 2 days after which the insects were transferred to a new plate containing fresh treated leaf discs. Thereafter, the insects were transferred to a plate containing untreated leaf discs every day until day 7. Insect mortality and weight scores were recorded.

Feeding potato leaf discs with surface-applied intact naked dsRNA of target LD002 to *L.*
35   *decemlineata* larvae resulted in a significant increase in larval mortalities (i.e. at day 7 all insects were dead; 100 % mortality) whereas control gfp dsRNA had no effect on CPB survival. Target LD002 dsRNA severely affected the growth of the larvae after 2 to 3 days whereas the larvae fed with gfp dsRNA at the same concentration developed as normal (**Figure 3-LD**).

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E. Screening shorter versions of dsRNAs using artificial diet for activity against *Leptinotarsa decemlineata*

This example exemplifies the finding that shorter (60 or 100bp) dsRNA fragments on their own or as concatemer constructs are sufficient in causing toxicity towards the Colorado potato
5   beetle.

LD014, a target known to induce lethality in Colorado potato beetle, was selected for this example. This gene encodes a V-ATPase subunit E (SEQ ID NO 15).

A 100 base pair fragment, LD014_F1, at position 195-294 on SEQ ID NO 15 (SEQ ID NO 159) and a 60 base pair fragment, LD014_F2, at position 235-294 on SEQ ID NO 15 (SEQ ID NO
10   160) were further selected. See also **Table 7-LD**.

Two concatemers of 300 base pairs, LD014_C1 and LD014_C2, were designed (SEQ ID NO 161 and SEQ ID NO 162). LD014_C1 contained 3 repeats of the 100 base pair fragment described above (SEQ ID NO 159) and LD014_C2 contained 5 repeats of the 60 base pair fragment described above (SEQ ID NO 160). See also **Table 7-LD**.

15   The fragments LD014_F1 and LD014_F2 were synthesized as sense and antisense primers. These primers were annealed to create the double strands DNA molecules prior to cloning. *Xba*I and *Xma*I restrictions sites were included at the 5′ and 3′ ends of the primers, respectively, to facilitate the cloning.

The concatemers were made as 300 base pairs synthetic genes. *Xba*I and *Xma*I
20   restrictions sites were included at the 5′ and 3′ ends of the synthetic DNA fragments, respectively, to facilite the cloning.

The 4 DNA molecules, i.e. the 2 single units (LD014_F1 & LD014_F2) and the 2 concatemers (LD014_C1 & LD014_C2), were digested with *Xba*I and *Xma*I and subcloned in pBluescriptII SK+ linearised by *Xba*I and *Xma*I digests, resulting in recombinant plasmids p1, p2,
25   p3, & p4, respectively.

Double-stranded RNA production: dsRNA was synthesized using the commercially available kit T7 Ribomax™ Express RNAi System (Cat. Nr. P1700, Promega). First two separate single 5′ T7 RNA polymerase promoter templates were generated in two separate PCR reactions, each reaction containing the target sequence in a different orientation relative to the T7 promoter.
30   For LD014_F1, the sense T7 template was generated using the specific T7 forward primer oGBM159 and the specific reverse primer oGBM164 (represented herein as SEQ ID NO 204 and SEQ ID NO 205, respectively) in a PCR reaction with the following conditions: 4 minutes at 95°C, followed by 35 cycles of 30 seconds at 95°C, 30 seconds at 55°C and 1 minute at 72°C, followed by 10 minutes at 72°C. The anti-sense T7 template was generated using the specific forward
35   primer oGBM163 and the specific T7 reverse primer oGBM160 (represented herein as SEQ ID NO 206 and SEQ ID NO 207, respectively) in a PCR reaction with the same conditions as described above. The resulting PCR products were analyzed on agarose gel and purified by PCR purification kit (Qiaquick PCR Purification Kit, Cat. Nr. 28106, Qiagen) and NaClO₄ precipitation. The generated T7 forward and reverse templates were mixed to be transcribed and the resulting RNA
40   strands were annealed, Dnase and Rnase treated, and purified by sodium acetate, following the

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manufacturer's instructions. The sense strand of the resulting dsRNA is herein represented by SEQ ID NO 203.

For LD014_F2, the sense T7 template was generated using the specific T7 forward primer oGBM161 and the specific reverse primer oGBM166 (represented herein as SEQ ID NO 209 and SEQ ID NO 210, respectively) in a PCR reaction with the following conditions: 4 minutes at 95°C, followed by 35 cycles of 30 seconds at 95°C, 30 seconds at 55°C and 1 minute at 72°C, followed by 10 minutes at 72°C. The anti-sense T7 template was generated using the specific forward primer oGBM165 and the specific T7 reverse primer oGBM162 (represented herein as SEQ ID NO 211 and SEQ ID NO 212, respectively) in a PCR reaction with the same conditions as described above. The resulting PCR products were analyzed on agarose gel and purified by PCR purification kit (Qiaquick PCR Purification Kit, Cat. Nr. 28106, Qiagen) and $NaClO_4$ precipitation. The generated T7 forward and reverse templates were mixed to be transcribed and the resulting RNA strands were annealed, Dnase and Rnase treated, and purified by sodium acetate, following the manufacturer's instructions. The sense strand of the resulting dsRNA is herein represented by SEQ ID NO 208.

Also for the concatemers, separate single 5' T7 RNA polymerase promoter templates were generated in two separate PCR reactions, each reaction containing the target sequence in a different orientation relative to the T7 promoter. The recombinant plasmids p3 and p4 containing LD014_C1 & LD014_C2 were linearised with *Xba*I or *Xma*I, the two linear fragments for each construct purified and used as template for the *in vitro* transcription assay, using the T7 promoters flanking the cloning sites. Double-stranded RNA was prepared by *in vitro* transcription using the T7 RiboMAX[TM] Express RNAi System (Promega). The sense strands of the resulting dsRNA for LD014_C1 and LD014_C2 are herein represented by SEQ ID NO 213 and2114, respectively.

Shorter sequences of target LD014 and concatemers were able to induce lethality in *Leptinotarsa decemlineata*, as shown in **Figure 4-LD**.

F. Screening dsRNAs at different concentrations using artificial diet for activity against *Leptinotarsa decemlineata*

Fifty µl of a solution of dsRNA at serial ten-fold concentrations from 1 µg/µl (for target LD027 from 0.1 µg/µl)down to 0.01 ng/µl was applied topically onto the solid artificial diet in the wells of a 24-well plate (Nunc). The diet was dried in a laminair flow cabin. Per treatment, twenty-four Colorado potato beetle larvae (2nd stage), with two insects per well, were tested. The plates were stored in the insect rearing chamber at 25 ± 2 °C, 60 % relative humidity, with a 16:8 hours light:dark photoperiod. The beetles were assessed as live or dead at regular intervals up to day 14. After seven days, the diet was replaced with fresh diet with topically applied dsRNA at the same concentrations. The dsRNA targets were compared to diet only.

Feeding artificial diet containing intact naked dsRNAs of different targets to *L. decemlineata* larvae resulted in high larval mortalities at concentrations as low as between 0.1 and 10 ng dsRNA/µl as shown in **Figure 5-LD**.

G. Cloning of a CPB gene fragment in a vector suitable for bacterial production of insect-active double-stranded RNA

While any efficient bacterial promoter may be used, a DNA fragment corresponding to an CPB gene target was cloned in a vector for the expression of double-stranded RNA in a bacterial host (See WO 00/01846).

The sequences of the specific primers used for the amplification of target genes are provided in **Table 8-LD**. The template used is the pCR8/GW/topo vector containing any of target sequences. The primers are used in a PCR reaction with the following conditions: 5 minutes at 98°C, followed by 30 cycles of 10 seconds at 98°C, 30 seconds at 55°C and 2 minutes at 72°C, followed by 10 minutes at 72°C. The resulting PCR fragment is analyzed on agarose gel, purified (QIAquick Gel Extraction kit, Cat. Nr. 28706, Qiagen), blunt-end cloned into *Srf* I-linearized pGNA49A vector (reference to WO00188121A1), and sequenced. The sequence of the resulting PCR product corresponds to the respective sequence as given in **Table 8-LD**. The recombinant vector harboring this sequence is named pGBNJ003.

The sequences of the specific primers used for the amplification of target gene fragment LD010 are provided in **Table 8-LD** (forward primer SEQ ID NO 191 and reverse primer SEQ ID NO 190). The template used was the pCR8/GW/topo vector containing the LD010 sequence (SEQ ID NO 11). The primers were used in a PCR reaction with the following conditions: 5 minutes at 98°C, followed by 30 cycles of 10 seconds at 98°C, 30 seconds at 55°C and 2 minutes at 72°C, followed by 10 minutes at 72°C. The resulting PCR fragment was analyzed on agarose gel, purified (QIAquick Gel Extraction kit, Cat. Nr. 28706, Qiagen), blunt-end cloned into *Srf* I-linearized pGNA49A vector (reference to WO 00/188121A1), and sequenced. The sequence of the resulting PCR product corresponds to SEQ ID NO 188 as given in **Table 8-LD**. The recombinant vector harboring this sequence was named pGBNJ003.

H. Expression and production of a double-stranded RNA target in two strains of *Escherichia coli*: **(1) AB301-105(DE3), and, (2) BL21(DE3)**

The procedures described below were followed in order to express suitable levels of insect-active double-stranded RNA of target LD010 in bacteria. An RNaseIII-deficient strain, AB301-105(DE3), was used in comparison to wild-type RNaseIII-containing bacteria, BL21(DE3).

Transformation of AB301-105(DE3) and BL21(DE3)

Three hundred ng of the plasmid was added to and gently mixed in a 50 µl aliquot of ice-chilled chemically competent *E.* coli strain AB301-105(DE3) or BL21(DE3). The cells were incubated on ice for 20 minutes before subjecting them to a heat shock treatment of 37 °C for 5 minutes, after which the cells were placed back on ice for a further 5 minutes. Four hundred and fifty µl of room temperature SOC medium was added to the cells and the suspension incubated on a shaker (250 rpm) at 37 °C for 1 hour. One hundred µl of the bacterial cell suspension was transferred to a 500 ml conical flask containing 150 ml of liquid Luria-Bertani (LB) broth supplemented with 100 µg/ml carbenicillin antibiotic. The culture was incubated on an Innova 4430 shaker (250 rpm) at 37 °C overnight (16 to 18 hours).

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Chemical induction of double-stranded RNA expression in AB301-105(DE3) and BL21(DE3)

Expression of double-stranded RNA from the recombinant vector, pGBNJ003, in the bacterial strain AB301-105(DE3) or BL21(DE3) was made possible since all the genetic components for controlled expression are present. In the presence of the chemical inducer isopropylthiogalactoside, or IPTG, the T7 polymerase will drive the transcription of the target sequence in both antisense and sense directions since these are flanked by oppositely oriented T7 promoters.

The optical density at 600 nm of the overnight bacterial culture was measured using an appropriate spectrophotometer and adjusted to a value of 1 by the addition of fresh LB broth. Fifty ml of this culture was transferred to a 50 ml Falcon tube and the culture then centrifuged at 3000 g at 15 °C for 10 minutes. The supernatant was removed and the bacterial pellet resuspended in 50 ml of fresh S complete medium (SNC medium plus 5 µg/ml cholesterol) supplemented with 100 µg/ml carbenicillin and 1 mM IPTG. The bacteria were induced for 2 to 4 hours at room temperature.

Heat treatment of bacteria

Bacteria were killed by heat treatment in order to minimize the risk of contamination of the artificial diet in the test plates. However, heat treatment of bacteria expressing double-stranded RNA is not a prerequisite for inducing toxicity towards the insects due to RNA interference. The induced bacterial culture was centrifuged at 3000 g at room temperature for 10 minutes, the supernatant discarded and the pellet subjected to 80 °C for 20 minutes in a water bath. After heat treatment, the bacterial pellet was resuspended in 1.5 ml MilliQ water and the suspension transferred to a microfuge tube. Several tubes were prepared and used in the bioassays for each refreshment. The tubes were stored at -20 °C until further use.

I. Laboratory trials to test Escherichia coli expressing dsRNA target LD010 against *Leptinotarsa decemlineata*

Two bioassay methods were employed to test double-stranded RNA produced in *Escherichia coli* against larvae of the Colorado potato beetle: (1) artificial diet-based bioassay, and, (2) plant-based bioassay.

Artificial diet-based bioassays

Artificial diet for the Colorado potato beetle was prepared as described previously in Example 3C. A half milliliter of diet was dispensed into each of the wells of a 48-well multiwell test plate (Nunc). For every treatment, fifty µl of an OD 1 suspension of heat-treated bacteria (which is equivalent to approximately 5×10^7 bacterial cells) expressing dsRNA was applied topically onto the solid diet in the wells and the plates were allowed to dry in a laminair flow cabin. Per treatment, forty-eight 2nd stage Colorado potato beetle larvae, one in each well containing diet and bacteria, were tested. Each row of a plate (i.e. 8 wells) was considered as one replicate. The plates were kept in the insect rearing chamber at 25 ± 2 °C, 60 ± 5 % relative humidity, with a 16:8 hours light:dark photoperiod. After every 4 days, the beetles were transferred to fresh diet containing

topically-applied bacteria. The beetles were assessed as alive or dead every one or three days post infestation. For the survivors, growth and development in terms of larval weight was recorded on day 7 post infestation.

For RNaseIII-deficient *E. coli* strain *AB301-105(DE3)*, bacteria containing plasmid pGBNJ003 and those containing the empty vector pGN29 (reference to WO 00/188121A1) were tested in bioassays for CPB toxicity. Bacteria harboring the pGBNJ003 plasmid showed a clear increase in insect mortality with time, whereas little or no mortality was observed for pGN29 and diet only control (**Figures 6a-LD & 7a-LD**). The growth and development of Colorado potato beetle larval survivors, 7 days after feeding on artificial diet containing bacteria expressing dsRNA target LD010, was severely impeded (**Table 10-LD, Figure 8a-LD, Figure 13-LD**).

For *E. coli* strain BL21(DE3), bacteria containing plasmid pGBNJ003 and those containing the empty vector pGN29 were tested against the Colorado potato beetle larvae. Similar detrimental effects were observed on larvae fed diet supplemented with BL21(DE3) bacteria as for the RNAseIII-deficient strain, AB301-105(DE3) (**Figures 6b-LD & 7b-LD**). However, the number of survivors for the five clones were higher for BL21(DE3) than for *AB301-105(DE3)*; at day 12, average mortality values were approximately 25 % lower for this strain compared to the RNase III deficient strain. Also, the average weights of survivors fed on diet containing BL21(DE3) expressing dsRNA corresponding to target LD010 was severely reduced (**Table 10-LD, Figure 8b-LD**).

The delay in growth and development of the CPB larvae fed on diet containing either of the two bacterial strains harboring plasmid pGBNJ003 was directly correlated to feeding inhibition since no frass was visible in the wells of refreshed plates from day 4 onwards when compared to bacteria harboring the empty vector pGN29 or the diet only plate. This observation was similar to that where CPB was fed on *in vitro* transcribed double-stranded RNA topically applied to artificial diet (see Example 3D); here, cessation of feeding occurred from day 2 onwards on treated diet.

Plant-based bioassays

Whole potato plants were sprayed with suspensions of chemically induced bacteria expressing dsRNA prior to feeding the plants to CPB larvae. The potato plants of variety "line V" (Wageningen University) were grown from tubers to the 8-12 unfolded leaf stage in a plant growth room chamber with the following conditions: 25 ± 2°C, 60 % relative humidity, 16:8 hour light:dark photoperiod. The plants were caged by placing a 500 ml plastic bottle upside down over the plant with the neck of the bottle firmly placed in the soil in a pot and the base cut open and covered with a fine nylon mesh to permit aeration, reduce condensation inside and prevent larval escape. Fifteen Colorado potato beetle larvae at the L1 stage were placed on each treated plant in the cage. Plants were treated with a suspension of *E. coli* AB301-105(DE3) harboring the pGBNJ003 plasmids (clone 1; **Figure 7a-LD**) or pGN29 plasmid (clone 1; see **Figure 7a-LD**). Different quantities of bacteria were applied to the plants: 66, 22, and 7 units, where one unit is defined as 10^9 bacterial cells in 1 ml of a bacterial suspension at optical density value of 1 at 600 nm wavelength. In each case, a total volume of 1.6 ml was sprayed on the plant with the aid of a

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· vaporizer. One plant was used per treatment in this trial. The number of survivors were counted and the weight of each survivor recorded.

Spraying plants with a suspension of *E. coli* bacterial strain AB301-105(DE3) expressing target dsRNA from pGBNJ003 led to a dramatic increase in insect mortality when compared to
5   pGN29 control. The mortality count was maintained when the amount of bacteria cell suspension was diluted 9-fold (**Figure 9-LD**). The average weights of the larval survivors at day 11 on plants sprayed with bacteria harboring the pGBNJ003 vector were approximately 10-fold less than that of pGN29 (**Figure 10-LD**). Feeding damage by CPB larvae of the potato plant sprayed with bacteria containing the pGBNJ003 plasmid was much reduced when compared to the damage incurred on
10   a potato plant sprayed with bacteria containing the empty vector pGN29 (**Figure 11-LD**).

These experiments showed that double-stranded RNA corresponding to an insect gene target sequence produced in either wild-type or RNaseIII-deficient bacterial expression systems is toxic towards the insect in terms of substantial increases in insect mortality and growth/development delay for larval survivors. It is also clear from these experiments that an
15   exemplification was provided for the effective protection of plants/crops from insect damage by the use of a spray of a formulation consisting of bacteria expressing double-stranded RNA corresponding to an insect gene target.

J. Testing various culture suspension densities of *Escherichia coli* expressing dsRNA target LD010 against *Leptinotarsa decemlineata*

20   Preparation and treatment of bacterial cultures are described in Example 3J. Three-fold serial dilutions of cultures (starting from 0.25 unit equivalents) of *Escherichia coli* RNAseIII-deficient strain AB301-105(DE3) expressing double-stranded RNA of target LD010 were applied to foliages of the potato plant of variety 'Bintje' at the 8-12 unfolded leaf stage. Ten L1 larvae of the *L. decemlineata* were placed on the treated plants with one plant per treatment. Scoring for insect
25   mortality and growth impediment was done on day 7 (i.e., 7 days post infestation).

As shown in **Figure 14-LD**, high CPB larval mortality (90 to 100 %) was recorded after 1 week when insects were fed potato plants treated with a topical application by fine spray of heat-inactivated cultures of *E.coli* harboring plasmid pGBNJ003 (for target 10 dsRNA expression) at densities 0.25, 0.08 and 0.025 bacterial units. At 0.008 units, about a third of the insects were
30   dead, however, the surviving insects were significantly smaller than those in the control groups (*E. coli* harboring the empty vector pGN29 and water only). Feeding damage by CPB larvae of the potato plant sprayed with bacteria containing the pGBNJ003 plasmid at concentrations 0.025 or 0.008 units was much reduced when compared to the damage incurred on a potato plant sprayed with bacteria containing the empty vector pGN29 (**Figure 15-LD**).

35   **K. Adults are extremely susceptible to orally ingested dsRNA corresponding to target genes.**

The example provided below highlights the finding that adult insects (and not only insects of the larval stage) are extremely susceptible to orally ingested dsRNA corresponding to target genes.

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Four targets were chosen for this experiment: targets 2, 10, 14 and 16 (SEQ ID NO 168, 188, 198 and 220, respectively). GFP fragment dsRNA (SEQ ID NO 235) was used as a control. Young adults (2 to 3 days old) were picked at random from our laboratory-reared culture with no bias towards insect gender. Ten adults were chosen per treatment. The adults were prestarved for
5   at least 6 hours before the onset of the treatment. On the first day of treatment, each adult was fed four potato leaf discs (diameter 1.5 cm^2) which were pretreated with a topical application of 25 µl of 0.1µg/µl target dsRNA (synthesized as described in Example 3A; topical application as described in Example 3E) per disc. Each adult was confined to a small petridish (diameter 3 cm) in order to make sure that all insects have ingested equal amounts of food and thus received equal doses of
10   dsRNA. The following day, each adult was again fed four treated leaf discs as described above. On the third day, all ten adults per treatment were collected and placed together in a cage consisting of a plastic box (dimensions 30 cm x 20 cm x 15 cm) with a fine nylon mesh built into the lid to provide good aeration. Inside the box, some moistened filter paper was placed in the base. Some (untreated) potato foliage was placed on top of the paper to maintain the adults during the
15   experiment. From day 5, regular assessments were carried out to count the number of dead, alive (mobile) and moribund insects. For insect moribundity, adults were laid on their backs to check whether they could right themselves within several minutes; an insect was considered moribund only if it was not able to turn onto its front.

Clear specific toxic effects of double-stranded RNA correpsonding to different targets
20   towards adults of the Colorado potato beetle, *Leptinotarsa decemlineata*, were demonstrated in this experiment (**Figure 12-LD**). Double-stranded RNA corresponding to a gfp fragment showed no toxicity towards CPB adults on the day of the final assessment (day 19). This experiment clearly showed that the survival of CPB adults was severely reduced only after a few days of exposure to dsRNA when delivered orally. For example, for target 10, on day 5, 5 out of 10 adults were
25   moribund (sick and slow moving); on day 6, 4 out of 10 adults were dead with three of the survivors moribund; on day 9 all adults were observed dead.

As a consequence of this experiment, the application of target double-stranded RNAs against insect pests may be broadened to include the two life stages of an insect pest (i.e. larvae and adults) which could cause extensive crop damage, as is the case with the Colorado potato
30   beetle.

Example 4: *Phaedon cochleariae* (Mustard leaf beetle)

A. Cloning of a partial sequence of the *Phaedon cochleariae* (mustard leaf beetle) PC001, PC003, PC005, PC010, PC014, PC016 and PC027 genes via family PCR

35   High quality, intact RNA was isolated from the third larval stage of *Phaedon cochleariae* (mustard leaf beetle; source: Dr. Caroline Muller, Julius-von-Sachs-Institute for Biosciences, Chemical Ecology Group, University of Wuerzburg, Julius-von-Sachs-Platz 3, D-97082 Wuerzburg, Germany) using TRIzol Reagent (Cat. Nr. 15596-026/15596-018, Invitrogen, Rockville, Maryland, USA) following the manufacturer's instructions. Genomic DNA present in the RNA preparation was

removed by DNase (Cat. Nr. 1700, Promega) treatment following the manufacturer's instructions. cDNA was generated using a commercially available kit (SuperScript ™ III Reverse Transcriptase, Cat. Nr. 18080044, Invitrogen, Rockville, Maryland, USA) following the manufacturer's instructions.

5   To isolate cDNA sequences comprising a portion of the PC001, PC003, PC005, PC010, PC014, PC016 and PC027 genes, a series of PCR reactions with degenerate primers were performed using Amplitaq Gold (Cat. Nr. N8080240, Applied Biosystems) following the manafacturer's instructions.

       The sequences of the degenerate primers used for amplification of each of the genes are given in **Table 2-PC**. These primers were used in respective PCR reactions with the following
10   conditions: 10 minutes at 95°C, followed by 40 cycles of 30 seconds at 95°C, 1 minute at 55°C and 1 minute at 72°C, followed by 10 minutes at 72°C. The resulting PCR fragments were analyzed on agarose gel, purified (QIAquick Gel Extraction kit, Cat. Nr. 28706, Qiagen), cloned into the pCR4/TOPO vector (Cat. Nr. K4530-20, Invitrogen) and sequenced. The sequences of the resulting PCR products are represented by the respective SEQ ID NOs as given in **Table 2-PC** and
15   are referred to as the partial sequences.

       The corresponding partial amino acid sequence are represented by the respective SEQ ID NOs as given in **Table 3-PC.** Table 3-PC provides amino acid sequences of cDNA clones, and the start of the reading frame is indicated in brackets.

B. dsRNA production of the *Phaedon cochleariae* genes

20   dsRNA was synthesized in milligram amounts using the commercially available kit T7 Ribomax™ Express RNAi System (Cat. Nr. P1700, Promega). First two separate single 5' T7 RNA polymerase promoter templates were generated in two separate PCR reactions, each reaction containing the target sequence in a different orientation relative to the T7 promoter.

       For each of the target genes, the sense T7 template was generated using specific T7
25   forward and specific reverse primers. The sequences of the respective primers for amplifying the sense template for each of the target genes are given in **Table 8-PC**. Table 8-PC provides details for preparing ds RNA fragments of *Phaedon cochleariae* target sequences, including primer sequences.

       The conditions in the PCR reactions were as follows: 1 minute at 95°C, followed by 20
30   cycles of 30 seconds at 95°C, 30 seconds at 60°C and 1 minute at 72°C, followed by 15 cycles of 30 seconds at 95°C, 30 seconds at 50°C and 1 minute at 72°C followed by 10 minutes at 72°C. The anti-sense T7 template was generated using specific forward and specific T7 reverse primers in a PCR reaction with the same conditions as described above. The sequences of the respective primers for amplifying the anti-sense template for each of the target genes are given in **Table 8-PC**.
35   The resulting PCR products were analyzed on agarose gel and purified by PCR purification kit (Qiaquick PCR Purification Kit, Cat. Nr. 28106, Qiagen) and NaClO₄ precipitation. The generated T7 forward and reverse templates were mixed to be transcribed and the resulting RNA strands were annealed, DNase and RNase treated, and purified by sodium acetate, following the

manufacturer's instructions. The sense strand of the resulting dsRNA for each of the target genes is given in **Table 8-PC**.

C. Laboratory trials of *Myzus periscae* (green peach aphid) infestation on transgenic *Arabidopsis thaliana* plants

5   *Generation of transgenic plants*

Arabidopsis thaliana plants were transformed using the floral dip method (Clough and Bent (1998) *Plant Journal* 16:735-743). Aerial parts of the plants were incubated for a few seconds in a solution containing 5% sucrose, resuspended *Agrobacterium tumefaciens* strain C58C1 Rif cells from an overnight culture and 0.03% of the surfactant Silwet L-77. After inoculation, plants were

10   covered for 16 hours with a transparent plastic to maintain humidity. To increase the transformation efficiency, the procedure was repeated after one week. Watering was stopped as seeds matured and dry seeds were harvested and cold-treated for two days. After sterilization, seeds were plated on a kanamycin-containing growth medium for selection of transformed plants.

The selected plants are transferred to soil for optimal T2 seed production.

15   *Bioassay*

Transgenic *Arabidopsis thaliana* plants are selected by allowing the segregating T2 seeds to germinate on appropriate selection medium. When the roots of these transgenics are well-established they are then transferred to fresh artificial growth medium or soil and allowed to grow under optimal conditions. Whole transgenic plants are tested against nymphs of the green peach

20   aphid (*Myzus persicae*) to show (1) a significant resistance to plant damage by the feeding nymph, (2) increased nymphal mortality, and/or (3) decreased weight of nymphal survivors (or any other aberrant insect development).

D. Laboratory trials to test dsRNA targets, using oilseed rape leaf discs for activity against *Phaedon cochleariae* larvae

25   The example provided below is an exemplification of the finding that the mustard leaf beetle (MLB) larvae are susceptible to orally ingested dsRNA corresponding to own target genes.

To test the different double-stranded RNA samples against MLB larvae, a leaf disc assay was employed using oilseed rape (*Brassica napus* variety SW Oban; source: Nick Balaam, Sw Seed Ltd., 49 North Road, Abington, Cambridge, CB1 6AS, UK) leaf material as food source. The

30   insect cultures were maintained on the same variety of oilseed rape in the insect chamber at 25 ± 2 °C and 60 ± 5 % relative humidity with a photoperiod of 16h light/8h dark. Discs of approximately 1.1 cm in diameter (or 0.95 cm^2) were cut out off leaves of 4- to 6-week old rape plants using a suitably-sized cork borer. Double-stranded RNA samples were diluted to 0.1 µg/µl in Milli-Q water containing 0.05% Triton X-100. Treated leaf discs were prepared by applying 25 µl of the diluted

35   solution of target PC001, PC003, PC005, PC010, PC014, PC016, PC027 dsRNA and control gfp dsRNA or 0.05 % Triton X-100 on the adaxial leaf surface. The leaf discs were left to dry and placed individually in each of the 24 wells of a 24-well multiplate containing 1 ml of gellified 2% agar which helps to prevent the leaf disc from drying out. Two neonate MLB larvae were placed into each well of the plate, which was then covered with a multiwell plastic lid. The plate (one

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treatment containing 48 insects) was divided into 4 replicates of 12 insects per replicate (each row). The plate containing the insects and leaf discs were kept in an insect chamber at 25 ± 2 °C and 60 ± 5 % relative humidity with a photoperiod of 16h light/8h dark. The insects were fed leaf discs for 2 days after which they were transferred to a new plate containing freshly treated leaf discs.

5 Thereafter, 4 days after the start of the bioassay, the insects from each replicate were collected and transferred to a Petri dish containing untreated fresh oilseed rape leaves. Larval mortality and average weight were recorded at days 2, 4 7, 9 and 11.

P. cochleariae larvae fed on intact naked target dsRNA-treated oilseed rape leaves resulted in significant increases in larval mortalities for all targets tested, as indicated in Figure 1(a).

10 Tested double-stranded RNA for target PC010 led to 100 % larval mortality at day 9 and for target PC027 at day 11. For all other targets, signficantly high mortality values were reached at day 11 when compared to control gfp dsRNA, 0.05% Trition X-100 alone or untreated leaf only: (average value in percentage ± confidence interval with alpha 0.05) PC001 (94.4 ± 8.2); PC003 (86.1 ± 4.1); PC005 (83.3 ± 7.8); PC014 (63.9 ± 20.6); PC016 (75.0 ± 16.8); gfp dsRNA (11.1 ± 8.2); 0.05%

15 Trition X-100 (19.4 ± 10.5); leaf only (8.3 ± 10.5).

Larval survivors were assessed based on their average weight. For all targets tested, the mustard leaf beetle larvae had significantly reduced average weights after day 4 of the bioassay; insects fed control gfp dsRNA or 0.05% Triton X-100 alone developed normally, as for the larvae on leaf only (Figure 1(b)-PC).

20 **E. Laboratory trials to screen dsRNAs at different concentrations using oilseed rape leaf discs for activity against Phaedon cochleariae larvae**

Twenty-five µl of a solution of dsRNA from target PC010 or PC027 at serial ten-fold concentrations from 0.1 µg/µl down to 0.1 ng/µl was applied topically onto the oilseed rape leaf disc, as described in Example 4D above. As a negative control, 0.05% Triton X-100 only was

25 administered to the leaf disc. Per treatment, twenty-four mustard leaf beetle neonate larvae, with two insects per well, were tested. The plates were stored in the insect rearing chamber at 25 ± 2 °C, 60 ± 5 % relative humidity, with a 16:8 hours light:dark photoperiod. At day 2, the larvae were transferred on to a new plate containing fresh dsRNA-treated leaf discs. At day 4 for target PC010 and day 5 for target PC027, insects from each replicate were transferred to a Petri dish containing

30 abundant untreated leaf material. The beetles were assessed as live or dead on days 2, 4, 7, 8, 9, and 11 for target PC010, and 2, 5, 8, 9 and 12 for target PC027.

Feeding oilseed rape leaf discs containing intact naked dsRNAs of the two different targets, PC010 and PC027, to P. cochleariae larvae resulted in high mortalities at concentrations down to as low as 1 ng dsRNA/µl solution, as shown in Figures 2 (a) and (b). Average mortality values in

35 percentage ± confidence interval with alpha 0.05 for different concentrations of dsRNA for target PC010 at day 11, 0 µg/µl: 8.3 ± 9.4; 0.1 µg/µl: 100; 0.01 µg/µl: 79.2 ± 20.6; 0.001 µg/µl: 58.3 ± 9.4; 0.0001 µg/µl: 12.5 ± 15.6; and for target PC027 at day 12, 0 µg/µl: 8.3 ± 9.4; 0.1 µg/µl: 95.8 ± 8.2; 0.01 µg/µl: 95.8 ± 8.2; 0.001 µg/µl: 83.3 ± 13.3; 0.0001 µg/µl: 12.5 ± 8.2.

F. Cloning of a MLB gene fragment in a vector suitable for bacterial production of insect-active double-stranded RNA

What follows is an example of cloning a DNA fragment corresponding to an MLB gene target in a vector for the expression of double-stranded RNA in a bacterial host, although any vector comprising a T7 promoter or any other promoter for efficient transcription in bacteria, may be used (reference to WO0001846):

The sequences of the specific primers used for the amplification of target gene fragment PC010 are provided in **Table 8-PC**. The template used was the pCR8/GW/topo vector containing the PC010 sequence (SEQ ID NO 253). The primers were used in a touch-down PCR reaction with the following conditions: 1 minute at 95°C, followed by 20 cycles of 30 seconds at 95°C, 30 seconds at 60°C with temperature decrease of -0.5 °C per cycle and 1 minute at 72°C, followed by 15 cycles of 30 seconds at 95°C, 30 seconds at 50°C and 1 minute at 72°C, followed by 10 minutes at 72°C. The resulting PCR fragment was analyzed on agarose gel, purified (QIAquick Gel Extraction kit, Cat. Nr. 28706, Qiagen), blunt-end cloned into *Srf* I-linearized pGNA49A vector (reference to WO00188121A1), and sequenced. The sequence of the resulting PCR product corresponds to SEQ ID NO 488 as given in **Table 8-PC**. The recombinant vector harboring this sequence was named pGCDJ001.

G. Expression and production of a double-stranded RNA target in one strain of *Escherichia coli* AB301-105(DE3)

The procedures described below are followed in order to express suitable levels of insect-active double-stranded RNA of insect target in bacteria. In this experiment, an RNaseIII-deficient strain, AB301-105(DE3) was used.

Transformation of AB301-105(DE3)

Three hundred ng of the plasmid were added to and gently mixed in a 50 µl aliquot of ice-chilled chemically competent *E. coli* strain AB301-105(DE3). The cells were incubated on ice for 20 minutes before subjecting them to a heat shock treatment of 37 °C for 5 minutes, after which the cells were placed back on ice for a further 5 minutes. Four hundred and fifty µl of room temperature SOC medium was added to the cells and the suspension incubated on a shaker (250 rpm) at 37 °C for 1 hour. One hundred µl of the bacterial cell suspension was transferred to a 500 ml conical flask containing 150 ml of liquid Luria-Bertani (LB) broth supplemented with 100 µg/ml carbenicillin antibiotic. The culture was incubated on an Innova 4430 shaker (250 rpm) at 37 °C overnight (16 to 18 hours).

Chemical induction of double-stranded RNA expression in AB301-105(DE3)

Expression of double-stranded RNA from the recombinant vector, pGXXX0XX, in the bacterial strain AB301-105(DE3) was made possible since all the genetic components for controlled expression are present. In the presence of the chemical inducer isopropylthiogalactoside, or IPTG, the T7 polymerase will drive the transcription of the target sequence in both antisense and sense directions since these are flanked by oppositely oriented T7 promoters.

The optical density at 600 nm of the overnight bacterial culture was measured using an appropriate spectrophotometer and adjusted to a value of 1 by the addition of fresh LB broth. Fifty ml of this culture was transferred to a 50 ml Falcon tube and the culture then centrifuged at 3000 g at 15 °C for 10 minutes. The supernatant was removed and the bacterial pellet resuspended in 50 ml of fresh S complete medium (SNC medium plus 5 µg/ml cholesterol) supplemented with 100 µg/ml carbenicillin and 1 mM IPTG. The bacteria were induced for 2 to 4 hours at room temperature.

Heat treatment of bacteria

Bacteria were killed by heat treatment in order to minimize the risk of contamination of the artificial diet in the test plates. However, heat treatment of bacteria expressing double-stranded RNA is not a prerequisite for inducing toxicity towards the insects due to RNA interference. The induced bacterial culture was centrifuged at 3000 g at room temperature for 10 minutes, the supernatant discarded and the pellet subjected to 80 °C for 20 minutes in a water bath. After heat treatment, the bacterial pellet was resuspended in a total volume of 50 ml of 0.05% Triton X-100 solution. The tube was stored at 4 °C until further use

H. Laboratory trials to test *Escherichia coli* expressing dsRNA target against *Phaedon cochleariae*

Leaf disc bioassays

The leaf-disc bioassay method was employed to test double-stranded RNA from target PC010 produced in *Escherichia coli* (from plasmid pGCDJ001) against larvae of the mustard leaf beetle. Leaf discs were prepared from oilseed rape foliage, as described in Example 4. Twenty µl of a bacterial suspension, with an optical density measurement of 1 at 600 nm wavelength, was pipetted onto each disc. The leaf disc was placed in a well of a 24-multiwell plate containing 1 ml gellified agar. On each leaf disc were added two neonate larvae. For each treatment, 3 replicates of 16 neonate larvae per replicate were prepared. The plates were kept in the insect rearing chamber at 25 ± 2 °C and 60 ± 5 % relative humidity, with a 16:8 hours light:dark photoperiod. At day 3 (i.e. 3 days post start of bioassay), larvae were transferred to a new plate containing fresh treated (same dosage) leaf discs. The leaf material was refreshed every other day from day 5 onwards. The bioassay was scored on mortality and average weight. Negative controls were leaf discs treated with bacteria harboring plasmid pGN29 (empty vector) and leaf only.

A clear increase in mortality of *P. cochleariae* larvae with time was shown after the insects were fed on oilseed rape leaves treated with a suspension of RNaseIII-deficient *E. coli* strain AB301-105(DE3) containing plasmid pGCDJ001, whereas very little or no insect mortality was observed in the case of bacteria with plasmid pGN29 or leaf only control (**Figure 3-PC**).

Plant-based bioassays

Whole plants are sprayed with suspensions of heat-inactivated chemically induced bacteria expressing dsRNA prior to feeding the plants to MLB. The are grown from in a plant growth room chamber. The plants are caged by placing a 500 ml plastic bottle upside down over the plant with the neck of the bottle firmly placed in the soil in a pot and the base cut open and covered with a

fine nylon mesh to permit aeration, reduce condensation inside and prevent insect escape. MLB are placed on each treated plant in the cage. Plants are treated with a suspension of *E. coli* AB301-105(DE3) harboring the pGCDJ001 plasmids or pGN29 plasmid. Different quantities of bacteria are applied to the plants: for instance 66, 22, and 7 units, where one unit is defined as 10^9 bacterial cells in 1 ml of a bacterial suspension at optical density value of 1 at 600 nm wavelength. In each case, a total volume of between 1 and 10 ml s sprayed on the plant with the aid of a vaporizer. One plant is used per treatment in this trial. The number of survivors are counted and the weight of each survivor recorded.

Spraying plants with a suspension of *E. coli* bacterial strain AB301-105(DE3) expressing target dsRNA from pGCDJ001 leads to a dramatic increase in insect mortality when compared to pGN29 control. These experiments show that double-stranded RNA corresponding to an insect gene target sequence produced in either wild-type or RNaseIII-deficient bacterial expression systems is toxic towards the insect in terms of substantial increases in insect mortality and growth/development delay for larval survivors. It is also clear from these experiments that an exemplification is provided for the effective protection of plants/crops from insect damage by the use of a spray of a formulation consisting of bacteria expressing double-stranded RNA corresponding to an insect gene target.

Example 5: *Epilachna varivetis* (Mexican bean beetle)

A. Cloning *Epilachna varivetis* partial gene sequences

High quality, intact RNA was isolated from 4 different larval stages of *Epilachna varivetis* (Mexican bean beetle; source: Thomas Dorsey, Supervising Entomologist, New Jersey Department of Agriculture, Division of Plant Industry, Bureau of Biological Pest Control, Phillip Alampi Beneficial Insect Laboratory, PO Box 330, Trenton, New Jersey 08625-0330, USA) using TRIzol Reagent (Cat. Nr. 15596-026/15596-018, Invitrogen, Rockville, Maryland, USA) following the manufacturer's instructions. Genomic DNA present in the RNA preparation was removed by DNase treatment following the manafacturer's instructions (Cat. Nr. 1700, Promega). cDNA was generated using a commercially available kit (SuperScript ™ III Reverse Transcriptase, Cat. Nr. 18080044, Invitrogen, Rockville, Maryland, USA) following the manufacturer's instructions.

To isolate cDNA sequences comprising a portion of the EV005, EV009, EV010, EV015 and EV016 genes, a series of PCR reactions with degenerate primers were performed using Amplitaq Gold (Cat. Nr. N8080240, Applied Biosystems) following the manufacturer's instructions.

The sequences of the degenerate primers used for amplification of each of the genes are given in **Table 2-EV**, which displays *Epilachna varivetis* target genes including primer sequences and cDNA sequences obtained. These primers were used in respective PCR reactions with the following conditions: for EV005 and EV009, 10 minutes at 95°C, followed by 40 cycles of 30 seconds at 95°C, 1 minute at 50°C and 1 minute 30 seconds at 72°C, followed by 7 minutes at 72°C; for EV014, 10 minutes at 95°C, followed by 40 cycles of 30 seconds at 95°C, 1 minute at 53°C and 1 minute at 72°C, followed by 7 minutes at 72°C; for EV010 and EV016, 10 minutes at

95°C, followed by 40 cycles of 30 seconds at 95°C, 1 minute at 54°C and 1 minute 40 seconds at 72°C, followed by 7 minutes at 72°C. The resulting PCR fragments were analyzed on agarose gel, purified (QIAquick Gel Extraction kit, Cat. Nr. 28706, Qiagen), cloned into the pCR4/TOPO vector (Cat. Nr. K4530-20, Invitrogen), and sequenced. The sequences of the resulting PCR products are

5   represented by the respective SEQ ID NOs as given in **Table 2-EV** and are referred to as the partial sequences. The corresponding partial amino acid sequences are represented by the respective SEQ ID NOs as given in **Table 3-EV**, where the start of the reading frame is indicated in brackets.

B. dsRNA production of the *Epilachna varivetis* genes

10   dsRNA was synthesized in milligram amounts using the commercially available kit T7 Ribomax™ Express RNAi System (Cat. Nr. P1700, Promega). First two separate single 5' T7 RNA polymerase promoter templates were generated in two separate PCR reactions, each reaction containing the target sequence in a different orientation relative to the T7 promoter.

For each of the target genes, the sense T7 template was generated using specific T7

15   forward and specific reverse primers. The sequences of the respective primers for amplifying the sense template for each of the target genes are given in **Table 8-EV**.

The conditions in the PCR reactions were as follows: 1 minute at 95°C, followed by 20 cycles of 30 seconds at 95°C, 30 seconds at 60°C and 1 minute at 72°C, followed by 15 cycles of 30 seconds at 95°C, 30 seconds at 50°C and 1 minute at 72°C followed by 10 minutes at 72°C.

20   The anti-sense T7 template was generated using specific forward and specific T7 reverse primers in a PCR reaction with the same conditions as described above. The sequences of the respective primers for amplifying the anti-sense template for each of the target genes are given in **Table 8-EV**. The resulting PCR products were analyzed on agarose gel and purified by PCR purification kit (Qiaquick PCR Purification Kit, Cat. Nr. 28106, Qiagen) and NaClO$_4$ precipitation. The generated

25   T7 forward and reverse templates were mixed to be transcribed and the resulting RNA strands were annealed, DNase and RNase treated, and purified by sodium acetate, following the manufacturer's instructions. The sense strand of the resulting dsRNA for each of the target genes is given in **Table 8-EV**.

C. Laboratory trials to test dsRNA targets using bean leaf discs for activity against

30   *Epilachna varivetis* larvae

The example provided below is an exemplification of the finding that the Mexican bean beetle (MBB) larvae are susceptible to orally ingested dsRNA corresponding to own target genes.

To test the different double-stranded RNA samples against MBB larvae, a leaf disc assay was employed using snap bean (*Phaseolus vulgaris* variety Montano; source: Aveve NV, Belgium)

35   leaf material as food source. The same variety of beans was used to maintain insect cultures in the insect chamber at 25 ± 2 °C and 60 ± 5 % relative humidity with a photoperiod of 16h light/8h dark. Discs of approximately 1.1 cm in diameter (or 0.95 cm^2) were cut out off leaves of 1- to 2-week old bean plants using a suitably-sized cork borer. Double-stranded RNA samples were diluted to 1 µg/µl in Milli-Q water containing 0.05% Triton X-100. Treated leaf discs were prepared by applying

25 µl of the diluted solution of target Ev005, Ev010, Ev015, Ev016 dsRNA and control gfp dsRNA or 0.05 % Triton X-100 on the adaxial leaf surface. The leaf discs were left to dry and placed individually in each of the 24 wells of a 24-well multiplate containing 1 ml of gellified 2 % agar which helps to prevent the leaf disc from drying out. A single neonate MBB larva was placed into each

5   well of a plate, which was then covered with a multiwell plastic lid. The plate was divided into 3 replicates of 8 insects per replicate (row). The plate containing the insects and leaf discs were kept in an insect chamber at 25 ± 2 °C and 60 ± 5 % relative humidity with a photoperiod of 16h light/8h dark. The insects were fed on the leaf discs for 2 days after which the insects were transferred to a new plate containing freshly treated leaf discs. Thereafter, 4 days after the start of the bioassay,

10   the insects were transferred to a petriplate containing untreated fresh bean leaves every day until day 10. Insect mortality was recorded at day 2 and every other day thereafter.

Feeding snap bean leaves containing surface-applied intact naked target dsRNAs to *E. varivestis* larvae resulted in significant increases in larval mortalities, as indicated in Figure 1. Tested double-stranded RNAs of targets Ev010, Ev015, & Ev016 led to 100 % mortality after 8

15   days, whereas dsRNA of target Ev005 took 10 days to kill all larvae. The majority of the insects fed on treated leaf discs containing control gfp dsRNA or only the surfactant Triton X-100 were sustained throughout the bioassay **(Figure 1-EV)**.

D. Laboratory trials to test dsRNA targets using bean leaf discs for activity against *Epilachna varivestis* adults

20   The example provided below is an exemplification of the finding that the Mexican bean beetle adults are susceptible to orally ingested dsRNA corresponding to own target genes.

In a similar bioassay set-up as for Mexican bean beetle larvae, adult MBBs were tested against double-stranded RNAs topically-applied to bean leaf discs. Test dsRNA from each target Ev010, Ev015 and Ev016 was diluted in 0.05 % Triton X-100 to a final concentration of 0.1 µg/µl.

25   Bean leaf discs were treated by topical application of 30 µl of the test solution onto each disc. The discs were allowed to dry completely before placing each on a slice of gellified 2 % agar in each well of a 24-well multiwell plate. Three-day-old adults were collected from the culture cages and fed nothing for 7-8 hours prior to placing one adult to each well of the bioassay plate (thus 24 adults per treatment). The plates were kept in the insect rearing chamber (under the same conditions as

30   for MBB larvae for 24 hours) after which the adults were transferred to a new plate containing fresh dsRNA-treated leaf discs. After a further 24 hours, the adults from each treatment were collected and placed in a plastic box with dimensions 30 cm x 15 cm x 10 cm containing two potted and untreated 3-week-old bean plants. Insect mortality was assessed from day 4 until day 11.

All three target dsRNAs (Ev010, Ev015 and Ev016) ingested by adults of *Epilachna*

35   *varivestis* resulted in significant increases in mortality from day 4 (4 days post bioassay start), as shown in **Figure 2(a)-EV**. From day 5, dramatic changes in feeding patterns were observed between insects fed initially with target-dsRNA-treated bean leaf discs and those that were fed discs containing control gfp dsRNA or surfactant Triton X-100. Reductions in foliar damage by MBB adults of untreated bean plants were clearly visible for all three targets when compared to gfp

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dsRNA and surfactant only controls, albeit at varying levels; insects fed target 15 caused the least damage to bean foliage (**Figure 2(b)-EV**).

E. Cloning of a MBB gene fragment in a vector suitable for bacterial production of insect-active double-stranded RNA

5   What follows is an example of cloning a DNA fragment corresponding to an MBB gene target in a vector for the expression of double-stranded RNA in a bacterial host, although any vector comprising a T7 promoter or any other promoter for efficient transcription in bacteria, may be used (reference to WO0001846).

The sequences of the specific primers used for the amplification of target genes are

10   provided in **Table 8-EV**. The template used is the pCR8/GW/topo vector containing any of target sequences. The primers are used in a PCR reaction with the following conditions: 5 minutes at 98°C, followed by 30 cycles of 10 seconds at 98°C, 30 seconds at 55°C and 2 minutes at 72°C, followed by 10 minutes at 72°C. The resulting PCR fragment is analyzed on agarose gel, purified (QIAquick Gel Extraction kit, Cat. Nr. 28706, Qiagen), blunt-end cloned into *Srf* I-linearized

15   pGNA49A vector (reference to WO00188121A1), and sequenced. The sequence of the resulting PCR product corresponds to the respective sequence as given in **Table 8-EV**. The recombinant vector harboring this sequence is named pGXXX0XX.

F. Expression and production of a double-stranded RNA target in two strains of *Escherichia coli*: (1) AB301-105(DE3), and, (2) BL21(DE3)

20   The procedures described below are followed in order to express suitable levels of insect-active double-stranded RNA of insect target in bacteria. An RNaseIII-deficient strain, AB301-105(DE3), is used in comparison to wild-type RNaseIII-containing bacteria, BL21(DE3).

Transformation of AB301-105(DE3) and BL21(DE3)

Three hundred ng of the plasmid are added to and gently mixed in a 50 μl aliquot of ice-

25   chilled chemically competent *E. coli* strain AB301-105(DE3) or BL21(DE3). The cells are incubated on ice for 20 minutes before subjecting them to a heat shock treatment of 37 °C for 5 minutes, after which the cells are placed back on ice for a further 5 minutes. Four hundred and fifty μl of room temperature SOC medium is added to the cells and the suspension incubated on a shaker (250 rpm) at 37 °C for 1 hour. One hundred μl of the bacterial cell suspension is transferred to a 500 ml

30   conical flask containing 150 ml of liquid Luria-Bertani (LB) broth supplemented with 100 μg/ml carbenicillin antibiotic. The culture is incubated on an Innova 4430 shaker (250 rpm) at 37 °C overnight (16 to 18 hours).

Chemical induction of double-stranded RNA expression in AB301-105(DE3) and BL21(DE3)

Expression of double-stranded RNA from the recombinant vector, pGXXX0XX, in the

35   bacterial strain AB301-105(DE3) or BL21(DE3) is made possible since all the genetic components for controlled expression are present. In the presence of the chemical inducer isopropylthiogalactoside, or IPTG, the T7 polymerase will drive the transcription of the target sequence in both antisense and sense directions since these are flanked by oppositely oriented T7 promoters.

The optical density at 600 nm of the overnight bacterial culture is measured using an appropriate spectrophotometer and adjusted to a value of 1 by the addition of fresh LB broth. Fifty ml of this culture is transferred to a 50 ml Falcon tube and the culture then centrifuged at 3000 g at 15 °C for 10 minutes. The supernatant is removed and the bacterial pellet resuspended in 50 ml of

5   fresh S complete medium (SNC medium plus 5 µg/ml cholesterol) supplemented with 100 µg/ml carbenicillin and 1 mM IPTG. The bacteria are induced for 2 to 4 hours at room temperature.

Heat treatment of bacteria

Bacteria are killed by heat treatment in order to minimize the risk of contamination of the artificial diet in the test plates. However, heat treatment of bacteria expressing double-stranded

10   RNA is not a prerequisite for inducing toxicity towards the insects due to RNA interference. The induced bacterial culture is centrifuged at 3000 g at room temperature for 10 minutes, the supernatant discarded and the pellet subjected to 80 °C for 20 minutes in a water bath. After heat treatment, the bacterial pellet is resuspended in 1.5 ml MilliQ water and the suspension transferred to a microfuge tube. Several tubes are prepared and used in the bioassays for each refreshment.

15   The tubes are stored at -20 °C until further use.

G. Laboratory trials to test *Escherichia coli* expressing dsRNA targets against *Epilachna varivetis*

Plant-based bioassays

Whole plants are sprayed with suspensions of chemically induced bacteria expressing

20   dsRNA prior to feeding the plants to MBB. The are grown from in a plant growth room chamber. The plants are caged by placing a 500 ml plastic bottle upside down over the plant with the neck of the bottle firmly placed in the soil in a pot and the base cut open and covered with a fine nylon mesh to permit aeration, reduce condensation inside and prevent insect escape. MMB are placed on each treated plant in the cage. Plants are treated with a suspension of *E. coli* AB301-105(DE3)

25   harboring the pGBNJ001 plasmids or pGN29 plasmid. Different quantities of bacteria are applied to the plants: for instance 66, 22, and 7 units, where one unit is defined as 10^9 bacterial cells in 1 ml of a bacterial suspension at optical density value of 1 at 600 nm wavelength. In each case, a total volume of between 1 and 10 ml s sprayed on the plant with the aid of a vaporizer. One plant is used per treatment in this trial. The number of survivors are counted and the weight of each

30   survivor recorded.

Spraying plants with a suspension of *E. coli* bacterial strain AB301-105(DE3) expressing target dsRNA from pGXXX0XX lead to a dramatic increase in insect mortality when compared to pGN29 control. These experiments show that double-stranded RNA corresponding to an insect gene target sequence produced in either wild-type or RNaseIII-deficient bacterial expression

35   systems is toxic towards the insect in terms of substantial increases in insect mortality and growth/development delay for larval survivors. It is also clear from these experiments that an exemplification is provided for the effective protection of plants/crops from insect damage by the use of a spray of a formulation consisting of bacteria expressing double-stranded RNA corresponding to an insect gene target.

Example 6: *Anthonomus grandis* (Cotton boll weevil)

A. Cloning *Anthonomus grandis* partial sequences

High quality, intact RNA was isolated from the 3 instars of *Anthonomus grandis* (cotton boll weevil; source: Dr. Gary Benzon, Benzon Research Inc., 7 Kuhn Drive, Carlisle, Pennsylvania 17013, USA) using TRIzol Reagent (Cat. Nr. 15596-026/15596-018, Invitrogen, Rockville, Maryland, USA) following the manufacturer's instructions. Genomic DNA present in the RNA preparation was removed by DNase treatment following the manafacturer's instructions (Cat. Nr. 1700, Promega). cDNA was generated using a commercially available kit (SuperScript ™ III Reverse Transcriptase, Cat. Nr. 18080044, Invitrogen, Rockville, Maryland, USA) following the manufacturer's instructions.

To isolate cDNA sequences comprising a portion of the AG001, AG005, AG010, AG014 and AG016 genes, a series of PCR reactions with degenerate primers were performed using Amplitaq Gold (Cat. Nr. N8080240, Applied Biosystems) following the manafacturer's instructions.

The sequences of the degenerate primers used for amplification of each of the genes are given in **Table 2-AG**. These primers were used in respective PCR reactions with the following conditions: for AG001, AG005 and AG016, 10 minutes at 95°C, followed by 40 cycles of 30 seconds at 95°C, 1 minute at 50°C and 1 minute and 30 seconds at 72°C, followed by 7 minutes at 72°C; for AG010, 10 minutes at 95°C, followed by 40 cycles of 30 seconds at 95°C, 1 minute at 54°C and 2 minutes and 30 seconds at 72°C, followed by 7 minutes at 72°C; for AG014, 10 minutes at 95°C, followed by 40 cycles of 30 seconds at 95°C, 1 minute at 55°C and 1 minute at 72°C, followed by 7 minutes at 72°C. The resulting PCR fragments were analyzed on agarose gel, purified (QIAquick Gel Extraction kit, Cat. Nr. 28706, Qiagen), cloned into the pCR8/GW/TOPO vector (Cat. Nr. K2500-20, Invitrogen) and sequenced. The sequences of the resulting PCR products are represented by the respective SEQ ID NOs as given in **Table 2-AG** and are referred to as the partial sequences. The corresponding partial amino acid sequence are represented by the respective SEQ ID NOs as given in **Table 3-AG**.

B. dsRNA production of the *Anthonomus grandis* (cotton boll weevil) genes

dsRNA was synthesized in milligram amounts using the commercially available kit T7 Ribomax™ Express RNAi System (Cat. Nr. P1700, Promega). First two separate single 5' T7 RNA polymerase promoter templates were generated in two separate PCR reactions, each reaction containing the target sequence in a different orientation relative to the T7 promoter.

For each of the target genes, the sense T7 template was generated using specific T7 forward and specific reverse primers. The sequences of the respective primers for amplifying the sense template for each of the target genes are given in **Table 8-AG**. A touchdown PCR was performed as follows: 1 minute at 95°C, followed by 20 cycles of 30 seconds at 95°C, 30 seconds at 60°C with a decrease in temperature of 0.5°C per cycle and 1 minute at 72°C, followed by 15 cycles of 30 seconds at 95°C, 30 seconds at 50°C and 1 minute at 72°C, followed by 10 minutes at 72°C. The anti-sense T7 template was generated using specific forward and specific T7 reverse

primers in a PCR reaction with the same conditions as described above. The sequences of the respective primers for amplifying the anti-sense template for each of the target genes are given in **Table 8-AG**. The resulting PCR products were analyzed on agarose gel and purified by PCR purification kit (Qiaquick PCR Purification Kit, Cat. Nr. 28106, Qiagen) and NaClO₄ precipitation.

5   The generated T7 forward and reverse templates were mixed to be transcribed and the resulting RNA strands were annealed, DNase and RNase treated, and purified by sodium acetate, following the manufacturer's instructions. The sense strand of the resulting dsRNA for each of the target genes is given in **Table 8-AG**.

        C. Cloning of a CBW gene fragment in a vector suitable for bacterial production of
10   **insect-active double-stranded RNA**

        What follows is an example of cloning a DNA fragment corresponding to a CBW gene target in a vector for the expression of double-stranded RNA in a bacterial host, although any vector comprising a T7 promoter or any other promoter for efficient transcription in bacteria, may be used (reference to WO0001846).

15   The sequences of the specific primers used for the amplification of target genes are provided in **Table 8-AG**. The template used is the pCR8/GW/topo vector containing any of target sequences. The primers are used in a PCR reaction with the following conditions: 5 minutes at 98°C, followed by 30 cycles of 10 seconds at 98°C, 30 seconds at 55°C and 2 minutes at 72°C, followed by 10 minutes at 72°C. The resulting PCR fragment is analyzed on agarose gel, purified

20   (QIAquick Gel Extraction kit, Cat. Nr. 28706, Qiagen), blunt-end cloned into *Srf* I-linearized pGNA49A vector (reference to WO00188121A1), and sequenced. The sequence of the resulting PCR product corresponds to the respective sequence as given in **Table 8-AG**. The recombinant vector harboring this sequence is named pGXXX0XX.

        D. Expression and production of a double-stranded RNA target in two strains of
25   *Escherichia coli*: (1) AB301-105(DE3), and, (2) BL21(DE3)

        The procedures described below are followed in order to express suitable levels of insect-active double-stranded RNA of insect target in bacteria. An RNaseIII-deficient strain, **AB301-105(DE3)**, is used in comparison to wild-type RNaseIII-containing bacteria, BL21(DE3).

Transformation of AB301-105(DE3) and BL21(DE3)

30   Three hundred ng of the plasmid are added to and gently mixed in a 50 µl aliquot of ice-chilled chemically competent *E.* coli strain AB301-105(DE3) or BL21(DE3). The cells are incubated on ice for 20 minutes before subjecting them to a heat shock treatment of 37 °C for 5 minutes, after which the cells are placed back on ice for a further 5 minutes. Four hundred and fifty µl of room temperature SOC medium is added to the cells and the suspension incubated on a shaker (250

35   rpm) at 37 °C for 1 hour. One hundred µl of the bacterial cell suspension is transferred to a 500 ml conical flask containing 150 ml of liquid Luria-Bertani (LB) broth supplemented with 100 µg/ml carbenicillin antibiotic. The culture is incubated on an Innova 4430 shaker (250 rpm) at 37 °C overnight (16 to 18 hours).

Chemical induction of double-stranded RNA expression in AB301-105(DE3) and BL21(DE3)

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Expression of double-stranded RNA from the recombinant vector, pGXXX0XX, in the bacterial strain AB301-105(DE3) or BL21(DE3) is made possible since all the genetic components for controlled expression are present. In the presence of the chemical inducer isopropylthiogalactoside, or IPTG, the T7 polymerase will drive the transcription of the target

5   sequence in both antisense and sense directions since these are flanked by oppositely oriented T7 promoters.

The optical density at 600 nm of the overnight bacterial culture is measured using an appropriate spectrophotometer and adjusted to a value of 1 by the addition of fresh LB broth. Fifty ml of this culture is transferred to a 50 ml Falcon tube and the culture then centrifuged at 3000 g at

10   15 °C for 10 minutes. The supernatant is removed and the bacterial pellet resuspended in 50 ml of fresh S complete medium (SNC medium plus 5 µg/ml cholesterol) supplemented with 100 µg/ml carbenicillin and 1 mM IPTG. The bacteria are induced for 2 to 4 hours at room temperature.

Heat treatment of bacteria

Bacteria are killed by heat treatment in order to minimise the risk of contamination of the

15   artificial diet in the test plates. However, heat treatment of bacteria expressing double-stranded RNA is not a prerequisite for inducing toxicity towards the insects due to RNA interference. The induced bacterial culture is centrifuged at 3000 g at room temperature for 10 minutes, the supernatant discarded and the pellet subjected to 80 °C for 20 minutes in a water bath. After heat treatment, the bacterial pellet is resuspended in 1.5 ml MilliQ water and the suspension transferred

20   to a microfuge tube. Several tubes are prepared and used in the bioassays for each refreshment. The tubes are stored at -20 °C until further use.

E. Laboratory trials to test *Escherichia coli* expressing dsRNA targets against *Anthonomus grandis*

Plant-based bioassays

25   Whole plants are sprayed with suspensions of chemically induced bacteria expressing dsRNA prior to feeding the plants to CBW. The are grown from in a plant growth room chamber. The plants are caged by placing a 500 ml plastic bottle upside down over the plant with the neck of the bottle firmly placed in the soil in a pot and the base cut open and covered with a fine nylon mesh to permit aeration, reduce condensation inside and prevent insect escape. CBW are placed

30   on each treated plant in the cage. Plants are treated with a suspension of *E. coli* AB301-105(DE3) harboring the pGXXX0XX plasmids or pGN29 plasmid. Different quantities of bacteria are applied to the plants: for instance 66, 22, and 7 units, where one unit is defined as 10^9 bacterial cells in 1 ml of a bacterial suspension at optical density value of 1 at 600 nm wavelength. In each case, a total volume of between 1 and 10 ml s sprayed on the plant with the aid of a vaporizer. One plant is

35   used per treatment in this trial. The number of survivors are counted and the weight of each survivor recorded.

Spraying plants with a suspension of *E. coli* bacterial strain AB301-105(DE3) expressing target dsRNA from pGXXX0XX lead to a dramatic increase in insect mortality when compared to pGN29 control. These experiments show that double-stranded RNA corresponding to an insect

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gene target sequence produced in either wild-type or RNaseIII-deficient bacterial expression systems is toxic towards the insect in terms of substantial increases in insect mortality and growth/development delay for larval survivors. It is also clear from these experiments that an exemplification is provided for the effective protection of plants/crops from insect damage by the
5   use of a spray of a formulation consisting of bacteria expressing double-stranded RNA corresponding to an insect gene target.

Example 7: *Tribolium castaneum* (Red flour beetle)

A. Cloning *Tribolium castaneum* partial sequences

10   High quality, intact RNA was isolated from all the different insect stages of *Tribolium castaneum* (red flour beetle; source: Dr. Lara Senior, Insect Investigations Ltd., Capital Business Park, Wentloog, Cardiff, CF3 2PX, Wales, UK) using TRIzol Reagent (Cat. Nr. 15596-026/15596-018, Invitrogen, Rockville, Maryland, USA) following the manufacturer's instructions. Genomic DNA present in the RNA preparation was removed by DNase treatment following the manafacturer's
15   instructions (Cat. Nr. 1700, Promega). cDNA was generated using a commercially available kit (SuperScript ™ III Reverse Transcriptase, Cat. Nr. 18080044, Invitrogen, Rockville, Maryland, USA) following the manufacturer's instructions.

To isolate cDNA sequences comprising a portion of the TC001, TC002, TC010, TC014 and TC015 genes, a series of PCR reactions with degenerate primers were performed using Amplitaq
20   Gold (Cat. Nr. N8080240, Applied Biosystems) following the manafacturer's instructions.

The sequences of the degenerate primers used for amplification of each of the genes are given in **Table 2-TC**. These primers were used in respective PCR reactions with the following conditions: 10 minutes at 95°C, followed by 40 cycles of 30 seconds at 95°C, 1 minute at 50°C and 1 minute and 30 seconds at 72°C, followed by 7 minutes at 72°C (TC001, TC014, TC015); 10
25   minutes at 95°C, followed by 40 cycles of 30 seconds at 95°C, 1 minute at 54°C and 2 minutes and 30 seconds at 72°C, followed by 7 minutes at 72°C (TC010); 10 minutes at 95°C, followed by 40 cycles of 30 seconds at 95°C, 1 minute at 53°C and 1 minute at 72°C, followed by 7 minutes at 72°C (TC002) . The resulting PCR fragments were analyzed on agarose gel, purified (QIAquick Gel Extraction kit, Cat. Nr. 28706, Qiagen), cloned into the pCR8/GW/TOPO vector (Cat. Nr. K2500-20,
30   Invitrogen), and sequenced. The sequences of the resulting PCR products are represented by the respective SEQ ID NOs as given in **Table 2-TC** and are referred to as the partial sequences. The corresponding partial amino acid sequences are represented by the respective SEQ ID NOs as given in **Table 3-TC**.

B. dsRNA production of the *Tribolium castaneum* genes

35   dsRNA was synthesized in milligram amounts using the commercially available kit T7 Ribomax™ Express RNAi System (Cat. Nr. P1700, Promega). First two separate single 5' T7 RNA polymerase promoter templates were generated in two separate PCR reactions, each reaction containing the target sequence in a different orientation relative to the T7 promoter.

For each of the target genes, the sense T7 template was generated using specific T7 forward and specific reverse primers. The sequences of the respective primers for amplifying the sense template for each of the target genes are given in **Table 8-TC**. The conditions in the PCR reactions were as follows: 1 minute at 95°C, followed by 20 cycles of 30 seconds at 95°C, 30

5   seconds at 60°C (-0.5°C/cycle) and 1 minute at 72°C, followed by 15 cycles of 30 seconds at 95°C, 30 seconds at 50°C and 1 minute at 72°C, followed by 10 minutes at 72°C. The anti-sense T7 template was generated using specific forward and specific T7 reverse primers in a PCR reaction with the same conditions as described above. The sequences of the respective primers for amplifying the anti-sense template for each of the target genes are given in **Table 8-TC**. The

10   resulting PCR products were analyzed on agarose gel and purified by PCR purification kit (Qiaquick PCR Purification Kit, Cat. Nr. 28106, Qiagen) and $NaClO_4$ precipitation. The generated T7 forward and reverse templates were mixed to be transcribed and the resulting RNA strands were annealed, DNase and RNase treated, and purified by sodium acetate, following the manufacturer's instructions. The sense strand of the resulting dsRNA for each of the target genes

15   is given in **Table 8-TC**.

**C. Laboratory trials to test dsRNA targets, using artificial diet for activity against
Tribolium castaneum larvae**

The example provided below is an exemplification of the finding that the red flour beetle (RFB) larvae are susceptible to orally ingested dsRNA corresponding to own target genes. -

20   Red flour beetles, *Tribolium castaneum*, were maintained at Insect Investigations Ltd. (origin: Imperial College of Science, Technology and Medicine, Silwood Park, Berkshire, UK). Insects were cultured according to company SOP/251/01. Briefly, the beetles were housed in plastic jars or tanks. These have an open top to allow ventilation. A piece of netting was fitted over the top and secured with an elastic band to prevent escape. The larval rearing medium (flour) was

25   placed in the container where the beetles can breed. The stored product beetle colonies were maintained in a controlled temperature room at 25 ± 3 °C with a 16:8 hour light:dark cycle.

Double-stranded RNA from target TC014 (with sequence corresponding to SEQ ID NO - 799) was incorporated into a mixture of flour and milk powder (wholemeal flour: powdered milk in the ratio 4:1) and left to dry overnight. Each replicate was prepared separately: 100 µl of a 10 µg/µl

30   dsRNA solution (1 mg dsRNA) was added to 0.1 g flour/milk mixture. The dried mixture was ground to a fine powder. Insects were maintained within Petri dishes (55 mm diameter), lined with a double layer of filter paper. The treated diet was placed between the two filter paper layers. Ten first instar, mixed sex larvae were placed in each dish (replicate). Four replicates were performed for each treatment. Control was Milli-Q water. Assessments (number of survivors) were made on a regular

35   basis. During the trial, the test conditions were 25 – 33 °C and 20 – 25 % relative humidity, with a 12:12 hour light:dark photoperiod.

Survival of larvae of *T. castaneum* over time on artificial diet treated with target TC014 dsRNA was significantly reduced when compared to diet only control, as shown in **Figure 1-TC**.

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D. Cloning of a RFB gene fragment in a vector suitable for bacterial production of insect-active double-stranded RNA

What follows is an example of cloning a DNA fragment corresponding to an RFB gene target in a vector for the expression of double-stranded RNA in a bacterial host, although any
5   vector comprising a T7 promoter or any other promoter for efficient transcription in bacteria, may be used (reference to WO0001846).

The sequences of the specific primers used for the amplification of target genes are provided in **Table 8-TC**. The template used is the pCR8/GW/topo vector containing any of target sequences. The primers are used in a PCR reaction with the following conditions: 5 minutes at
10 98°C, followed by 30 cycles of 10 seconds at 98°C, 30 seconds at 55°C and 2 minutes at 72°C, followed by 10 minutes at 72°C. The resulting PCR fragment is analyzed on agarose gel, purified (QIAquick Gel Extraction kit, Cat. Nr. 28706, Qiagen), blunt-end cloned into *Srf* I-linearized pGNA49A vector (reference to WO00188121A1), and sequenced. The sequence of the resulting PCR product corresponds to the respective sequence as given in **Table 8-TC**. The recombinant
15 vector harboring this sequence is named pGXXX0XX.

E. Expression and production of a double-stranded RNA target in two strains of *Escherichia coli*: (1) AB301-105(DE3), and, (2) BL21(DE3)

The procedures described below are followed in order to express suitable levels of insect-active double-stranded RNA of insect target in bacteria. An RNaseIII-deficient strain, AB301-
20 105(DE3), is used in comparison to wild-type RNaseIII-containing bacteria, BL21(DE3).

Transformation of AB301-105(DE3) and BL21(DE3)

Three hundred ng of the plasmid are added to and gently mixed in a 50 µl aliquot of ice-chilled chemically competent *E. coli* strain AB301-105(DE3) or BL21(DE3). The cells are incubated on ice for 20 minutes before subjecting them to a heat shock treatment of 37 °C for 5 minutes, after
25 which the cells are placed back on ice for a further 5 minutes. Four hundred and fifty µl of room temperature SOC medium is added to the cells and the suspension incubated on a shaker (250 rpm) at 37 °C for 1 hour. One hundred µl of the bacterial cell suspension is transferred to a 500 ml conical flask containing 150 ml of liquid Luria-Bertani (LB) broth supplemented with 100 µg/ml carbenicillin antibiotic. The culture is incubated on an Innova 4430 shaker (250 rpm) at 37 °C
30 overnight (16 to 18 hours).

Chemical induction of double-stranded RNA expression in AB301-105(DE3) and BL21(DE3)

Expression of double-stranded RNA from the recombinant vector, pGXXX0XX, in the bacterial strain AB301-105(DE3) or BL21(DE3) is made possible since all the genetic components for controlled expression are present. In the presence of the chemical inducer
35 isopropylthiogalactoside, or IPTG, the T7 polymerase will drive the transcription of the target sequence in both antisense and sense directions since these are flanked by oppositely oriented T7 promoters.

The optical density at 600 nm of the overnight bacterial culture is measured using an appropriate spectrophotometer and adjusted to a value of 1 by the addition of fresh LB broth. Fifty

ml of this culture is transferred to a 50 ml Falcon tube and the culture then centrifuged at 3000 g at 15 °C for 10 minutes. The supernatant is removed and the bacterial pellet resuspended in 50 ml of fresh S complete medium (SNC medium plus 5 µg/ml cholesterol) supplemented with 100 µg/ml carbenicillin and 1 mM IPTG. The bacteria are induced for 2 to 4 hours at room temperature.

5   *Heat treatment of bacteria*

Bacteria are killed by heat treatment in order to minimise the risk of contamination of the artificial diet in the test plates. However, heat treatment of bacteria expressing double-stranded RNA is not a prerequisite for inducing toxicity towards the insects due to RNA interference. The induced bacterial culture is centrifuged at 3000 g at room temperature for 10 minutes, the

10   supernatant discarded and the pellet subjected to 80 °C for 20 minutes in a water bath. After heat treatment, the bacterial pellet is resuspended in 1.5 ml MilliQ water and the suspension transferred to a microfuge tube. Several tubes are prepared and used in the bioassays for each refreshment. The tubes are stored at -20 °C until further use.

F. Laboratory trials to test *Escherichia coli* expressing dsRNA targets against

15   ***Tribolium castaneum***

Plant-based bioassays

Whole plants are sprayed with suspensions of chemically induced bacteria expressing dsRNA prior to feeding the plants to RFB. The are grown from in a plant growth room chamber. The plants are caged by placing a 500 ml plastic bottle upside down over the plant with the neck of

20   the bottle firmly placed in the soil in a pot and the base cut open and covered with a fine nylon mesh to permit aeration, reduce condensation inside and prevent insect escape. RFB are placed on each treated plant in the cage. Plants are treated with a suspension of *E. coli* AB301-105(DE3) harboring the pGXXX0XX plasmids or pGN29 plasmid. Different quantities of bacteria are applied to the plants: for instance 66, 22, and 7 units, where one unit is defined as 10^9 bacterial cells in 1

25   ml of a bacterial suspension at optical density value of 1 at 600 nm wavelength. In each case, a total volume of between 1 and 10 ml s sprayed on the plant with the aid of a vaporizer. One plant is used per treatment in this trial. The number of survivors are counted and the weight of each survivor recorded.

Spraying plants with a suspension of *E. coli* bacterial strain AB301-105(DE3) expressing

30   target dsRNA from pGXXX0XX leed to a dramatic increase in insect mortality when compared to pGN29 control. These experiments show that double-stranded RNA corresponding to an insect gene target sequence produced in either wild-type or RNaseIII-deficient bacterial expression systems is toxic towards the insect in terms of substantial increases in insect mortality and growth/development delay for larval survivors. It is also clear from these experiments that an

35   exemplification is provided for the effective protection of plants/crops from insect damage by the use of a spray of a formulation consisting of bacteria expressing double-stranded RNA corresponding to an insect gene target.

Example 8: *Myzus persicae* (Green peach aphid)

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A. Cloning *Myzus persicae* partial sequences

High quality, intact RNA was isolated from nymphs of *Myzus persicae* (green peach aphid; source: Dr. Rachel Down, Insect & Pathogen Interactions, Central Science Laboratory, Sand Hutton, York, YO41 1LZ, UK) using TRIzol Reagent (Cat. Nr. 15596-026/15596-018, Invitrogen,
5   Rockville, Maryland, USA) following the manufacturer's instructions. Genomic DNA present in the RNA preparation was removed by DNase treatment following the manafacturer's instructions (Cat. Nr. 1700, Promega). cDNA was generated using a commercially available kit (SuperScript ™ III Reverse Transcriptase, Cat. Nr. 18080044, Invitrogen, Rockville, Maryland, USA) following the manufacturer's instructions.
10   To isolate cDNA sequences comprising a portion of the MP001, MP002, MP010, MP016 and MP027 genes, a series of PCR reactions with degenerate primers were performed using Amplitaq Gold (Cat. Nr. N8080240, Applied Biosystems) following the manafacturer's instructions.

The sequences of the degenerate primers used for amplification of each of the genes are given in **Table 2-MP**. These primers were used in respective PCR reactions with the following
15   conditions: for MP001, MP002 and MP016, 10 minutes at 95°C, followed by 40 cycles of 30 seconds at 95°C, 1 minute at 50°C and 1 minute 30 seconds at 72°C, followed by 7 minutes at 72°C; for MP027, a touchdown program was used: 10 minutes at 95°C, followed by 10 cycles of 30 seconds at 95°C, 40 seconds at 60°C with a decrease in temperature of 1°C per cycle and 1 minute 10 seconds at 72°C, followed by 30 cycles of 30 seconds at 95°C, 40 seconds at 50°C and
20   1 minute 10 seconds at 72°C, followed by 7 minutes at 72°C; for MP010, 10 minutes at 95°C, followed by 40 cycles of 30 seconds at 95°C, 1 minute at 54°C and 3 minutes at 72°C, followed by 7 minutes at 72°C. The resulting PCR fragments were analyzed on agarose gel, purified (QIAquick Gel Extraction kit, Cat. Nr. 28706, Qiagen), cloned into the pCR8/GW/TOPO vector (Cat. Nr. K2500-20, Invitrogen), and sequenced. The sequences of the resulting PCR products are
25   represented by the respective SEQ ID NOs as given in **Table 2-MP** and are referred to as the partial sequences. The corresponding partial amino acid sequences are represented by the respective SEQ ID NOs as given in **Table 3-MP**.

B. dsRNA production of *Myzus persicae* genes

dsRNA was synthesized in milligram amounts using the commercially available kit T7
30   Ribomax™ Express RNAi System (Cat. Nr. P1700, Promega). First two separate single 5' T7 RNA polymerase promoter templates were generated in two separate PCR reactions, each reaction containing the target sequence in a different orientation relative to the T7 promoter.

For each of the target genes, the sense T7 template was generated using specific T7 forward and specific reverse primers. The sequences of the respective primers for amplifying the
35   sense template for each of the target genes are given in **Table 8-MP**. A touchdown PCR was performed as follows: 1 minute at 95°C, followed by 20 cycles of 30 seconds at 95°C, 30 seconds at 55°C (for MP001, MP002, MP016, MP027 and gfp) or 30 seconds at 50°C (for MP010) with a decrease in temperature of 0.5°C per cycle and 1 minute at 72°C, followed by 15 cycles of 30 seconds at 95°C, 30 seconds at 45°C and 1 minute at 72°C followed by 10 minutes at 72°C. The

anti-sense T7 template was generated using specific forward and specific T7 reverse primers in a PCR reaction with the same conditions as described above. The sequences of the respective primers for amplifying the anti-sense template for each of the target genes are given in **Table 8-MP**. The resulting PCR products were analyzed on agarose gel and purified by PCR purification kit

5 (Qiaquick PCR Purification Kit, Cat. Nr. 28106, Qiagen) and $NaClO_4$ precipitation. The generated T7 forward and reverse templates were mixed to be transcribed and the resulting RNA strands were annealed, DNase and RNase treated, and purified by sodium acetate, following the manufacturer's instructions. The sense strand of the resulting dsRNA for each of the target genes is given in **Table 8-MP**.

10 **C. Laboratory trials of *Myzus periscae* (green peach aphid) infestation on transgenic *Arabidopsis thaliana* plants**

Generation of transgenic plants

Arabidopsis thaliana plants were transformed using the floral dip method (Clough and Bent (1998) *Plant Journal* 16:735-743). Aerial parts of the plants were incubated for a few seconds in a

15 solution containing 5% sucrose, resuspended *Agrobacterium tumefaciens* strain C58C1 Rif cells from an overnight culture and 0.03% of the surfactant Silwet L-77. After inoculation, plants were covered for 16 hours with a transparent plastic to maintain humidity. To increase the transformation efficiency, the procedure was repeated after one week. Watering was stopped as seeds matured and dry seeds were harvested and cold-treated for two days. After sterilization, seeds were plated

20 on a kanamycin-containing growth medium for selection of transformed plants.

The selected plants are transferred to soil for optimal T2 seed production.

Bioassay

Transgenic *Arabidopsis thaliana* plants are selected by allowing the segregating T2 seeds to germinate on appropriate selection medium. When the roots of these transgenics are well-

25 established they are then transferred to fresh artificial growth medium or soil and allowed to grow under optimal conditions. Whole transgenic plants are tested against nymphs of the green peach aphid (*Myzus persicae*) to show (1) a significant resistance to plant damage by the feeding nymph, (2) increased nymphal mortality, and/or (3) decreased weight of nymphal survivors (or any other aberrant insect development).

30 **D. Laboratory trials to test dsRNA targets using liquid artificial diet for activity against *Myzus persicae***

Liquid artificial diet for the green peach aphid, *Myzus persicae*, was prepared based on the diet suitable for pea aphids (*Acyrthosiphon pisum*), as described by Febvay et al. (1988) [Influence of the amino acid balance on the improvement of an artificial diet for a biotype of *Acyrthosiphon*

35 *pisum* (Homoptera: Aphididae). *Can. J. Zool.* 66: 2449-2453], but with some modifications. The amino acids component of the diet was prepared as follows: in mg/100ml, alanine 178.71, beta-alanine 6.22, arginine 244.9, asparagine 298.55, aspartic acid 88.25, cysteine 29.59, glutamic acid 149.36, glutamine 445.61, glycine 166.56, histidine 136.02, isoleucine 164.75, leucine 231.56, lysine hydrochloride 351.09, methionine 72.35, ornithine (HCl) 9.41, phenylalanine 293, proline

129.33, serine 124.28, threonine 127.16, tryptophane 42.75, tyrosine 38.63, L-valine 190.85. The amino acids were dissolved in 30 ml Milli-Q H_2O except for tyrosine which was first dissolved in a few drops of 1 M HCl before adding to the amino acid mix. The vitamin mix component of the diet was prepared as a 5 x concentrate stock as follows: in mg/L, amino benzoic acid 100, ascorbic acid

5   1000, biotin 1, calcium panthothenate 50, choline chloride 500, folic acid 10, myoinositol 420, nicotinic acid 100; pyridoxine hydrochloride 25, riboflavin 5, thiamine hydrochloride 25. The riboflavin was dissolved in 1 ml H2O at 50 °C and then added to the vitamin mix stock. The vitamin mix was aliquoted in 20 ml per aliquot and stored at -20 °C. One aliquot of vitamin mix was added to the amino acid solution. Sucrose and $MgSO_4.7H_2O$ was added with the following amounts to the

10 mix: 20 g and 242 mg, respectively. Trace metal stock solution was prepared as follows: in mg/100ml, $CuSO_4.5H_2O$ 4.7, $FeCl_3.6H_2O$ 44.5, $MnCl_2.4H2O$ 6.5, NaCl 25.4, $ZnCl_2$ 8.3. Ten ml of the trace metal solution and 250 mg KH_2PO_4 was added to the diet and Milli-Q water was added to a final liquid diet volume of 100 ml. The pH of the diet was adjusted to 7 with 1 M KOH solution. The liquid diet was filter-sterilised through an 0.22 μm filter disc (Millipore).

15   Green peach aphids (*Myzus persicae*; source: Dr. Rachel Down, Insect & Pathogen Interactions, Central Science Laboratory, Sand Hutton, York, YO41 1LZ, UK) were reared on 4- to 6-week-old oilseed rape (*Brassica napus* variety SW Oban; source: Nick Balaam, Sw Seed Ltd., 49 North Road, Abington, Cambridge, CB1 6AS, UK) in aluminium-framed cages containing 70 μm mesh in a controlled environment chamber with the following conditions: 23 ±2 °C and 60 ±5 %

20 relative humidity, with a 16:8 hours light:dark photoperiod.

One day prior to the start of the bioassay, adults were collected from the rearing cages and placed on fresh detached oilseed rape leaves in a Petri dish and left overnight in the insect chamber. The following day, first-instar nymphs were picked and transferred to feeding chambers. A feeding chamber comprised of 10 first instar nymphs placed in a small Petri dish (with diameter 3

25 cm) covered with a single layer of thinly stretched parafilm M onto which 50 μl of diet was added. The chamber was sealed with a second layer of parafilm and incubated under the same conditions as the adult cultures. Diet with dsRNA was refreshed every other day and the insects' survival assessed on day 8 i.e. 8th day post bioassay start. Per treatment, 5 bioassay feeding chambers (replicates) were set up simultaneously. Test and control (gfp) dsRNA solutions were incorporated

30 into the diet to a final concentration of 2 μg/μl. The feeding chambers were kept at 23 ±2 °C and 60 ±5 % relative humidity, with a 16:8 hours light:dark photoperiod. A Mann-Whitney test was determined by GraphPad Prism version 4 to establish whether the medians do differ significantly between target 27 (MP027) and gfp dsRNA.

In the bioassay, feeding liquid artificial diet supplemented with intact naked dsRNA from

35 target 27 (SEQ ID NO 1061) to nymphs of *Myzus persicae* using a feeding chamber, resulted in a significant increase in mortality, as shown in Figure 1. Average percentage survivors for target 27, gfp dsRNA and diet only treatment were 2, 34 and 82, respectively. Comparison of target 027 with gfp dsRNA groups using the Mann-Whitney test resulted in an one-tailed P-value of 0.004 which indicates that the median of target 027 is significantly different (P < 0.05) from the expected larger

40 median of gfp dsRNA. The green peach aphids on the liquid diet with incorporated target 27

dsRNA were noticeably smaller than those that were fed on diet only or with gfp dsRNA control (data not presented).

E. Cloning of a GPA gene fragment in a vector suitable for bacterial production of insect-active double-stranded RNA

5   What follows is an example of cloning a DNA fragment corresponding to a GPA gene target in a vector for the expression of double-stranded RNA in a bacterial host, although any vector comprising a T7 promoter or any other promoter for efficient transcription in bacteria, may be used (reference to WO0001846).

          The sequences of the specific primers used for the amplification of target genes are
10   provided in **Table 8-MP**. The template used is the pCR8/GW/topo vector containing any of target sequences. The primers are used in a PCR reaction with the following conditions: 5 minutes at 98°C, followed by 30 cycles of 10 seconds at 98°C, 30 seconds at 55°C and 2 minutes at 72°C, followed by 10 minutes at 72°C. The resulting PCR fragment is analyzed on agarose gel, purified (QIAquick Gel Extraction kit, Cat. Nr. 28706, Qiagen), blunt-end cloned into *Srf* I-linearized
15   pGNA49A vector (reference to WO00188121A1), and sequenced. The sequence of the resulting PCR product corresponds to the respective sequence as given in **Table 8-MP**. The recombinant vector harboring this sequence is named pGXXX0XX.

          F. Expression and production of a double-stranded RNA target in two strains of *Escherichia coli*: (1) AB301-105(DE3), and, (2) BL21(DE3)

20   The procedures described below are followed in order to express suitable levels of insect-active double-stranded RNA of insect target in bacteria. An RNaseIII-deficient strain, AB301-105(DE3), is used in comparison to wild-type RNaseIII-containing bacteria, BL21(DE3).
Transformation of AB301-105(DE3) and BL21(DE3)

          Three hundred ng of the plasmid are added to and gently mixed in a 50 µl aliquot of ice-
25   chilled chemically competent *E.* coli strain AB301-105(DE3) or BL21(DE3). The cells are incubated on ice for 20 minutes before subjecting them to a heat shock treatment of 37 °C for 5 minutes, after which the cells are placed back on ice for a further 5 minutes. Four hundred and fifty µl of room temperature SOC medium is added to the cells and the suspension incubated on a shaker (250 rpm) at 37 °C for 1 hour. One hundred µl of the bacterial cell suspension is transferred to a 500 ml
30   conical flask containing 150 ml of liquid Luria-Bertani (LB) broth supplemented with 100 µg/ml carbenicillin antibiotic. The culture is incubated on an Innova 4430 shaker (250 rpm) at 37 °C overnight (16 to 18 hours).
Chemical induction of double-stranded RNA expression in AB301-105(DE3) and BL21(DE3)

          Expression of double-stranded RNA from the recombinant vector, pGXXX0XX, in the
35   bacterial strain AB301-105(DE3) or BL21(DE3) is made possible since all the genetic components for controlled expression are present. In the presence of the chemical inducer isopropylthiogalactoside, or IPTG, the T7 polymerase will drive the transcription of the target sequence in both antisense and sense directions since these are flanked by oppositely oriented T7 promoters.

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The optical density at 600 nm of the overnight bacterial culture is measured using an appropriate spectrophotometer and adjusted to a value of 1 by the addition of fresh LB broth. Fifty ml of this culture is transferred to a 50 ml Falcon tube and the culture then centrifuged at 3000 g at 15 °C for 10 minutes. The supernatant is removed and the bacterial pellet resuspended in 50 ml of

5   fresh S complete medium (SNC medium plus 5 µg/ml cholesterol) supplemented with 100 µg/ml carbenicillin and 1 mM IPTG. The bacteria are induced for 2 to 4 hours at room temperature.

Heat treatment of bacteria

Bacteria are killed by heat treatment in order to minimise the risk of contamination of the artificial diet in the test plates. However, heat treatment of bacteria expressing double-stranded

10 RNA is not a prerequisite for inducing toxicity towards the insects due to RNA interference. The induced bacterial culture is centrifuged at 3000 g at room temperature for 10 minutes, the supernatant discarded and the pellet subjected to 80 °C for 20 minutes in a water bath. After heat treatment, the bacterial pellet is resuspended in 1.5 ml MilliQ water and the suspension transferred to a microfuge tube. Several tubes are prepared and used in the bioassays for each refreshment.

15 The tubes are stored at -20 °C until further use.

G. Laboratory trials to test *Escherichia coli* expressing dsRNA targets against *Myzus persicae*

Plant-based bioassays

Whole plants are sprayed with suspensions of chemically induced bacteria expressing

20 dsRNA prior to feeding the plants to GPA. The are grown from in a plant growth room chamber. The plants are caged by placing a 500 ml plastic bottle upside down over the plant with the neck of the bottle firmly placed in the soil in a pot and the base cut open and covered with a fine nylon mesh to permit aeration, reduce condensation inside and prevent insect escape. GPA are placed on each treated plant in the cage. Plants are treated with a suspension of *E. coli* AB301-105(DE3)

25 harboring the pGXXX0XX plasmids or pGN29 plasmid. Different quantities of bacteria are applied to the plants: for instance 66, 22, and 7 units, where one unit is defined as 10^9 bacterial cells in 1 ml of a bacterial suspension at optical density value of 1 at 600 nm wavelength. In each case, a total volume of between 1 and 10 ml s sprayed on the plant with the aid of a vaporizer. One plant is used per treatment in this trial. The number of survivors are counted and the weight of each

30 survivor recorded.

Spraying plants with a suspension of *E. coli* bacterial strain AB301-105(DE3) expressing target dsRNA from pGXXX0XX lead to a dramatic increase in insect mortality when compared to pGN29 control. These experiments show that double-stranded RNA corresponding to an insect gene target sequence produced in either wild-type or RNaseIII-deficient bacterial expression

35 systems is toxic towards the insect in terms of substantial increases in insect mortality and growth/development delay for larval survivors. It is also clear from these experiments that an exemplification is provided for the effective protection of plants/crops from insect damage by the use of a spray of a formulation consisting of bacteria expressing double-stranded RNA corresponding to an insect gene target.

Example 9: *Nilaparvata lugens* (Brown plant hopper)

A. Cloning *Nilaparvata lugens* partial sequences

From high quality total RNA of *Nilaparvata lugens* (source: Dr. J. A. Gatehouse, Dept.
5 Biological Sciences, Durham University, UK) cDNA was generated using a commercially available
kit (SuperScriptTM III Reverse Transcriptase, Cat N°. 18080044, Invitrogen, Rockville, Maryland,
USA) following the manufacturer's protocol.

To isolate cDNA sequences comprising a portion of the *Nilaparvata lugens* NL001, NL002,
NL003, NL004, NL005, NL006, NL007, NL008, NL009, NL010, NL011, NL012, NL013, NL014,
10 NL015, NL016, NL018, NL019, NL021, NL022, and NL027 genes, a series of PCR reactions with
degenerate primers were performed using Amplitaq Gold (Cat N°. N8080240; Applied Biosystems)
following the manufacturer's protocol.

The sequences of the degenerate primers used for amplification of each of the genes are
given in **Table 2-NL**. These primers were used in respective PCR reactions with the following
15 conditions: for NL001: 5 minutes at 95°C, followed by 40 cycles of 30 seconds at 95°C, 1 minute at
55°C and 1 minute at 72°C, followed by 10 minutes at 72°C: for NL002: 3 minutes at 95°C,
followed by 40 cycles of 30 seconds at 95°C, 1 minute at 55°C and 1 minute at 72°C, followed by
10 minutes at 72°C; for NL003: 3 minutes at 95 °C, followed by 40 cycles of 30 seconds at 95 °C, 1
minute at 61 °C and 1 minute at 72 °C, followed by 10 minutes at 72°C; for NL004: 10 minutes at
20 95 °C, followed by 40 cycles of 30 seconds at 95 °C, 1 minute at 51 °C and 1 minute at 72 °C; for
NL005: 10 minutes at 95 °C, followed by 40 cycles of 30 seconds at 95 °C, 1 minute at 54 °C and 1
minute at 72 °C, followed by 10 minutes at 72°C; for NL006: 10 minutes at 95 °C, followed by 40
cycles of 30 seconds at 95 °C, 1 minute at 55 °C and 3 minute 30 seconds at 72 °C, followed by 10
minutes at 72°C; for NL007: 10 minutes at 95 °C, followed by 40 cycles of 30 seconds at 95 °C, 1
25 minute at 54 °C and 1 minute 15 seconds at 72 °C, followed by 10 minutes at 72°C; for NL008 &
NL014: 10 minutes at 95 °C, followed by 40 cycles of 30 seconds at 95 °C, 1 minute at 53 °C and 1
minute at 72 °C, followed by 10 minutes at 72°C; for NL009, NL011, NL012 & NL019: 10 minutes at
95 °C, followed by 40 cycles of 30 seconds at 95 °C, 1 minute at 55 °C and 1 minute at 72 °C,
followed by 10 minutes at 72°C; for NL010: 10 minutes at 95 °C, followed by 40 cycles of 30
30 seconds at 95 °C, 1 minute at 54 °C and 2 minute 30 seconds at 72 °C, followed by 10 minutes at
72°C; for NL013: 10 minutes at 95 °C, followed by 40 cycles of 30 seconds at 95 °C, 1 minute at 54
°C and 1 minute 10 seconds at 72 °C, followed by 10 minutes at 72°C; for NL015 & NL016: 10
minutes at 95 °C, followed by 40 cycles of 30 seconds at 95 °C, 1 minute at 54 °C and 1 minute 40
seconds at 72 °C, followed by 10 minutes at 72°C; for NL018: 10 minutes at 95 °C, followed by 40
35 cycles of 30 seconds at 95 °C, 1 minute at 54 °C and 1 minute 35 seconds at 72 °C, followed by 10
minutes at 72°C; for NL021, NL022 & NL027: 10 minutes at 95 °C, followed by 40 cycles of 30
seconds at 95 °C, 1 minute at 54 °C and 1 minute 45 seconds at 72 °C, followed by 10 minutes at
72°C. The resulting PCR fragments were analyzed on agarose gel, purified (QIAquick Gel
Extraction kit, Cat. Nr. 28706, Qiagen), cloned into the pCR8/GW/topo vector (Cat. Nr. K2500 20,

Invitrogen), and sequenced. The sequences of the resulting PCR products are represented by the respective SEQ ID NOs as given in **Table 2-NL** and are referred to as the partial sequences. The corresponding partial amino acid sequences are represented by the respective SEQ ID NOs as given in **Table 3-NL**.

5   **B. Cloning of a partial sequence of the *Nilaparvata lugens* NL023 gene via EST sequence**

From high quality total RNA of *Nilaparvata lugens* (source: Dr. J. A. Gatehouse, Dept. Biological Sciences, Durham University, UK) cDNA was generated using a commercially available kit (SuperScript™ III Reverse Transcriptase, Cat N°. 18080044, Invitrogen, Rockville, Maryland,
10   USA) following the manufacturer's protocol.

A partial cDNA sequence, NL023, was amplified from *Nilaparvata lugens* cDNA which corresponded to a *Nilaparvata lugens* EST sequence in the public database Genbank with accession number CAH65679.2. To isolate cDNA sequences comprising a portion of the NL023 gene, a series of PCR reactions with EST based specific primers were performed using
15   PerfectShot™ ExTaq (Cat N°. RR005A, Takara Bio Inc.) following the manafacturer's protocol.

For NL023, the specific primers oGBKW002 and oGBKW003 (represented herein as SEQ ID NO 1157 and SEQ ID NO 1158, respectively) were used in two independent PCR reactions with the following conditions: 3 minutes at 95 °C, followed by 30 cycles of 30 seconds at 95 °C, 30 seconds at 56 °C and 2 minutes at 72°C, followed by 10 minutes at 72°C. The resulting PCR
20   products were analyzed on agarose gel, purified (QIAquick® Gel Extraction Kit; Cat. N°. 28706, Qiagen), cloned into the pCR4-TOPO vector (Cat N°. K4575-40, Invitrogen) and sequenced. The consensus sequence resulting from the sequencing of both PCR products is herein represented by SEQ ID NO 1111 and is referred to as the partial sequence of the NL023 gene. The corresponding partial amino acid sequence is herein repreresented as SEQ ID NO 1112.

25   **C. dsRNA production of *Nilaparvata lugens* genes**

dsRNA was synthesized in milligram amounts using the commercially available kit T7 Ribomax™ Express RNAi System (Cat. Nr. P1700, Promega). First two separate single 5' T7 RNA polymerase promoter templates were generated in two separate PCR reactions, each reaction containing the target sequence in a different orientation relative to the T7 promoter.
30   For each of the target genes, the sense T7 template was generated using specific T7 forward and specific reverse primers. The sequences of the respective primers for amplifying the sense template for each of the target genes are given in **Table 8-NL**. The conditions in the PCR reactions were as follows: for NL001 & NL002: 4 minutes at 94 °C, followed by 35 cycles of 30 seconds at 94 °C, 30 seconds at 60 °C and 1 minute at 72 °C, followed by 10 minutes at 72°C; for
35   NL003: 4 minutes at 94 °C, followed by 35 cycles of 30 seconds at 94 °C, 30 seconds at 66 °C and 1 minute at 72 °C, followed by 10 minutes at 72°C; for NL004, NL006, NL008, NL009, NL010 & NL019: 4 minutes at 95 °C, followed by 35 cycles of 30 seconds at 95 °C, 30 seconds at 54 °C and 1 minute at 72 °C, followed by 10 minutes at 72°C; for NL005 & NL016: 4 minutes at 95 °C, followed by 35 cycles of 30 seconds at 95 °C, 30 seconds at 57 °C and 1 minute at 72 °C, followed

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by 10 minutes at 72°C; for NL007 & NL014: 4 minutes at 95 °C, followed by 35 cycles of 30 seconds at 95 °C, 30 seconds at 51 °C and 1 minute at 72 °C, followed by 10 minutes at 72°C; for NL011, NL012 & NL022: 4 minutes at 95 °C, followed by 35 cycles of 30 seconds at 95 °C, 30 seconds at 53 °C and 1 minute at 72 °C, followed by 10 minutes at 72°C; for NL013, NL015, NL018

5   & NL021: 4 minutes at 95 °C, followed by 35 cycles of 30 seconds at 95 °C, 30 seconds at 55 °C and 1 minute at 72 °C, followed by 10 minutes at 72°C; for NL023 & NL027: 4 minutes at 95 °C, followed by 35 cycles of 30 seconds at 95 °C, 30 seconds at 52 °C and 1 minute at 72 °C, followed by 10 minutes at 72°C. The anti-sense T7 template was generated using specific forward and specific T7 reverse primers in a PCR reaction with the same conditions as described above. The

10 sequences of the respective primers for amplifying the anti-sense template for each of the target genes are given in Table 8-NL. The resulting PCR products were analyzed on agarose gel and purified by PCR purification kit (Qiaquick PCR Purification Kit, Cat. Nr. 28106, Qiagen). The generated T7 forward and reverse templates were mixed to be transcribed and the resulting RNA strands were annealed, DNase and RNase treated, and purified by sodium acetate, following the

15 manufacturer's instructions, but with the following modification: RNA peppet is washed twice in 70% ethanol. The sense strand of the resulting dsRNA for each of the target genes is given in Table 8-NL.

The template DNA used for the PCR reactions with T7 primers on the green fluorescent protein (gfp) control was the plasmid pPD96.12 (the Fire Lab, http://genome-

20 www.stanford.edu/group/fire/), which contains the wild-type gfp coding sequence interspersed by 3 synthetic introns. Double-stranded RNA was synthesized using the commercially available kit T7 RiboMAX™ Express RNAi System (Cat.N°. P1700, Promega). First two separate single 5' T7 RNA polymerase promoter templates were generated in two separate PCR reactions, each reaction containing the target sequence in a different orientation relative to the T7 promoter. For gfp, the

25 sense T7 template was generated using the specific T7 FW primer oGAU183 and the specific RV primer oGAU182 (represented herein as SEQ ID NO 236 and SEQ ID NO 237 , respectively) in a PCR reaction with the following conditions: 4 minutes at 95 °C, followed by 35 cycles of 30 seconds at 95 °C, 30 seconds at 55 °C and 1 minute at 72 °C, followed by 10 minutes at 72°C. The anti-sense T7 template was generated using the specific FW primer oGAU181 and the specific T7 RV

30 primer oGAU184 (represented herein as SEQ ID NO 238 and SEQ ID NO 239 , respectively) in a PCR reaction with the same conditions as described above. The resulting PCR products were analyzed on agarose gel and purified (QIAquick® PCR Purification Kit; Cat. N°. 28106, Qiagen). The generated T7 FW and RV templates were mixed to be transcribed and the resulting RNA strands were annealed, DNase and RNase treated, and purified by precipitation with sodium

35 acetate and isopropanol, following the manufacturer's protocol, but with the following modification: RNA peppet is washed twice in 70% ethanol. The sense strands of the resulting dsRNA is herein represented by SEQ ID NO 235.

D. Laboratory trials to screen dsRNA targets using liquid artificial diet for activity against _Nilaparvata lugens_

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Liquid artificial diet (MMD-1) for the rice brown planthopper, *Nilaparvata lugens*, was prepared as described by Koyama (1988) [Artificial rearing and nutritional physiology of the planthoppers and leafhoppers (Homoptera: Delphacidae and Deltocephalidae) on a holidic diet. *JARQ* 22: 20–27], but with a modification in final concentration of diet component sucrose: 14.4 %

5   (weight over volume) was used. Diet components were prepared as separate concentrates: 10 x mineral stock (stored at 4 °C), 2 x amino acid stock (stored at -20 °C) and 10 x vitamin stock (stored at -20 °C). The stock components were mixed immediately prior to the start of a bioassay to 4/3 x concentration to allow dilution with the test dsRNA solution (4 x concentration), pH adjusted to 6.5, and filter-sterilised into approximately 500 µl aliquots.

10   Rice brown planthopper (*Nilaparvata lugens*) was reared on two-to-three month old rice (*Oryza sativa* cv Taichung Native 1) plants in a controlled environment chamber: 27 ± 2 °C, 80 % relative humidity, with a 16:8 hours light:dark photoperiod. A feeding chamber comprised 10 first or second instar nymphs placed in a small petri dish (with diameter 3 cm) covered with a single layer of thinly stretched parafilm M onto which 50 µl of diet was added. The chamber was sealed with a

15   second layer of parafilm and incubated under the same conditions as the adult cultures but with no direct light exposure. Diet with dsRNA was refreshed every other day and the insects' survival assessed daily. Per treatment, 5 bioassay feeding chambers (replicates) were set up simultaneously. Test and control (gfp) dsRNA solutions were incorporated into the diet to a final concentration of 2 mg/ml. The feeding chambers were kept at 27 ± 2 °C, 80 % relative humidity,

20   with a 16:8 hours light:dark photoperiod. Insect survival data were analysed using the Kaplan-Meier survival curve model and the survival between groups were compared using the logrank test (Prism version 4.0).

Feeding liquid artificial diet supplemented with intact naked dsRNAs to *Nilaparvata lugens in vitro* using a feeding chamber resulted in significant increases in nymphal mortalities as shown in

25   four separate bioassays (**Figures 1(a)-(d)-NL; Tables 10-NL(a)-(d)**) (Durham University). These results demonstrate that dsRNAs corresponding to different essential BPH genes showed significant toxicity towards the rice brown planthopper.

Effect of gfp dsRNA on BPH survival in these bioassays is not significantly different to survival on diet only

30   **Tables 10-NL(a)-(d)** show a summary of the survival of *Nilaparvata lugens* on artificial diet supplemented with 2 mg/ml (final concentration) of the following targets; in **Table 10-NL(a)**: NL002, NL003, NL005, NL010; in **Table 10-NL(b)**: NL009, NL016; in **Table 10-NL(c)**: NL014, NL018; and in **Table 10-NL(d)**: NL013, NL015, NL021. In the survival analysis column, the effect of RNAi is indicated as follows: + = significantly decreased survival compared to gfp dsRNA control (alpha <

35   0.05); - = no significant difference in survival compared to gfp dsRNA control. Survival curves were compared (between diet only and diet supplemented with test dsRNA, gfp dsRNA and test dsRNA, and diet only and gfp dsRNA) using the logrank test.

E. Laboratory trials to screen dsRNAs at different concentrations using artificial diet for activity against *Nilaparvata lugens*

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Fifty µl of liquid artificial diet supplemented with different concentrations of target NL002 dsRNA, namely 1, 0.2, 0.08, and 0.04 mg/ml (final concentration), was applied to the brown planthopper feeding chambers. Diet with dsRNA was refreshed every other day and the insects' survival assessed daily. Per treatment, 5 bioassay feeding chambers (replicates) were set up simultaneously. The feeding chambers were kept at 27 ± 2 °C, 80 % relative humidity, with a 16:8 hours light:dark photoperiod. Insect survival data were analysed using the Kaplan-Meier survival curve model and the survival between groups were compared using the logrank test (Prism version 4.0).

Feeding liquid artificial diet supplemented with intact naked dsRNAs of target NL002 at different concentrations resulted in significantly higher BPH mortalities at final concentrations of as low as 0.04 mg dsRNA per ml diet when compared with survival on diet only, as shown in **Figure 2-NL** and **Table 11-NL**. **Table 11-NL** summarizes the survival of *Nilaparvata lugens* artificial diet feeding trial supplemented with 1, 0.2, 0.08, & 0.04 mg/ml (final concentration) of target NL002. In the survival analysis column the effect of RNAi is indicated as follows: + = significantly decreases survival compared to diet only control (alpha < 0.05); - = no significant differences in survival compared to diet only control. Survival curves were compared using the logrank test.

F. Cloning of a BPH gene fragment in a vector suitable for bacterial production of insect-active double-stranded RNA

What follows is an example of cloning a DNA fragment corresponding to a BPH gene target in a vector for the expression of double-stranded RNA in a bacterial host, although any vector comprising a T7 promoter or any other promoter for efficient transcription in bacteria, may be used (reference to WO0001846).

The sequences of the specific primers used for the amplification of target genes are provided in **Table 8-NL**. The template used is the pCR8/GW/topo vector containing any of target sequences. The primers are used in a PCR reaction with the following conditions: 5 minutes at 98°C, followed by 30 cycles of 10 seconds at 98°C, 30 seconds at 55°C and 2 minutes at 72°C, followed by 10 minutes at 72°C. The resulting PCR fragment is analyzed on agarose gel, purified (QIAquick Gel Extraction kit, Cat. Nr. 28706, Qiagen), blunt-end cloned into *Srf* I-linearized pGNA49A vector (reference to WO00188121A1), and sequenced. The sequence of the resulting PCR product corresponds to the respective sequence as given in **Table 8-NL**. The recombinant vector harboring this sequence is named pGXXX0XX.

G. Expression and production of a double-stranded RNA target In two strains of *Escherichia coli*: (1) AB301-105(DE3), and, (2) BL21(DE3)

The procedures described below are followed in order to express suitable levels of insect-active double-stranded RNA of insect target in bacteria. An RNaseIII-deficient strain, AB301-105(DE3), is used in comparison to wild-type RNaseIII-containing bacteria, BL21(DE3).

Transformation of AB301-105(DE3) and BL21(DE3)

Three hundred ng of the plasmid are added to and gently mixed in a 50 µl aliquot of ice-chilled chemically competent *E. coli* strain AB301-105(DE3) or BL21(DE3). The cells are incubated

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on ice for 20 minutes before subjecting them to a heat shock treatment of 37 °C for 5 minutes, after which the cells are placed back on ice for a further 5 minutes. Four hundred and fifty µl of room temperature SOC medium is added to the cells and the suspension incubated on a shaker (250 rpm) at 37 °C for 1 hour. One hundred µl of the bacterial cell suspension is transferred to a 500 ml

5   conical flask containing 150 ml of liquid Luria-Bertani (LB) broth supplemented with 100 µg/ml carbenicillin antibiotic. The culture is incubated on an Innova 4430 shaker (250 rpm) at 37 °C overnight (16 to 18 hours).

Chemical induction of double-stranded RNA expression in AB301-105(DE3) and BL21(DE3)

Expression of double-stranded RNA from the recombinant vector, pGXXX0XX, in the

10   bacterial strain AB301-105(DE3) or BL21(DE3) is made possible since all the genetic components for controlled expression are present. In the presence of the chemical inducer isopropylthiogalactoside, or IPTG, the T7 polymerase will drive the transcription of the target sequence in both antisense and sense directions since these are flanked by oppositely oriented T7 promoters.

15   The optical density at 600 nm of the overnight bacterial culture is measured using an appropriate spectrophotometer and adjusted to a value of 1 by the addition of fresh LB broth. Fifty ml of this culture is transferred to a 50 ml Falcon tube and the culture then centrifuged at 3000 g at 15 °C for 10 minutes. The supernatant is removed and the bacterial pellet resuspended in 50 ml of fresh S complete medium (SNC medium plus 5 µg/ml cholesterol) supplemented with 100 µg/ml

20   carbenicillin and 1 mM IPTG. The bacteria are induced for 2 to 4 hours at room temperature.

Heat treatment of bacteria

Bacteria are killed by heat treatment in order to minimise the risk of contamination of the artificial diet in the test plates. However, heat treatment of bacteria expressing double-stranded RNA is not a prerequisite for inducing toxicity towards the insects due to RNA interference. The

25   induced bacterial culture is centrifuged at 3000 g at room temperature for 10 minutes, the supernatant discarded and the pellet subjected to 80 °C for 20 minutes in a water bath. After heat treatment, the bacterial pellet is resuspended in 1.5 ml MilliQ water and the suspension transferred to a microfuge tube. Several tubes are prepared and used in the bioassays for each refreshment. The tubes are stored at -20 °C until further use.

30   **H. Laboratory trials to test *Escherichia coli* expressing dsRNA targets against *Nilaparvata lugens***

Plant-based bioassays

. Whole plants are sprayed with suspensions of chemically induced bacteria expressing dsRNA prior to feeding the plants to BPH. The are grown from in a plant growth room chamber.

35   The plants are caged by placing a 500 ml plastic bottle upside down over the plant with the neck of the bottle firmly placed in the soil in a pot and the base cut open and covered with a fine nylon mesh to permit aeration, reduce condensation inside and prevent insect escape. BPH are placed on each treated plant in the cage. Plants are treated with a suspension of *E. coli* AB301-105(DE3) harboring the pGXXX0XX plasmids or pGN29 plasmid. Different quantities of bacteria are applied

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to the plants: for instance 66, 22, and 7 units, where one unit is defined as 10^9 bacterial cells in 1 ml of a bacterial suspension at optical density value of 1 at 600 nm wavelength. In each case, a total volume of between 1 and 10 ml s sprayed on the plant with the aid of a vaporizer. One plant is used per treatment in this trial. The number of survivors are counted and the weight of each
5   survivor recorded.

Spraying plants with a suspension of E. coli bacterial strain AB301-105(DE3) expressing target dsRNA from pGXXX0XX leed to a dramatic increase in insect mortality when compared to pGN29 control. These experiments show that double-stranded RNA corresponding to an insect gene target sequence produced in either wild-type or RNaseIII-deficient bacterial expression
10   systems is toxic towards the insect in terms of substantial increases in insect mortality and growth/development delay for larval survivors. It is also clear from these experiments that an exemplification is provided for the effective protection of plants/crops from insect damage by the use of a spray of a formulation consisting of bacteria expressing double-stranded RNA corresponding to an insect gene target.

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Example 10: *Chilo suppressalis* (Rice striped stem borer)

A. Cloning of partial sequence of the *Chilo suppressalis* genes via family PCR

High quality, intact RNA was isolated from the 4 different larval stages of Chilo suppressalis (rice striped stem borer) using TRIzol Reagent (Cat. Nr. 15596-026/15596-018,
20. Invitrogen, Rockville, Maryland, USA) following the manufacturer's instructions. Genomic DNA present in the RNA preparation was removed by DNase treatment following the manafacturer's instructions (Cat. Nr. 1700, Promega). cDNA was generated using a commercially available kit (SuperScript ™ III Reverse Transcriptase, Cat. Nr. 18080044, Invitrogen, Rockville, Maryland, USA) following the manufacturer's instructions.
25   To isolate cDNA sequences comprising a portion of the CS001, CS002, CS003, CS006, CS007, CS009, CS011, CS013, CS014, CS015, CS016 and CS018 genes, a series of PCR reactions with degenerate primers were performed using Amplitaq Gold (Cat. Nr. N8080240, Applied Biosystems) following the manafacturer's instructions.

The sequences of the degenerate primers used for amplification of each of the genes are
30   given in Table 2-CS. These primers were used in respective PCR reactions with the following conditions: 10 minutes at 95°C, followed by 40 cycles of 30 seconds at 95°C, 1 minute at 55°C and 1 minute at 72°C, followed by 10 minutes at 72°C. The resulting PCR fragments were analyzed on agarose gel, purified (QIAquick Gel Extraction kit, Cat. Nr. 28706, Qiagen), cloned into the pCR4/TOPO vector (Cat. Nr. K2500-20, Invitrogen), and sequenced. The sequences of the
35   resulting PCR products are represented by the respective SEQ ID NOs as given in Table 2-CS and are referred to as the partial sequences. The corresponding partial amino acid sequences are represented by the respective SEQ ID NOs as given in **Table 3-CS**.

B. dsRNA production of the *Chilo suppressalis* genes

dsRNA was synthesized in milligram amounts using the commercially available kit T7 Ribomax™ Express RNAi System (Cat. Nr. P1700, Promega). First two separate single 5' T7 RNA polymerase promoter templates were generated in two separate PCR reactions, each reaction containing the target sequence in a different orientation relative to the T7 promoter.

5   For each of the target genes, the sense T7 template was generated using specific T7 forward and specific reverse primers. The sequences of the respective primers for amplifying the sense template for each of the target genes are given in **Table 8-CS**. The conditions in the PCR reactions were as follows: 4 minutes at 95°C, followed by 35 cycles of 30 seconds at 95°C, 30 seconds at 55°C and 1 minute at 72°C, followed by 10 minutes at 72°C. The anti-sense T7

10   template was generated using specific forward and specific T7 reverse primers in a PCR reaction with the same conditions as described above. The sequences of the respective primers for amplifying the anti-sense template for each of the target genes are given in **Table 8-CS**. The resulting PCR products were analyzed on agarose gel and purified by PCR purification kit (Qiaquick PCR Purification Kit, Cat. Nr. 28106, Qiagen) and NaClO$_4$ precipitation. The generated

15   T7 forward and reverse templates were mixed to be transcribed and the resulting RNA strands were annealed, DNase and RNase treated, and purified by sodium acetate, following the manufacturer's instructions. The sense strand of the resulting dsRNA for each of the target genes is given in **Table 8-CS**.

C. Laboratory trials to test dsRNA targets, using artificial diet for activity against

20   *Chilo suppressalis* **larvae**

Rice striped stem borers, *Chilo suppressalis*, (origin: Syngenta, Stein, Switzerland) were maintained on a modified artificial diet based on that described by Kamano and Sato, 1985 (in: Handbook of Insect Rearing. Volumes I & II. P Singh and RF Moore, eds., Elsevier Science Publishers, Amsterdam and New York, 1985, pp 448). Briefly, a litre diet was made up as follows:

25   20 g of agar added to 980 ml of Milli-Q water and autoclaved; the agar solution was cooled down to approximately 55 °C and the remaining ingredients were added and mixed thoroughly: 40 g corn flour (Polenta), 20 g cellulose, 30 g sucrose, 30 g casein, 20 g wheat germ (toasted), 8 g Wesson salt mixture, 12 g Vanderzant vitamin mix, 1.8 g sorbic acid, 1.6 g nipagin (methylparaben), 0.3 g aureomycin, 0.4 g cholesterol and 0.6 g L-cysteine. The diet was cooled down to approx. 45 °C and

30   poured into rearing trays or cups. The diet was left to set in a horizontal laminair flow cabin. Rice leaf sections with oviposited eggs were removed from a cage housing adult moths and pinned to the solid diet in the rearing cup or tray. Eggs were left to hatch and neonate larvae were available for bioassays and the maintenance of the insect cultures. During the trials and rearings, the conditions were 28 ± 2 °C and 80 ± 5 % relative humidity, with a 16:8 hour light:dark photoperiod.

35   The same artificial diet is used for the bioassays but in this case the diet is poured equally in 24 multiwell plates, with each well containing 1 ml diet. Once the diet is set, the test formulations are applied to the diet's surface (2 cm^2), at the rate of 50 µl of 1 µg/µl dsRNA of target. The dsRNA solutions are left to dry and two first instar moth larvae are placed in each well. After 7 days, the larvae are transferred to fresh treated diet in multiwell plates. At day 14 (i.e. 14 days post bioassay

start) the number of live and dead insects is recorded and examined for abnormalities. Twenty-four larvae in total are tested per treatment.

An alternative bioassay is performed in which treated rice leaves are fed to neonate larvae of the rice striped stem borer. Small leaf sections of *Indica* rice variety Taichung native 1 are dipped in 0.05 % Triton X-100 solution containing 1 µg/µl of target dsRNA, left to dry and each section placed in a well of a 24 multiwell plate containing gellified 2 % agar. Two neonates are transferred from the rearing tray to each dsRNA treated leaf section (24 larvae per treatment). After 4 and 8 days, the larvae are transferred to fresh treated rice leaf sections. The number of live and dead larvae are assessed on days 4, 8 and 12; any abnormalities are also recorded.

D. Cloning of a SSB gene fragment in a vector suitable for bacterial production of insect-active double-stranded RNA

What follows is an example of cloning a DNA fragment corresponding to an SSB gene target in a vector for the expression of double-stranded RNA in a bacterial host, although any vector comprising a T7 promoter or any other promoter for efficient transcription in bacteria, may be used (reference to WO0001846).

The sequences of the specific primers used for the amplification of target genes are provided in **Table 8-CS**. The template used is the pCR8/GW/topo vector containing any of target sequences. The primers are used in a PCR reaction with the following conditions: 5 minutes at 98°C, followed by 30 cycles of 10 seconds at 98°C, 30 seconds at 55°C and 2 minutes at 72°C, followed by 10 minutes at 72°C. The resulting PCR fragment is analyzed on agarose gel, purified (QIAquick Gel Extraction kit, Cat. Nr. 28706, Qiagen), blunt-end cloned into *Srf* I-linearized pGNA49A vector (reference to WO00188121A1), and sequenced. The sequence of the resulting PCR product corresponds to the respective sequence as given in **Table 8-CS**. The recombinant vector harboring this sequence is named pGXXX0XX.

E. Expression and production of a double-stranded RNA target in two strains of *Escherichia coli*: (1) AB301-105(DE3), and, (2) BL21(DE3)

The procedures described below are followed in order to express suitable levels of insect-active double-stranded RNA of insect target in bacteria. An RNaseIII-deficient strain, AB301-105(DE3), is used in comparison to wild-type RNaseIII-containing bacteria, BL21(DE3).

Transformation of AB301-105(DE3) and BL21(DE3)

Three hundred ng of the plasmid are added to and gently mixed in a 50 µl aliquot of ice-chilled chemically competent *E. coli* strain AB301-105(DE3) or BL21(DE3). The cells are incubated on ice for 20 minutes before subjecting them to a heat shock treatment of 37 °C for 5 minutes, after which the cells are placed back on ice for a further 5 minutes. Four hundred and fifty µl of room temperature SOC medium is added to the cells and the suspension incubated on a shaker (250 rpm) at 37 °C for 1 hour. One hundred µl of the bacterial cell suspension is transferred to a 500 ml conical flask containing 150 ml of liquid Luria-Bertani (LB) broth supplemented with 100 µg/ml carbenicillin antibiotic. The culture is incubated on an Innova 4430 shaker (250 rpm) at 37 °C overnight (16 to 18 hours).

Chemical induction of double-stranded RNA expression in AB301-105(DE3) and BL21(DE3)

      Expression of double-stranded RNA from the recombinant vector, pGXXX0XX, in the bacterial strain AB301-105(DE3) or BL21(DE3) is made possible since all the genetic components for controlled expression are present. In the presence of the chemical inducer isopropylthiogalactoside, or IPTG, the T7 polymerase will drive the transcription of the target sequence in both antisense and sense directions since these are flanked by oppositely oriented T7 promoters.

      The optical density at 600 nm of the overnight bacterial culture is measured using an appropriate spectrophotometer and adjusted to a value of 1 by the addition of fresh LB broth. Fifty ml of this culture is transferred to a 50 ml Falcon tube and the culture then centrifuged at 3000 g at 15 °C for 10 minutes. The supernatant is removed and the bacterial pellet resuspended in 50 ml of fresh S complete medium (SNC medium plus 5 µg/ml cholesterol) supplemented with 100 µg/ml carbenicillin and 1 mM IPTG. The bacteria are induced for 2 to 4 hours at room temperature.

Heat treatment of bacteria

      Bacteria are killed by heat treatment in order to minimise the risk of contamination of the artificial diet in the test plates. However, heat treatment of bacteria expressing double-stranded RNA is not a prerequisite for inducing toxicity towards the insects due to RNA interference. The induced bacterial culture is centrifuged at 3000 g at room temperature for 10 minutes, the supernatant discarded and the pellet subjected to 80 °C for 20 minutes in a water bath. After heat treatment, the bacterial pellet is resuspended in 1.5 ml MilliQ water and the suspension transferred to a microfuge tube. Several tubes are prepared and used in the bioassays for each refreshment. The tubes are stored at -20 °C until further use.

      F. Laboratory trials to test *Escherichia coli* expressing dsRNA targets against *Chilo suppressalis*

Plant-based bioassays

      Whole plants are sprayed with suspensions of chemically induced bacteria expressing dsRNA prior to feeding the plants to SSB. The are grown from in a plant growth room chamber. The plants are caged by placing a 500 ml plastic bottle upside down over the plant with the neck of the bottle firmly placed in the soil in a pot and the base cut open and covered with a fine nylon mesh to permit aeration, reduce condensation inside and prevent insect escape. SSB are placed on each treated plant in the cage. Plants are treated with a suspension of *E. coli* AB301-105(DE3) harboring the pGXXX0XX plasmids or pGN29 plasmid. Different quantities of bacteria are applied to the plants: for instance 66, 22, and 7 units, where one unit is defined as 10^9 bacterial cells in 1 ml of a bacterial suspension at optical density value of 1 at 600 nm wavelength. In each case, a total volume of between 1 and 10 ml s sprayed on the plant with the aid of a vaporizer. One plant is used per treatment in this trial. The number of survivors are counted and the weight of each survivor recorded.

      Spraying plants with a suspension of *E. coli* bacterial strain AB301-105(DE3) expressing target dsRNA from pGXXX0XX leed to a dramatic increase in insect mortality when compared to

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pGN29 control. These experiments show that double-stranded RNA corresponding to an insect gene target sequence produced in either wild-type or RNaseIII-deficient bacterial expression systems is toxic towards the insect in terms of substantial increases in insect mortality and growth/development delay for larval survivors. It is also clear from these experiments that an

5   exemplification is provided for the effective protection of plants/crops from insect damage by the use of a spray of a formulation consisting of bacteria expressing double-stranded RNA corresponding to an insect gene target.

Example 11: *Plutella xylostella* (Diamondback moth)

10   A. Cloning of a partial sequence of the *Plutella xylostella*

High quality, intact RNA was isolated from all the different larval stages of Plutella xylostella (Diamondback moth; source: Dr. Lara Senior, Insect Investigations Ltd., Capital Business Park, Wentloog, Cardiff, CF3 2PX, Wales, UK) using TRIzol Reagent (Cat. Nr. 15596-026/15596-018, Invitrogen, Rockville, Maryland, USA) following the manufacturer's instructions. Genomic DNA

15 present in the RNA preparation was removed by DNase treatment following the manufacturer's instructions (Cat. Nr. 1700, Promega). cDNA was generated using a commercially available kit (SuperScript ^{TM} III Reverse Transcriptase, Cat. Nr. 18080044, Invitrogen, Rockville, Maryland, USA) following the manufacturer's instructions.

To isolate cDNA sequences comprising a portion of the PX001, PX009, PX010, PX015,

20 PX016 genes, a series of PCR reactions with degenerate primers were performed using Amplitaq Gold (Cat. Nr. N8080240, Applied Biosystems) following the manufacturer's instructions.

The sequences of the degenerate primers used for amplification of each of the genes are given in **Table 2-PX**. These primers were used in respective PCR reactions with the following conditions: 10 minutes at 95°C, followed by 40 cycles of 30 seconds at 95°C, 1 minute at 50°C and

25 1 minute and 30 seconds at 72°C, followed by 7 minutes at 72°C (for PX001, PX009, PX015, PX016); 10 minutes at 95°C, followed by 40 cycles of 30 seconds at 95°C, 1 minute at 54°C and 2 minute and 30 seconds at 72°C, followed by 7 minutes at 72°C (for PX010). The resulting PCR fragments were analyzed on agarose gel, purified (QIAquick Gel Extraction kit, Cat. Nr. 28706, Qiagen), cloned into the pCR8/GW/TOPO vector (Cat. Nr. K2500-20, Invitrogen) and sequenced.

30 The sequences of the resulting PCR products are represented by the respective SEQ ID NOs as given in **Table 2-PX** and are referred to as the partial sequences. The corresponding partial amino acid sequence are represented by the respective SEQ ID NOs as given in **Table 3-PX**.

      B. dsRNA production of the *Plutella xylostella* genes

dsRNA was synthesized in milligram amounts using the commercially available kit T7

35 Ribomax^{TM} Express RNAi System (Cat. Nr. P1700, Promega). First two separate single 5' T7 RNA polymerase promoter templates were generated in two separate PCR reactions, each reaction containing the target sequence in a different orientation relative to the T7 promoter.

For each of the target genes, the sense T7 template was generated using specific T7 forward and specific reverse primers. The sequences of the respective primers for amplifying the

sense template for each of the target genes are given in **Table 8-PX**. The conditions in the PCR reactions were as follows: 1 minute at 95°C, followed by 20 cycles of 30 seconds at 95°C, 30 seconds at 60°C (-0.5°C/cycle) and 1 minute at 72°C, followed by 15 cycles of 30 seconds at 95°C, 30 seconds at 50°C and 1 minute at 72°C, followed by 10 minutes at 72°C. The anti-sense T7

5   template was generated using specific forward and specific T7 reverse primers in a PCR reaction with the same conditions as described above. The sequences of the respective primers for amplifying the anti-sense template for each of the target genes are given in **Table 8-PX**. The resulting PCR products were analyzed on agarose gel and purified by PCR purification kit (Qiaquick PCR Purification Kit, Cat. Nr. 28106, Qiagen) and $NaClO_4$ precipitation. The generated

10   T7 forward and reverse templates were mixed to be transcribed and the resulting RNA strands were annealed, DNase and RNase treated, and purified by sodium acetate, following the manufacturer's instructions. The sense strand of the resulting dsRNA for each of the target genes is given in **Table 8-PX**.

C. Laboratory trials to test dsRNA targets, using artificial diet for activity against
15   *Plutella xylostella* **larvae**

Diamond-back moths, *Plutella xylostella*, were maintained at Insect Investigations Ltd. (origin: Newcastle University, Newcastle-upon-Tyne, UK). The insects were reared on cabbage leaves. First instar, mixed sex larvae (approximately 1 day old) were selected for use in the trial. Insects were maintained in Eppendorf tubes (1.5 ml capacity). Commercially available Diamond-

20   back moth diet (Bio-Serv, NJ, USA), prepared following the manafacturer's instructions, was placed in the lid of each tube (0.25 ml capacity, 8 mm diameter). While still liquid, the diet was smoother over to remove excess and produce an even surface.

Once the diet has set the test formulations are applied to the diet's surface, at the rate of 25 µl undiluted formulation (1 µg/µl dsRNA of targets) per replicate. The test formulations are

25   allowed to dry and one first instar moth larva is placed in each tube. The larva is placed on the surface of the diet in the lid and the tube carefully closed. The tubes are stored upside down, on their lids such that each larva remains on the surface of the diet. Twice weekly the larvae are transferred to new Eppendorf tubes with fresh diet. The insects are provided with treated diet for the first two weeks of the trial and thereafter with untreated diet.

30   Assessments are made twice weekly for a total of 38 days at which point all larvae are dead. At each assessment the insects are assessed as live or dead and examined for abnormalities. Forty single larva replicates are performed for each of the treatments. During the trial the test conditions are 23 to 26 °C and 50 to 65 % relative humidity, with a 16:8 hour light:dark photoperiod.

35   **D. Cloning of a DBM gene fragment in a vector suitable for bacterial production of insect-active double-stranded RNA**

What follows is an example of cloning a DNA fragment corresponding to a DBM gene target in a vector for the expression of double-stranded RNA in a bacterial host, although any

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vector comprising a T7 promoter or any other promoter for efficient transcription in bacteria, may be used (reference to WO0001846).

The sequences of the specific primers used for the amplification of target genes are provided in **Table 8-PX**. The template used is the pCR8/GW/topo vector containing any of target sequences. The primers are used in a PCR reaction with the following conditions: 5 minutes at 98°C, followed by 30 cycles of 10 seconds at 98°C, 30 seconds at 55°C and 2 minutes at 72°C, followed by 10 minutes at 72°C. The resulting PCR fragment is analyzed on agarose gel, purified (QIAquick Gel Extraction kit, Cat. Nr. 28706, Qiagen), blunt-end cloned into *Srf* I-linearized pGNA49A vector (reference to WO00188121A1), and sequenced. The sequence of the resulting PCR product corresponds to the respective sequence as given in **Table 8-PX**. The recombinant vector harboring this sequence is named pGXXX0XX.

E. Expression and production of a double-stranded RNA target in two strains of *Escherichia coli*: (1) AB301-105(DE3), and, (2) BL21(DE3)

The procedures described below are followed in order to express suitable levels of insect-active double-stranded RNA of insect target in bacteria. An RNaseIII-deficient strain, AB301-105(DE3), is used in comparison to wild-type RNaseIII-containing bacteria, BL21(DE3).

Transformation of AB301-105(DE3) and BL21(DE3)

Three hundred ng of the plasmid are added to and gently mixed in a 50 µl aliquot of ice-chilled chemically competent *E. coli* strain AB301-105(DE3) or BL21(DE3). The cells are incubated on ice for 20 minutes before subjecting them to a heat shock treatment of 37 °C for 5 minutes, after which the cells are placed back on ice for a further 5 minutes. Four hundred and fifty µl of room temperature SOC medium is added to the cells and the suspension incubated on a shaker (250 rpm) at 37 °C for 1 hour. One hundred µl of the bacterial cell suspension is transferred to a 500 ml conical flask containing 150 ml of liquid Luria-Bertani (LB) broth supplemented with 100 µg/ml carbenicillin antibiotic. The culture is incubated on an Innova 4430 shaker (250 rpm) at 37 °C overnight (16 to 18 hours).

Chemical induction of double-stranded RNA expression in AB301-105(DE3) and BL21(DE3)

Expression of double-stranded RNA from the recombinant vector, pGXXX0XX, in the bacterial strain AB301-105(DE3) or BL21(DE3) is made possible since all the genetic components for controlled expression are present. In the presence of the chemical inducer isopropylthiogalactoside, or IPTG, the T7 polymerase will drive the transcription of the target sequence in both antisense and sense directions since these are flanked by oppositely oriented T7 promoters.

The optical density at 600 nm of the overnight bacterial culture is measured using an appropriate spectrophotometer and adjusted to a value of 1 by the addition of fresh LB broth. Fifty ml of this culture is transferred to a 50 ml Falcon tube and the culture then centrifuged at 3000 g at 15 °C for 10 minutes. The supernatant is removed and the bacterial pellet resuspended in 50 ml of fresh S complete medium (SNC medium plus 5 µg/ml cholesterol) supplemented with 100 µg/ml carbenicillin and 1 mM IPTG. The bacteria are induced for 2 to 4 hours at room temperature.

Heat treatment of bacteria

Bacteria are killed by heat treatment in order to minimise the risk of contamination of the artificial diet in the test plates. However, heat treatment of bacteria expressing double-stranded RNA is not a prerequisite for inducing toxicity towards the insects due to RNA interference. The induced bacterial culture is centrifuged at 3000 g at room temperature for 10 minutes, the supernatant discarded and the pellet subjected to 80 °C for 20 minutes in a water bath. After heat treatment, the bacterial pellet is resuspended in 1.5 ml MilliQ water and the suspension transferred to a microfuge tube. Several tubes are prepared and used in the bioassays for each refreshment. The tubes are stored at -20 °C until further use.

F. Laboratory trials to test *Escherichia coli* expressing dsRNA targets against *Plutella xylostella*

Plant-based bioassays

Whole plants are sprayed with suspensions of chemically induced bacteria expressing dsRNA prior to feeding the plants to DBM. The are grown from in a plant growth room chamber. The plants are caged by placing a 500 ml plastic bottle upside down over the plant with the neck of the bottle firmly placed in the soil in a pot and the base cut open and covered with a fine nylon mesh to permit aeration, reduce condensation inside and prevent insect escape. DBM are placed on each treated plant in the cage. Plants are treated with a suspension of *E. coli* AB301-105(DE3) harboring the pGXXX0XXplasmids or pGN29 plasmid. Different quantities of bacteria are applied to the plants: for instance 66, 22, and 7 units, where one unit is defined as 10^9 bacterial cells in 1 ml of a bacterial suspension at optical density value of 1 at 600 nm wavelength. In each case, a total volume of between 1 and 10 ml s sprayed on the plant with the aid of a vaporizer. One plant is used per treatment in this trial. The number of survivors are counted and the weight of each survivor recorded.

Spraying plants with a suspension of *E. coli* bacterial strain AB301-105(DE3) expressing target dsRNA from pGXXX0XX leed to a dramatic increase in insect mortality when compared to pGN29 control. These experiments show that double-stranded RNA corresponding to an insect gene target sequence produced in either wild-type or RNaseIII-deficient bacterial expression systems is toxic towards the insect in terms of substantial increases in insect mortality and growth/development delay for larval survivors. It is also clear from these experiments that an exemplification is provided for the effective protection of plants/crops from insect damage by the use of a spray of a formulation consisting of bacteria expressing double-stranded RNA corresponding to an insect gene target.

Example 12: *Acheta domesticus* (House cricket)

A. Cloning *Acheta domesticus* partial sequences

High quality, intact RNA was isolated from all the different insect stages of *Acheta domesticus* (house cricket; source: Dr. Lara Senior, Insect Investigations Ltd., Capital Business Park, Wentloog, Cardiff, CF3 2PX, Wales, UK) using TRIzol Reagent (Cat. Nr. 15596-026/15596-

018, Invitrogen, Rockville, Maryland, USA) following the manufacturer's instructions. Genomic DNA present in the RNA preparation was removed by DNase treatment following the manafacturer's instructions (Cat. Nr. 1700, Promega). cDNA was generated using a commercially available kit (SuperScript ™ III Reverse Transcriptase, Cat. Nr. 18080044, Invitrogen, Rockville, Maryland, USA) following the manufacturer's instructions.

To isolate cDNA sequences comprising a portion of the AD001, AD002, AD009, AD015 and AD016 genes, a series of PCR reactions with degenerate primers were performed using Amplitaq Gold (Cat. Nr. N8080240, Applied Biosystems) following the manafacturer's instructions.

The sequences of the degenerate primers used for amplification of each of the genes are given in **Table 2-AD**. These primers were used in respective PCR reactions with the following conditions: 10 minutes at 95°C, followed by 40 cycles of 30 seconds at 95°C, 1 minute at 50°C and 1 minute and 30 seconds at 72°C, followed by 7 minutes at 72°C. The resulting PCR fragments were analyzed on agarose gel, purified (QIAquick Gel Extraction kit, Cat. Nr. 28706, Qiagen), cloned into the pCR8/GW/topo vector (Cat. Nr. K2500 20, Invitrogen) and sequenced. The sequences of the resulting PCR products are represented by the respective SEQ ID NOs as given in **Table 2-AD** and are referred to as the partial sequences. The corresponding partial amino acid sequence are represented by the respective SEQ ID NOs as given in **Table 3-AD**.

B. dsRNA production of the *Acheta domesticus* genes

dsRNA was synthesized in milligram amounts using the commercially available kit T7 Ribomax™ Express RNAi System (Cat. Nr. P1700, Promega). First two separate single 5' T7 RNA polymerase promoter templates were generated in two separate PCR reactions, each reaction containing the target sequence in a different orientation relative to the T7 promoter.

For each of the target genes, the sense T7 template was generated using specific T7 forward and specific reverse primers. The sequences of the respective primers for amplifying the sense template for each of the target genes are given in **Table 8-AD**. The conditions in the PCR reactions were as follows: 1 minute at 95°C, followed by 20 cycles of 30 seconds at 95°C, 30 seconds at 60°C (-0.5°C/cycle) and 1 minute at 72°C, followed by 15 cycles of 30 seconds at 95°C, 30 seconds at 50°C and 1 minute at 72°C, followed by 10 minutes at 72°C. The anti-sense T7 template was generated using specific forward and specific T7 reverse primers in a PCR reaction with the same conditions as described above. The sequences of the respective primers for amplifying the anti-sense template for each of the target genes are given in **Table 8-AD**. The resulting PCR products were analyzed on agarose gel and purified by PCR purification kit (Qiaquick PCR Purification Kit, Cat. Nr. 28106, Qiagen) and NaClO₄ precipitation. The generated T7 forward and reverse templates were mixed to be transcribed and the resulting RNA strands were annealed, DNase and RNase treated, and purified by sodium acetate, following the manufacturer's instructions. The sense strand of the resulting dsRNA for each of the target genes is given in **Table 8-AD**.

C. Laboratory trials to test dsRNA targets, using artificial diet for activity against *Acheta domesticus* larvae

House crickets, *Acheta domesticus*, were maintained at Insect Investigations Ltd. (origin: Blades Biological Ltd., Kent, UK). The insects were reared on bran pellets and cabbage leaves. Mixed sex nymphs of equal size and no more than 5 days old were selected for use in the trial. Double-stranded RNA is mixed with a wheat-based pelleted rodent diet (rat and mouse standard diet, B & K Universal Ltd., Grimston, Aldbrough, Hull, UK). The diet, BK001P, contains the following ingredients in descending order by weight: wheat, soya, wheatfeed, barley, pellet binder, rodent 5 vit min, fat blend, dicalcium phosphate, mould carb. The pelleted rodent diet is finely ground and heat-treated in a microwave oven prior to mixing, in order to inactivate any enzyme components. All rodent diet is taken from the same batch in order to ensure consistency. The ground diet and dsRNA are mixed thoroughly and formed into small pellets of equal weight, which are allowed to dry overnight at room temperature.

Double-stranded RNA samples from targets and gfp control at concentrations 10 µg/µl were applied in the ratio 1 g ground diet plus 1 ml dsRNA solution, thereby resulting in an application rate of 10 mg dsRNA per g pellet. Pellets are replaced weekly. The insects are provided with treated pellets for the first three weeks of the trial. Thereafter untreated pellets are provided. Insects are maintained within lidded plastic containers (9 cm diameter, 4.5 cm deep), ten per container. Each arena contains one treated bait pellet and one water source (damp cotton wool ball), each placed in a separate small weigh boat. The water is replenished *ad lib* throughout the experiment.

Assessments are made at twice weekly intervals, with no more than four days between assessments, until all the control insects had either died or moulted to the adult stage (84 days). At each assessment the insects are assessed as live or dead, and examined for abnormalities. From day 46 onwards, once moulting to adult has commenced, all insects (live and dead) are assessed as nymph or adult. Surviving insects are weighed on day 55 of the trial. Four replicates are performed for each of the treatments. During the trial the test conditions are 25 to 33 °C and 20 to 25 % relative humidity, with a 12:12 hour light:dark photoperiod.

D. Cloning of a HC gene fragment in a vector suitable for bacterial production of insect-active double-stranded RNA

What follows is an example of cloning a DNA fragment corresponding to a HC gene target in a vector for the expression of double-stranded RNA in a bacterial host, although any vector comprising a T7 promoter or any other promoter for efficient transcription in bacteria, may be used (reference to WO0001846).

The sequences of the specific primers used for the amplification of target genes are provided in **Table 8-AD**. The template used is the pCR8/GW/topo vector containing any of target sequences. The primers are used in a PCR reaction with the following conditions: 5 minutes at 98°C, followed by 30 cycles of 10 seconds at 98°C, 30 seconds at 55°C and 2 minutes at 72°C, followed by 10 minutes at 72°C. The resulting PCR fragment is analyzed on agarose gel, purified (QIAquick Gel Extraction kit, Cat. Nr. 28706, Qiagen), blunt-end cloned into *Srf* I-linearized pGNA49A vector (reference to WO00188121A1), and sequenced. The sequence of the resulting

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PCR product corresponds to the respective sequence as given in **Table 8-AD**. The recombinant vector harboring this sequence is named pGXXX0XX.

E. Expression and production of a double-stranded RNA target in two strains of *Escherichia coli*: **(1) AB301-105(DE3), and, (2) BL21(DE3)**

5　　　　The procedures described below are followed in order to express suitable levels of insect-active double-stranded RNA of insect target in bacteria. An RNaseIII-deficient strain, AB301-105(DE3), is used in comparison to wild-type RNaseIII-containing bacteria, BL21(DE3).

Transformation of AB301-105(DE3) and BL21(DE3)

　　　　Three hundred ng of the plasmid are added to and gently mixed in a 50 µl aliquot of ice-
10　　chilled chemically competent *E. coli* strain AB301-105(DE3) or BL21(DE3). The cells are incubated on ice for 20 minutes before subjecting them to a heat shock treatment of 37 °C for 5 minutes, after which the cells are placed back on ice for a further 5 minutes. Four hundred and fifty µl of room temperature SOC medium is added to the cells and the suspension incubated on a shaker (250 rpm) at 37 °C for 1 hour. One hundred µl of the bacterial cell suspension is transferred to a 500 ml
15　　conical flask containing 150 ml of liquid Luria-Bertani (LB) broth supplemented with 100 µg/ml carbenicillin antibiotic. The culture is incubated on an Innova 4430 shaker (250 rpm) at 37 °C overnight (16 to 18 hours).

Chemical induction of double-stranded RNA expression in AB301-105(DE3) and BL21(DE3)

　　　　Expression of double-stranded RNA from the recombinant vector, pGXXX0XX, in the
20　　bacterial strain AB301-105(DE3) or BL21(DE3) is made possible since all the genetic components for controlled expression are present. In the presence of the chemical inducer isopropylthiogalactoside, or IPTG, the T7 polymerase will drive the transcription of the target sequence in both antisense and sense directions since these are flanked by oppositely oriented T7 promoters.

25　　　　The optical density at 600 nm of the overnight bacterial culture is measured using an appropriate spectrophotometer and adjusted to a value of 1 by the addition of fresh LB broth. Fifty ml of this culture is transferred to a 50 ml Falcon tube and the culture then centrifuged at 3000 g at 15 °C for 10 minutes. The supernatant is removed and the bacterial pellet resuspended in 50 ml of fresh S complete medium (SNC medium plus 5 µg/ml cholesterol) supplemented with 100 µg/ml
30　　carbenicillin and 1 mM IPTG. The bacteria are induced for 2 to 4 hours at room temperature.

Heat treatment of bacteria

　　　　Bacteria are killed by heat treatment in order to minimise the risk of contamination of the artificial diet in the test plates. However, heat treatment of bacteria expressing double-stranded RNA is not a prerequisite for inducing toxicity towards the insects due to RNA interference. The
35　　induced bacterial culture is centrifuged at 3000 g at room temperature for 10 minutes, the supernatant discarded and the pellet subjected to 80 °C for 20 minutes in a water bath. After heat treatment, the bacterial pellet is resuspended in 1.5 ml MilliQ water and the suspension transferred to a microfuge tube. Several tubes are prepared and used in the bioassays for each refreshment. The tubes are stored at -20 °C until further use.

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F. Laboratory trials to test *Escherichia coli* expressing dsRNA targets against *Acheta domesticus*

Plant-based bioassays

Whole plants are sprayed with suspensions of chemically induced bacteria expressing
5   dsRNA prior to feeding the plants to HC. The are grown from in a plant growth room chamber. The plants are caged by placing a 500 ml plastic bottle upside down over the plant with the neck of the bottle firmly placed in the soil in a pot and the base cut open and covered with a fine nylon mesh to permit aeration, reduce condensation inside and prevent insect escape. HC are placed on each treated plant in the cage. Plants are treated with a suspension of *E. coli* AB301-105(DE3) harboring
10 the pGXXX0XX plasmids or pGN29 plasmid. Different quantities of bacteria are applied to the plants: for instance 66, 22, and 7 units, where one unit is defined as 10^9 bacterial cells in 1 ml of a bacterial suspension at optical density value of 1 at 600 nm wavelength. In each case, a total volume of between 1 and 10 ml s sprayed on the plant with the aid of a vaporizer. One plant is used per treatment in this trial. The number of survivors are counted and the weight of each
15 survivor recorded.

Spraying plants with a suspension of *E. coli* bacterial strain AB301-105(DE3) expressing target dsRNA from pGXXX0XX leads to a dramatic increase in insect mortality when compared to pGN29 control. These experiments show that double-stranded RNA corresponding to an insect gene target sequence produced in either wild-type or RNaseIII-deficient bacterial expression
20 systems is toxic towards the insect in terms of substantial increases in insect mortality and growth/development delay for larval survivors. It is also clear from these experiments that an exemplification is provided for the effective protection of plants/crops from insect damage by the use of a spray of a formulation consisting of bacteria expressing double-stranded RNA corresponding to an insect gene target.

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Table 1A

C.elegans id	D. melanogaster id	description	devgen RNAi screen
B0250.1	CG1263	large ribosomal subunit L8 protein.	Acute lethal or lethal
B0336.10	CG3661	large ribosomal subunit L23 protein.	Acute lethal or lethal
B0336.2	CG8385	ADP-ribosylation factor.	Acute lethal or lethal
B0464.1	CG3821	Putative aspartyl(D) tRNA synthetase.	Acute lethal or lethal
C01G8.5	CG10701	Ortholog of the ERM family of cytoskeletal linkers	Acute lethal or lethal
C01H6.5	CG33183	Nuclear hormone receptor that is required in all larval molts	Acute lethal or lethal
C02C6.1	CG18102	Member of the DYNamin related gene class	Acute lethal or lethal
C03D6.8	CG6764	Large ribosomal subunit L24 protein (Rlp24p)	Acute lethal or lethal
C04F12.4	CG6253	rpl-14 encodes a large ribosomal subunit L14 protein.	Acute lethal or lethal
C04H5.6	CG10689	Product with RNA helicase activity (EC:2.7.7.-) involved in nuclear mRNA splicing, via spliceosome which is a component of the spliceosome complex	Embryonic lethal or sterile
C13B9.3	CG14813	Delta subunit of the coatomer (COPI) complex	Acute lethal or lethal
C17H12.14	CG1088	Member of the Vacuolar H ATPase gene class	Acute lethal or lethal
C26E6.4	CG3180	DNA-directed RNA polymerase II	Acute lethal or lethal
F23F12.6	CG16916	Triple A ATPase subunit of the 26S proteasome's 19S regulatory particle (RP) base subcomplex	Acute lethal or lethal
F57B9.10	CG10149	Member of the proteasome Regulatory Particle, Non-ATPase-like gene class	Acute lethal or lethal
K11D9.2	CG3725	sarco-endoplasmic reticulum Ca^{2+} ATPase homolog	Embryonic lethal or sterile
T20G5.1	CG9012	Clathrin heavy chain	Acute lethal or lethal
T20H4.3	CG5394	Predicted cytoplasmic prolyl-tRNA synthetase (ProRS)	Acute lethal or lethal
T21E12.4	CG7507	Cytoplasmic dynein heavy chain homolog	Acute lethal or lethal
C05C10.3	CG1140	Orthologue to the human gene 3-OXOACID COA TRANSFERASE	Acute lethal or lethal
C09D4.5	CG2746	Ribosomal protein L19, structural constituent of ribosome involved in protein biosynthesis which is localised to the ribosome	Acute lethal or lethal
C09E10.2	CG31140	Orthologue of diacylglyerol kinase involved in movement, egg laying, and synaptic transmission, and is expressed in neurons.	Acute lethal or lethal
C13B9.3	CG14813	Delta subunit of the coatomer (COPI)	Acute lethal or lethal

C14B9.7	CG12775	Large ribosomal subunit L21 protein (RPL-21) involved in protein biosynthesis	Acute lethal or lethal
C15H11.7	CG30382	Type 6 alpha subunit of the 26S proteasome's 20S protease core particle (CP)	Acute lethal or lethal
C17E4.9	CG9261	Protein involved with Na+/K+- exchanging ATPase complex	Embryonic lethal or sterile
C17H12.14	CG1088	V-ATPase E subunit	Acute lethal or lethal
C23G10.4	CG11888	Non-ATPase subunit of the 26S proteasome's 19S regulatory particle base subcomplex (RPN-2)	Acute lethal or lethal
C26D10.2	CG7269	Product with helicase activity involved in nuclear mRNA splicing, via spliceosome which is localized to the nucleus	Acute lethal or lethal
C26E6.4	CG3180	RNA polymerase II 140kD subunit (RpII140), DNA-directed RNA polymerase activity (EC:2.7.7.6) involved in transcription from Pol II promoter which is a component of the DNA-directed RNA polymerase II, core complex	Acute lethal or lethal
C26F1.4	CG15697	Product with function in protein biosynthesis and ubiquitin in protein degradation.	Acute lethal or lethal
C30C11.1	CG12220	Unknown function	Acute lethal or lethal
C30C11.2	CG10484	Member of the proteasome Regulatory Particle, Non-ATPase-like gene class	Acute lethal or lethal
C36A4.2	CG13977	cytochrome P450	Acute lethal or lethal
C37C3.6	CG33103	Orthologous to thrombospondin, papilin and lacunin	Acute lethal or lethal
C37H5.8	CG8542	Member of the Heat Shock Protein gene class	Acute lethal or lethal
C39F7.4	CG3320	Rab-protein 1 involved in cell adhesion	Acute lethal or lethal
C41C4.8	CG2331	Transitional endoplasmic reticulum ATPase TER94, Golgi organization and biogenesis	Growth delay or arrested in growth
C42D8.5	CG8827	ACE-like protein	Acute lethal or lethal
C47E12.5	CG1782	Ubiquitin-activating enzyme,function in an ATP-dependant reaction that activates ubiquitin prior to its conjugation to proteins that will subsequently be degraded by the 26S proteasome.	Acute lethal or lethal
C47E8.5	CG1242	Member of the abnormal DAuer Formation gene class	Acute lethal or lethal
C49H3.11	CG5920	Small ribosomal subunit S2 protein.	Acute lethal or lethal

C52E4.4	Member of the proteasome Regulatory Particle, ATPase-like gene class	Acute lethal or lethal
C56C10.3	Carrier protein with putatively involved in intracellular protein transport	Growth delay or arrested in growth
CD4.6	Type 1 alpha subunit of the 26S proteasome's 20S protease core particle (CP).	Acute lethal or lethal
D1007.12	Large ribosomal subunit L24 protein.	Acute lethal or lethal
D1054.2	Member of the Proteasome Alpha Subunit gene class	Acute lethal or lethal
D1081.8	MYB transforming protein	Acute lethal or lethal
F07D10.1	Large ribosomal subunit L11 protein (RPL-11.2) involved in protein biosynthesis.	Acute lethal or lethal
F11C3.3	Muscle myosin heavy chain (MHC B)	Acute lethal or lethal
F13B10.2	Large ribosomal subunit L3 protein (rpl-3)	Acute lethal or lethal
F16A11.2	Methanococcus hypothetical protein 0682 like	Acute lethal or lethal
F20B6.2	V-ATPase B subunit	Growth delay or arrested in growth
F23F12.6	Triple A ATPase subunit of the 26S proteasome's 19S regulatory particle (RP) base subcomplex (RPT-3)	Acute lethal or lethal
F25H5.4	Translation elongation factor 2 (EF-2), a GTP-binding protein involved in protein synthesis	Growth delay or arrested in growth
F26D10.3	Member of the Heat Shock Protein gene class	Acute lethal or lethal
F28C6.7	Large ribosomal subunit L26 protein (RPL-26) involved in protein biosynthesis	Embryonic lethal or sterile
F28D1.7	Small ribosomal subunit S23 protein (RPS-23) involved in protein biosynthesis	Acute lethal or lethal
F29G9.5	Member of the proteasome Regulatory Particle, ATPase-like gene class	Acute lethal or lethal
F32H2.5	Mitochondrial protein	Acute lethal or lethal
F37C12.11	Small ribosomal subunit S21 protein (RPS-21) involved in protein biosynthesis	Acute lethal or lethal
F37C12.4	Large ribosomal subunit L36 protein (RPL-36) involved in protein biosynthesis	Acute lethal or lethal

Note: The CG identifiers corresponding to each row (reading left column): CG1341, CG8055, CG4904, CG9282, CG5266, CG6905, CG7726, CG17927, CG4863, CG9987, CG17369, CG16916, CG2238, CG4264, CG6846, CG8415, CG5289, CG3523, CG2986, CG7622

F37C12.9	CG1527	Small ribosomal subunit S14 protein (RPS-14) involved in protein biosynthesis	Acute lethal or lethal
F38E11.5	CG6699	beta' (beta-prime) subunit of the coatomer (COPI) complex	Acute lethal or lethal
F39B2.6	CG10305	Small ribosomal subunit S26 protein (RPS-26) involved in protein biosynthesis	Acute lethal or lethal
F39H11.5	CG12000	Member of the Proteasome Beta Subunit gene class	Acute lethal or lethal
F40F8.10	CG3395	Ribosomal protein S9 (RpS9), structural constituent of ribosome involved in protein biosynthesis which is a component of the cytosolic small ribosomal subunit	Acute lethal or lethal
F42C5.8	CG7808	Small ribosomal subunit S8 protein (RPS-8) involved in protein biosynthesis	Acute lethal or lethal
F49C12.8	CG5378	Member of the proteasome Regulatory Particle, Non-ATPase-like gene class	Acute lethal or lethal
F53A3.3	CG2033	Small ribosomal subunit S15a protein.	Acute lethal or lethal
F53G12.10	CG4897	large ribosomal subunit L7 protein (rpl-7)	Acute lethal or lethal
F54A3.3	CG8977	Unknown function	Acute lethal or lethal
F54E2.3	CG1915	Product with sallimus (sls), myosin-light-chain kinase activity (EC:2.7.1.117) involved in mitotic chromosome condensation which is localized to the nucleus	
F54E7.2	CG11271	Small ribosomal subunit S12 protein (RPS-12) involved in protein biosynthesis	Acute lethal or lethal
F55A11.2	CG4214	Member of the SYNtaxin gene class	Acute lethal or lethal
F55A3.3	CG1828	transcritpion factor	Acute lethal or lethal
F55C10.1	CG11217	Ortholog of calcineurin B, the regulatory subunit of the protein phosphatase 2B	Acute lethal or lethal
F56F3.5	CG2168	rps-1 encodes a small ribosomal subunit S3A protein.	Acute lethal or lethal
F57B9.10	CG10149	Member of the proteasome Regulatory Particle, Non-ATPase-like gene class	Acute lethal or lethal
F58F12.1	CG2968	ATP synthase	Acute lethal or lethal
F59E10.3	CG3948	Zeta subunit of the coatomer (COPI) complex	Acute lethal or lethal
JC8.3	CG3195	Large ribosomal subunit L12 protein (rpl-12)	Acute lethal or lethal
K01G5.4	CG1404	Putative RAN small monomeric GTPase (cell adhesion)	Acute lethal or lethal
K04F10.4	CG18734	Subtilase	Acute lethal or lethal

K05C4.1	CG12323	Member of the Proteasome Beta Subunit gene class	Acute lethal or lethal
K07D4.3	CG18174	Putative proteasome regulatory particle, lid subcomplex, rpn11	Acute lethal or lethal
K11D9.2	CG3725	Sarco-endoplasmic reticulum Ca^{2+} ATPase	Embryonic lethal or sterile; Acute lethal or lethal
M03F4.2	CG4027	An actin that is expressed in body wall and vulval muscles and the spermatheca.	Acute lethal or lethal
R06A4.9	CG1109	six WD40 repeats	Acute lethal or lethal
R10E11.1	CG15319	Putative transcriptional cofactor	Acute lethal or lethal
R12E2.3	CG3416	Protein with endopeptidase activity involved in proteolysis and peptidolysis	Acute lethal or lethal
F10C1.2	CG10119	Member of the Intermediate Filament, B gene class	Embryonic lethal or sterile
F35G12.8	CG11397	Homolog of the SMC4 subunit of mitotic condensin	Embryonic lethal or sterile
F53G12.1	CG5771	GTPase homologue	Embryonic lethal or sterile
F54E7.3	CG5055	PDZ domain-containing protein	Embryonic lethal or sterile
H28O16.1	CG3612	ATP synthase	Growth delay or arrested in growth
K12C11.2	CG4494	Member of the SUMO (ubiquitin-related) homolog gene class	Embryonic lethal or sterile
R12E2.3	CG3416	Member of the proteasome Regulatory Particle, Non-ATPase-like gene class	Acute lethal or lethal
R13A5.8	CG6141	Ribosomal protein L9, structural constituent of ribosome involved in protein biosynthesis which is localised to the ribosome	Acute lethal or lethal
T01C3.6	CG4046	rps-16 encodes a small ribosomal subunit S16 protein.	Acute lethal or lethal
T01H3.1	CG7007	proteolipid protein PPA1 like protein	Acute lethal or lethal
T05C12.7	CG5374	Cytosolic chaperonin	Acute lethal or lethal
T05H4.6	CG5605	eukaryotic peptide chain release factor subunit 1	Acute lethal or lethal
T10H9.4	CG17248	N-synaptobrevin; v-SNARE, vesicle-mediated transport, synaptic vesicle	
T14F9.1	CG17332	ATPase subunit	Growth delay or arrested in growth
T20G5.1	CG9012	Clathrin heavy chain	Acute lethal or lethal
T21B10.7	CG7033	t-complex protein 1	Acute lethal or lethal
W09B12.1	CG17907	Acetylcholineesterase	Embryonic lethal or sterile
T27F2.1	CG8264	Member of the mammalian SKIP (Ski interacting protein) homolog gene	Acute lethal or lethal

		class	
ZC434.5	CG5394	predicted mitochondrial glutamyl-tRNA synthetase (GluRS)	Acute lethal or lethal
B0511.6	CG6375	helicase	Embryonic lethal or sterile
DY3.2	CG10119	Nuclear lamin; LMN-1 protein	Growth delay or arrested in growth
R13G10.1	CG11397	homolog of the SMC4 subunit of mitotic condensin	Wild Type
T26E3.7	CG3612	Predicted mitochondrial protein.	Growth delay or arrested in growth
Y113G7A.3	CG1250	GTPase activator, ER to Golgi prot transport, component of the Golgi stack	Acute lethal or lethal
Y43B11AR.4	CG11276	Ribosomal protein S4 (RpS4), structural constituent of ribosome involved in protein biosynthesis which is a component of the cytosolic small ribosomal subunit	Acute lethal or lethal
Y46G5A.4	CG5931	Y46G5A.4 gene	Acute lethal or lethal
Y71F9AL.17	CG7961	Alpha subunit of the coatomer (COPI) complex	Acute lethal or lethal
Y76B12C.7	CG10110	Gene cleavage and polyadenylation specificity factor	Embryonic lethal or sterile
Y37D8A.10	CG1751	Unknown function	Embryonic lethal or sterile
C06G3.2	CG7765	Member of the Kinesin-Like Protein gene class	
C44E4.4	CG10922	RNA-binding protein	Embryonic lethal or sterile
F01G12.5	CG4145	alpha-2 type IV collagen	Embryonic lethal or sterile
F28H1.3	CG13391	apredicted cytoplasmic alanyl-tRNA synthetase (AlaRS)	Growth delay or arrested in growth
R05D3.7	CG7765	Member of the UNCoordinated gene class	Embryonic lethal or sterile
R06A4.4	CG7398	Member of the IMportin Beta family gene class	Embryonic lethal or sterile
T17E9.2	CG7436	Unknown function	Embryonic lethal or sterile
T25G3.2	CG2666	putative chitin synthase	Embryonic lethal or sterile
W04A8.7	CG17603	TATA-binding protein associated factor TAF1L (TAFII250)	Embryonic lethal or sterile

Table 1-LD

Target ID	Dm Identifier	SEQ ID NO NA	SEQ ID NO AA	Function (based on Flybase)
LD001	CG11276	1	2	Ribosomal protein S4 (RpS4), structural constituent of ribosome involved in protein biosynthesis which is a component of the cytosolic small ribosomal subunit
LD002	CG8055	3	4	Carrier protein with putatively involved in intracellular protein transport
LD003	CG3395	5	6	Ribosomal protein S9 (RpS9), structural constituent of ribosome involved in protein biosynthesis which is a component of the cytosolic small ribosomal subunit
LD006	CG3180	7	8	RNA polymerase II 140kD subunit (RpII140), DNA-directed RNA polymerase activity (EC:2.7.7.6) involved in transcription from Pol II promoter which is a component of the DNA-directed RNA polymerase II, core complex
LD007	CG7269	9	10	Helicase at 25E (Hel25E), also known in FlyBase as Dbp25F, Hel, l(2)25Eb and l(2)k11511, pre-mRNA splicing factor activity involved in nuclear mRNA splicing, via spliceosome which is localized to the nucleus
LD010	CG1250	11	12	GTPase activator, ER to Golgi prot transport, component of the Golgi stack
LD011	CG1404	13	14	Tutative RAN small monomeric GTPase (cell adhesion)
LD014	CG1088	15	16	V-ATPase E subunit
LD015	CG2331	17	18	Transitional endoplasmic reticulum ATPase TER94, Golgi organization and biogenesis
LD016	CG17369	19	20	V-ATPase B subunit
LD018	CG1915	21	22	Sallimus (sls), myosin-light-chain kinase activity (EC:2.7.1.117) involved in mitotic chromosome condensation which is localized to the nucleus
LD027	CG6699	23	24	Beta-coatomer protein, subunit of a multimeric complex that forms a membrane vesicle coat

Table 1-PC

Target ID	Dm Identifier	SEQ ID NO NA	SEQ ID NO AA	Function (based on Flybase)
PC001	CG11276	247	248	Ribosomal protein S4 (RpS4), structural constituent of ribosome involved in protein biosynthesis which is a component of the cytosolic small ribosomal subunit
PC003	CG3395	249	250	Ribosomal protein S9 (RpS9), structural constituent of ribosome involved in protein biosynthesis

Target ID	Dm Identifier	SEQ ID NO NA	SEQ ID NO AA	Function
				which is a component of the cytosolic small ribosomal subunit
PC005	CG2746	251	252	Ribosomal protein L19, structural constituent of ribosome involved in protein biosynthesis which is localised to the ribosome
PC010	CG1250	253	254	GTPase activator, ER to Golgi prot transport, component of the Golgi stack
PC014	CG1088	255	256	V-ATPase E subunit
PC016	CG17369	257	258	V-ATPase B subunit
PC027	CG6699	259	260	Beta-coatamer protein, subunit of a multimeric complex that forms a membrane vesicle coat

Table 1-EV

Target ID	Dm Identifier	SEQ ID NO NA	SEQ ID NO AA	Function (based on Flybase)
EV005	CG2746	513	514	Ribosomal protein L19, structural constituent of ribosome involved in protein biosynthesis which is localised to the ribosome
EV009	CG9261	515	516	Protein involved with Na+/K+- exchanging ATPase complex
EV010	CG1250	517	518	GTPase activator, ER to Golgi prot transport, component of the Golgi stack
EV015	CG2331	519	520	Transitional endoplasmic reticulum ATPase TER94, Golgi organization and biogenesis
EV016	CG17369	521	522	V-ATPase B subunit

Table 1-AG

Target ID	Dm Identifier	SEQ ID NO NA	SEQ ID NO AA	Function (based on Flybase)
AG001	CG11276	601	602	Ribosomal protein S4 (RpS4), structural constituent of ribosome involved in protein biosynthesis which is a component of the cytosolic small ribosomal subunit
AG005	CG2746	603	604	Ribosomal protein L19, structural constituent of ribosome involved in protein biosynthesis which is localised to the ribosome
AG010	CG1250	605	606	GTPase activator, ER to Golgi prot transport, component of the Golgi stack
AG014	CG1088	607	608	V-ATPase E subunit

AG016	CG17369	609	610	V-ATPase B subunit

Table 1-TC

Target ID	Dm identifier	SEQ ID NO NA	SEQ ID NO AA	Function (based on Flybase)
TC001	CG11276	793	794	Ribosomal protein S4 (RpS4), structural constituent of ribosome involved in protein biosynthesis which is a component of the cytosolic small ribosomal subunit
TC002	CG8055	795	796	Protein with putatively involved in intracellular protein transport
TC010	CG1250	797	798	GTPase activator, ER to Golgi prot transport, component of the Golgi stack
TC014	CG1088	799	800	V-ATPase E subunit
TC015	CG2331	801	802	Transitional endoplasmic reticulum ATPase TER94, Golgi organization and biogenesis

Table 1-MP

Target ID	Dm Identifier	SEQ ID NO NA	SEQ ID NO AA	Function (based on Flybase)
MP001	CG11276	888	889	Ribosomal protein S4 (RpS4), structural constituent of ribosome involved in protein biosynthesis which is a component of the cytosolic small ribosomal subunit
MP002	CG8055	890	891	Carrier protein with putatively involved in intracellular protein transport
MP010	CG1250	892	893	GTPase activator, ER to Golgi prot transport, component of the Golgi stack
MP016	CG17369	894	895	V-ATPase B subunit
MP027	CG6699	896	897	Beta-coatamer protein, subunit of a multimeric complex that forms a membrane vesicle coat

Table 1-NL

Target ID	Dm identifier	SEQ ID NO NA	SEQ ID NO AA	Function (based on Flybase)
NL001	CG11276	1071	1072	Ribosomal protein S4 (RpS4), structural constituent of ribosome involved in protein biosynthesis which is a component of the cytosolic small ribosomal subunit

NL002	CG8055	1073	1074	Protein with putatively involved in intracellular protein transport
NL003	CG3395	1075	1076	Ribosomal protein S9 (RpS9), structural constituent of ribosome involved in protein biosynthesis which is a component of the cytosolic small ribosomal subunit
NL004	CG6141	1077	1078	Ribosomal protein L9, structural constituent of ribosome involved in protein biosynthesis which is localised to the ribosome
NL005	CG2746	1079	1080	Ribosomal protein L19, structural constituent of ribosome involved in protein biosynthesis which is localised to the ribosome
NL006	CG3180	1081	1082	RNA polymerase II 140kD subunit (RpII140), DNA-directed RNA polymerase activity (EC:2.7.7.6) involved in transcription from Pol II promoter which is a component of the DNA-directed RNA polymerase II, core complex
NL007	CG7269	1083	1084	Helicase at 25E (Hel25E), also known in FlyBase as Dbp25F, Hel, l(2)25Eb and l(2)k11511, pre-mRNA splicing factor activity involved in nuclear mRNA splicing, via spliceosome which is localized to the nucleus
NL008	CG3416	1085	1086	Protein with endopeptidase activity involved in proteolysis and peptidolysis which is a component of the proteasome regulatory particle, lid subcomplex (sensu Eukarya)
NL009	CG9261	1087	1088	Protein Involved with Na+/K+- exchanging ATPase complex
NL010	CG1250	1089	1090	GTPase activator, ER to Golgi prot transport, component of the Golgi stack
NL011	CG1404	1091	1092	Putative RAN small monomeric GTPase (cell adhesion)
NL012	CG17248	1093	1094	N-synaptobrevin; v-SNARE, vesicle-mediated transport, synaptic vesicle
NL013	CG18174	1095	1096	Putative proteasome regulatory particle, lid subcomplex, rpn11
NL014	CG1088	1097	1098	V-ATPase E subunit
NL015	CG2331	1099	1100	Transitional endoplasmic reticulum ATPase TER94, Golgi organization and biogenesis
NL016	CG17369	1101	1102	V-ATPase B subunit
NL018	CG1915	1103	1104	Sallimus (sls), myosin-light-chain kinase activity (EC:2.7.1.117) involved in mitotic chromosome condensation which is localized to the nucleus
NL019	CG3320	1105	1106	Rab-protein 1 involved in cell adhesion
NL021	CG10110	1107	1108	Gene cleavage and polyadenylation specificity factor

NL022	CG10689	1109	1110	Product with RNA helicase activity (EC:2.7.7.-) involved in nuclear mRNA splicing, via spliceosome which is a component of the spliceosome complex
NL023	CG17907	1111	1112	Acetylcholineesterase
NL027	CG6699	1113	1114	Beta-coatomer protein

Table 1-CS

Target ID	Dm Identifier	SEQ ID NO NA	SEQ ID NO AA	Function (based on Flybase)
CS001	CG11276	1682	1683	Ribosomal protein S4 (RpS4), structural constituent of ribosome involved in protein biosynthesis which is a component of the cytosolic small ribosomal subunit
CS002	CG8055	1684	1685	Carrier protein with putatively involved in intracellular protein transport
CS003	CG3395	1686	1687	Ribosomal protein S9 (RpS9), structural constituent of ribosome involved in protein biosynthesis which is a component of the cytosolic small ribosomal subunit
CS006	CG3180	1688	1689	RNA polymerase II 140kD subunit (RpII140), DNA-directed RNA polymerase activity (EC:2.7.7.6) involved in transcription from Pol II promoter which is a component of the DNA-directed RNA polymerase II, core complex
CS007	CG7269	1690	1691	Helicase at 25E (Hel25E), also known in FlyBase as Dbp25F, Hel, l(2)25Eb and l(2)k11511, pre-mRNA splicing factor activity involved in nuclear mRNA splicing, via spliceosome which is localized to the nucleus
CS009	CG9261	1692	1693	Protein involved with Na+/K+- exchanging ATPase complex
CS011	CG1404	1694	1695	Tutative RAN small monomeric GTPase
CS013	CG18174	1696	1697	Putative proteasome regulatory particle, lid subcomplex, rpn11
CS014	CG1088	1698	1699	V-ATPase E subunit
CS015	CG2331	1700	1701	Transitional endoplasmic reticulum ATPase TER94, Golgi organization and biogenesis
CS016	CG17369	1702	1703	V-ATPase B subunit
CS018	CG1915	1704	1705	Sallimus (sls), myosin-light-chain kinase activity (EC:2.7.1.117) involved in mitotic chromosome condensation which is localized to the nucleus

Table 1-PX

Target ID	Dm identifier	SEQ ID NO NA	SEQ ID NO AA	Function (based on Flybase)
PX001	CG11276	2100	2101	Ribosomal protein S4 (RpS4), structural constituent of ribosome involved in protein biosynthesis which is a component of the cytosolic small ribosomal subunit
PX009	CG9261	2102	2103	Protein involved with Na+/K+- exchanging ATPase complex
PX010	CG1250	2104	2105	GTPase activator, ER to Golgi prot transport, component of the Golgi stack
PX015	CG2331	2106	2107	Transitional endoplasmic reticulum ATPase TER94, Golgi organization and biogenesis
PX016	CG17369	2108	2109	V-ATPase B subunit

Table 1-AD

Target ID	Dm identifier	SEQ ID NO NA	SEQ ID NO AA	Function (based on Flybase)
AD001	CG11276	2364	2365	Ribosomal protein S4 (RpS4), structural constituent of ribosome involved in protein biosynthesis which is a component of the cytosolic small ribosomal subunit
AD002	CG8055	2366	2367	Carrier protein with putatively involved in intracellular protein transport
AD009	CG9261	2368	2369	Protein involved with Na+/K+- exchanging ATPase complex
AD015	CG2331	2370	2371	Transitional endoplasmic reticulum ATPase TER94, Golgi organization and biogenesis
AD016	CG17369	2372	2373	V-ATPase B subunit

Table 2-LD

Target ID	Primer Forward 5' → 3'	Primer Reverse 5' → 3'	cDNA Sequence (sense strand) 5' → 3'
LD001	SEQ ID NO: 25 GGCCCCAAGAA GCATTTGAAGC G	SEQ ID NO: 26 TAGCGGATGGT GCGGDCCRTCRT G	SEQ ID NO: 1 GGCCCCAAGAAGCATTTGAAGCGTTTGAATGCCCCAAAAGCATGGATGTTGGATAAAATTGG GAGGTGTTTCGCCACCTCGCCCATCTACAGGACCTCACAAATTGCGGAGAGTCTTTGCCCTT GGTGATCTTCCTACGTAACCGATTGAAGTATGCTTTGACTAACAGCGAAGTTACTAAGGATTG TTATGCAAAGGTTAATCAAAGTAGATGGAAAAGTGAGGACCGACTCCAATTACCCTGCTGG GTTTATGGATGTTATTACCATTGAAAAAACTGGTGAATTTTCCGACTCATCTATGATGTTTAA

LD002	SEQ ID NO: 27 GAGCGGCCAT GCAAGCVCTBA ARMRRAAG	AGGACGATTTGCAGTGCATCGTATTACTGCTGAGGAAGCAAGTACAAACTATGCAAAGTC AGGAGGATGCAAACTGGCCCCAAAGGAATTCCCTTCATAGTGACACGACGGCCGCCACC ATCCGCTA
	SEQ ID NO: 28 GCAATGTCATC CATCAKRTCRT GCAC	SEQ ID NO: 3 GCAATGTCATCCATCATGTCGTGTACATTGTCCACGTCCAAGTTTTTATGGGCTTTCTTAAG AGCTTCAGCTGCATTTTCATAGATTCCAATACTGTGGTGTTCGTACTAGCTCCCTCCAGAG CTTCTCGTTGAGTTCAATAGTAGTTAAAGTGCCATCTATTGCAACTGATTTTTTCTAATC GCTTCTTCCGCCTTCAGCGCTTCAGCGCCGTC
LD003	SEQ ID NO: 29 TCGGTTCTTCTC GAAGACNTAYG TKAC	SEQ ID NO: 5 CAGGTTCTTCCTCTTGACGCGTCCAGGGCGACCACCACCGAATGGAGATTTGAGCGGAGAA GTCAATATGCTTCTGGGAATCAAGTCTCACAATGAAGCTTGGAATATTCACGACCTGCTTAC GAACCCTGATATGTCTTTGACGGACCAGCACACGAGCTCGTTCCAAGCCC CAACTTGAAAACTTGTGTTTGGAGACGTCGGTTTCATCCAACACTCCAATACTTCAAACCCAAGA CGTAATCAAGCTTCATACGGGTTCATCCAACAACCTGCGCTGATCTTTCTTCTTCCAAGTCAGAGGTTCTCTGGCAG AGCATTGCCTTCAAACAACCTGCGCTGATCTTTCTTCTTCCAAGTCAGAGGTTCTCTGGCAG CTTTACGGATTTTTGCCAAGGTATACTTGACTCGGCCACACTTCACGTTTGTTCCTAAGACCA TATTCTCCTATGATTTTCAACTCCTGATCAAGACGTGCCTTTTCATAAGGTCGCCTGGGA
	SEQ ID NO: 30 CAGGTTCTTCC TCTTKACRCGD CC	
LD006	SEQ ID NO: 31 GGAGCGGAGAC TACAACAAYKA YRGYTGGC	SEQ ID NO: 7 GGAGCGGAGACTACAACAACTATGGCTGGCAGGTGTTGGTTGCTTCTGGTGTGGTGGAATAC ATCGACACTCTTGAAGAAGAAACTGTCATGATTGCGATGAATCCTGAGGATCTTCGGCAGG ACAAAGAATATGCTTATTGTACGACCTACACCCACTGCGAAATCCAGAACAACTAC GGGCGTTTGCGCGTCTATTATACCTTTCCCCGATCATAACCAGAGCCCAAGGAACACCTAC CAGAGCGCTATGGGTAAGCAAGCTATGGGGGTCTACATTACGAATTTCCACGTGCGGATG GACACCCTGGCCCACGTGCTATACTACCGGCACAAACCTCGGTCACTACCAGGTCTATG GAGTATCTGCGGTTCAGAGAATTACCAGCCGGGATCAACAGTATAGTTGCTATTGCTTGTT ATACTGGTTATAATCAAGAAGATTCGTTATTCTGAACGCGTCTGCTGTGAGAAGAGGATTT TTCCGATCCGTGTTTTATCGTTCCTATAAAGATGCCGAATCGAAGCGAATTGGGCGATCAAG AAGAGCAGTTCGAG
	SEQ ID NO: 32 CTCGAACTGCT CYTCYTGATCR CC	
LD007	SEQ ID NO: 33 CCGAAGAAGGA YGTSAAGGGYA C	SEQ ID NO: 9 CCGAAGAAGGATGTGAAGGGTACTTACGTATCCATACACAGTTCAGGCTTCAGGAGATTTTT TATTGAAACCAGAAATTCTAAGAGCTATAGTTGACTGGCGGTTTGAACACCCTTCAGAAGTT CAGCACGAATGTATTCCTCAAGCTGTCAAGCTGCATGGACATTTTATGTCAAGCCAAATCTGG TATGGGCAAAACGGCAGTGTTTGTTCTGGCGACACTGCAACAATTGGAACCAGCGGCGACAAT GTTGTTTTACGTTTTGGTGATGTGTCACACTCGTGAACTGCTTCCAAATCAGCAAAGAGTA CGAGAGGTTCAGTTAAATATATGCCCAGTGTCAAGGTGGGCGTCTCTTTTCGGAGGAATGCCT

LD010	SEQ ID NO: 35 CTCTCAAGGAT TCKYTRCARAT GTC	SEQ ID NO: 36 CGGCCATTGGGC RATGGTYTCKC C	SEQ ID NO: 11
			ATTGCTAACGATGAAGAAGTATTGAAAAAACAAATGTCCACACATTGTTGTGGGGACGCCTG GGCGTATTTGGCGCTTGTCAAGTCTCAGGAAGCTAGTCCTCAAGAACCTGAAACACTTCAT TCTTGATGAGTGCGATAAAATGTTTAGAACTGTTGGATATGAGCAAGACGTCCAGGAAATC TACAGAAACACCCTCACACCAAGCAAGTCAAGTGATGATGTTCAGTGCCACACTCAGCAAGAAA TCAGGCCGGTGTGCAAGAAATTCATGCAAGATCCAATGGAGGTGTATGTAGACGATGAAG CCAAATTGACGTTGCACGGATTACAACAGCATTACGTTAAACTCAAAGAAAAATGAAAGAAT AAAAATTATTTGAGTTGCTCGATGTCTCGAATTAATCAGGTGGTCATTTTGTGAAGTCC GTTCAAAGGTGTGGCGGAATGGACCAGAAAGAGAGGTTGTCTCGTATGAGCAGTTCAAAGATTTCCA GAAGAGAATATTGGTAGCTACGAATCTCTTTGGGCGTGGCGCATGGACAATTGAAAGGGTCAAC ATTGTCTTCAACTATGATATGCCAGAGGACTCCGAGACCTACTTGCATCG

LD011	SEQ ID NO: 37 CCCACTTTCAAGTGYGTRYTRGTCGG	SEQ ID NO: 38 GTGGAAGCAGGGCWGGCATKGCRAC	CAACCCGATAGAATTCTGCTCATGGCGACACGTTCTTCCAGATTCTGATATTCCATGGCGAAAC CATCGCCCAATGGCG SEQ ID NO: 13 GTGGAAGCAGGGCTGGCATGGCGACAAATTCTAGATTGGGATCACCAATAAGCTTCCTAG CTAGCCATAGGAAAGGCTTCTCAAAGTTGTAGTTAGATTGGCAGAGATATCATAGTACTGC AAATTCTTCCTATGAAAGACAATACTTTCGCTTTACTTTCTGTCTTTGATGTCAACCT TGTTCCCGCAAAGTACTATCGGGATATTTTCACAGACTCTGACAAGATCTCTGTGCCAATTT GGTACATTCTTGTATGTAACTCTGGAAGTTACATCAAACATGATAATAGCACACTGTCCCTG AATGTAATATCCATCACGGAGACCACCAAACTTCTCCTGACCGGCAGTGTCCCATACATTG AACCGAATAGGGCCCCTGTTTGTATGGAAGACCAGAGGATGGACTTCAACTCCCAAGTAG CTACATATCTTTTTCAAATTCACCAGTCATATGACGTTTCACAAATGTCGTTTTTCCAGTAC CTCCATCTCCGACCAACACACACTTGAAAGTGGG
LD014	SEQ ID NO: 39 CGCAGATCAARCAYATGATGGC	SEQ ID NO: 40 CGGATCTCGGGCASMARYTGC	SEQ ID NO: 15 CGCAGATCAAGCATATGATGGCTTTCATTGAACAAGAGGCAAACGAAAAGGCAGAGAAAT CGATGCCAAGGCCGAGGAAGAATTAATATTGAAAGGGGCGCCTTGTTCAGCAACAACGT CTCAAGATTATGGAATATTATGGAGAAGAAGAAAACAGGTCGAACTCCAGAAAAAATCCA ATCGTCTAACATGTTGAATCAGGCGCGTAAACGACGTTGGTCAGGTCACAAACGACCAGGT CGTACCGTACTAGAGGAGGCGCGTAAACCTCATTTTGCAGGGATTATATCAGCTTTTGAGAAAGATGT TATTCCCAAATCCTGGAAAGCCTCATTTTGCGGCCCCAGGACCGGAACTGGTCAAATCCATCTG TACCATTCGAGTTCGGCGCCACCGTAAGGACACCGGTAAGGAACTGGGCAGAAAAAACAAAATCAAGATCAG AACAAGTATAAAGATGCCACACGGGGGAATCGACCTGCTGCGCAGCAACTTCGCGCCGAGATCCG CAATACTATGGAGGCGTCGTCGTGATTCGGAGCTGATTTCGGCAGCAACTTCTGCCCGAGATCCG
LD014_F1			SEQ ID NO: 159 TCTAGAATGTTGAATCAGGCTCGCGATTGAAAGTATTGAAGGTTAGGGAAGATCACGTTCGTA CCGTACTAGAGGAGGCGCGTAAACGACTTGGTCAGGTCACAAACGCCCGGG
LD014_F2			SEQ ID NO: 160 TCTAGAAAGATCACGTTCGTACCGTACTAGAGGAGGCGCGTAAACGACTTGGTCAGGTCA CAAACGCCCGGG
LD014_C1			SEQ ID NO: 161 TCTAGAATGTTGAATCAGGCTCGCGATTGAAAGTATTGAAGGTTAGGGAAGATCACGTTCGTA CCGTACTAGAGGAGGCGCGTAAACGACTTGGTCAGGTCACAAACGATGTTGAATCAGGCT CGATTGAAGTATTGAAGGTTAGGGAAGATCACGTTCGTACCGTACTAGAGGAGGCGCGT AAACGACTTGGTCAGGTCACAAACGATGTTGAATCAGGCTCGATTGAAAGTATTGAAGGTT AGGGAAGATCACGTTCGTACCGTACTAGAGGAGGCGCGTAAACGACTTGGTCAGGTCACA

LD014_C2		AACGCCCGGG
		SEQ ID NO: 162
		TCTAGAAAGATCACGTTCGTACCGTACTAGAGGAGGCGCGTAAACGACTTGGTCAGGTCA CAAACGAAGATCACGTTCGTACCGTACTAGAGGAGGAGGCGCGTAAACGACTTGGTCAGGTCA CAAACGAAGATCACGTTCGTACCGTACTAGAGGAGGAGGCGCGTAAACGACTTGGTCAGGTCA CAAACGAAGATCACGTTCGTACCGTACTAGAGGAGGAGGCGCGTAAACGACTTGGTCAGGTCA CAAACGAAGATCACGTTCGTACCGTACTAGAGGAGGAGGCGCGTAAACGACTTGGTCAGGTCA CAAACGCCCGGG
LD015	SEQ ID NO: 41 CGCCATCCRTCGCTSTTCAAGGC	SEQ ID NO: 42 GCAATGGCATCAAKYTCRTCRATG
		SEQ ID NO: 17
		GCAATGGCATCAAGTTCATCGATGAAGATGCCGGAGAGTTTTGTCAGCTTCTTCAA AAGCTTTGCGCAAGTTACTCTCAGACTCGCCAGCGAGTTTGCTCATGATCTCCGGCCGTT TATCAAGAAGAAGAACGCCCCAGTCTCATTAGCCACGGCGCGAGCAATCAGGGTCTTACC CGTACCAGGGGGACCATACAGCAGTATACCCCTAGGGGGCTTCACGCCGATAGCCTTGAA GAGCGATGGATGGCG
LD016	SEQ ID NO: 43 GACTGTGTCTGGTGTRAACGGWCC	SEQ ID NO: 44 GGAATAGGATGGGGTRATRTCGTCG
		SEQ ID NO: 19
		GGAATAGGATGGGGTAATGTCGTCGTTGGGCATAGTCAATATAGGAATCTGGGTGATGGATC CGTTACGTCCTTCAACACGGCCGGCACGTTCATAGATGGTAGCTAATCGGTGTACATGTA ACCTGGGAAACCACGACGACCAGGCACCTCTTCTCTGGCGCAGCAGTACCTCACGCAAAGC TTCTGCATACGAAGACATATCTGTCAAGATGACCAAGACGTGCTTCTCACATTGGTAAGCC AAGAATTCGGCAGCTGTCAAAGCCAGAGGCAGACATTCTCCATAGAACCGTTCTCTTCAATGGTAGGATCGT TGGCCAAATTCAAGAACAGGCAGAACATTCTCCATAGAACCGAAAACAATAGCAAGTTATCTTC ATGATCATCAAGTACAGATTTACCAGGAATCTTGACTAAACCAGCTGTCTCTACAGATCTGGGG CAGCAATTTCATTGTGAGGCAGACCAGCTGCAGAGAAAATGGGGATCTTCTGACCACGAG CAATGGAGTTCATCACGGATTGATTGGTTGACCCTGGATGTCCATTCACAAGAAGTCTCCAACATATCTTCAGGATAGATA CGGGACCACGGATTGTCGATGGGTTTTCCTGATCCATTGAAAAACACGTCGGTGTTTTGGCGTCGATTCCTGAT GTGCCCTGCAACACTTGAACCACAGCTTTGACCCACTGACTTCCAGAACTTGTCCCGAAC GTATAGTGCCATCAGCCAGTTGAGTTGTACGATTTCATTGTACTTGGGGAACTTAACATCT TCGAGGATTACCAGGAGGACCGTTCACCACCAGACCAGTC
LD018	SEQ ID NO: 45 CACCTGGTTCAAGRATGGGVCARMG	SEQ ID NO: 46 GTGCATCGGTACCAHSCHGCRTC
		SEQ ID NO: 21
		CACCTGGTTCAAGGATGGGCAGCGGATAACGGAGTCGCAGAAATACGAGAGCCACCTTCTC GAACAACCAGCCTCCTTGAGGGTAAAACAAGCCCAGTCTGAGGACTCGGGACACTACAC TTTGTTGGGCGGAGAACCCTCAAGGCTGCATAGTGTCATCTGCTTACTTAGCCATAGAACCG

| | | | GTAACCACCCAGGAGGAAGGGTTGATCCACGAGTCCACCTTCAAGCAGCAACAGACGCGAAATG GAGCAAATCGACACGAGCAGCAAGACCTTGGGCGCCTAACTTCGTCGCGTCACTGGTCGTCCTATCCA GACGTGACCGAGGGCAGAGTGACCCGCTTCGACGTCGACAAGTCACCGACGACCACAACCACAGATTTTGG TTAACGAATCCGGAAACCATGCCCTGATCATCACCACCGTGAGCAGGAACGACTCAGGAG TAGTGACCTGCGTCGCCAGGAACAAGACGCGGAGAAACCTCCTTCCAGTGCAACCTTAACG TCATCGAAAAGGAACAGGTAGTCGCGCGCCCAAGTTCGTTGGACGAGATTTACCACAGTCAACGT GGCAGAAGGAGGAACCAGTGTCTCTGCGCGCCCCTAGCCCAGGCCCGAAGCGTTCGCATCGCGATT TCACTTGGCAGAGGACGGGCGCCCCTACTTTGAATATCTCGAGGCCAAGGCCTCGGATGCTGCATGGTAC CGATGCAC |
| LD027 | SEQ ID NO: 47 CCATGGTGGC GAYAARCCVTA C | SEQ ID NO: 48 GGTATAGATGA ARCARTCDCCV ACCCA | SEQ ID NO: 23 CCATGGTGGCGATAAACCATACTTGATATCGGGAGGCAGACGATCGGTTGGTTAAAATCTGG GACTATCAAAACAAAACGTGTCCAAACCTTGGAAGGACACACGCCCAAACGTAACCGCG GTTTGTTTCCACCCTGAACTACCTGTGGCTCTCACAGGCAGCGGAGATGGTACCGTTAGAG TTTGGCATACGAATACACACAGATTAGAGAATTGTTTGAATTATGGTTCGAGAGAGTGTG GACCATTTGTTGCTTGAAGGGTTCGAATAATGTTTCTCTGGGTATGACGAGGGCAGTATA TTAGTGAAAGTTGGAAGAGAAGAACCGGCAGTTAGTATGGATGCCAGTGCGGCGTAAAATAA TTTGGGCAAGGCACTCGGAATTACAACAAGCTAATTTGAAGGCGCTGCCAGAAGGTGGAG AAATAAGAGAGATGGGGAGCGTTTACCTGTCTCTGTAAAAGATATGGGAGCATGTGAAATATA CCCTCAAACAATCCAACATAATCCGAAGTGGAAGATTCGTTGTAGTATGCGGAGACGGCGAA TATATCATTTACACAGGACTCCAGCGAGTATGCCATTCAGCGCGAAGGAATCTACGGG TCTGGGCTCAGGACTCCAGCGAGTATGCCATTCAGCGGATTCAGCGTTTCAGGATATT CAAAACTTCAAAGAAAGGAAGAACTTCAAGTCGATTCGTCCGGTTAACGTTTACGATTGGGAAACTTTGGA GGTTTCTCTTGGGGATTAAATCGGTGTCCGGTTAACGTTTATTGGTCTGACAGTGGAAAATTA CTTGGTGAGACGGATTGAAATACAACCGAGGGCGGTTTATTCGTTTCTTATGATTCGGAGCAAGTTCAGA GTCTGTCTCGCAACGGAGGACAATCAAGTCGCAGAGGATGGGCGTAGAGGCCGCTTTCGATGTGTTGG AGGCCAGGGAGAACAATCAAGTCTGTCCGAACAGAGTCTTTGGGTCGGAGACTGTTTCATCTATACC GGGAAATGAACGAGTCGTTTGGGTCGGAGACTGTTTCATCTATACC |

Table 2-PC

Target ID	Primer Forward 5' → 3'	Primer Reverse 5' → 3'	cDNA Sequence (sense strand) 5' → 3'
PC001	SEQ ID NO: 261 CATTTGAAGCG	SEQ ID NO: 262 CTTCGTGCCCT	SEQ ID NO: 247 CATTTGAAGCGTTTAGCTGCTCCCAAAGCATGGATGTTGGACAAATTGGGGGTGTCTTCGCCC

	TTTWRMYGCY CC	TGCCRATKATR AABACG	CTCGTCCATCCACCGGGCCTCACAAGTTGCGCGAATCCCTGCCCTTTAGTGTGATTTCCTTCGTAAC AGGCTGAAGTATGCCCTTACAAACAGTGAAGTCACTAAAATTGTCATGCAAGGTTGATCAAAGT TGATGGTAAAGTGAGGACTGATTCTAATTACCCTGCTGGTTCATGGATGTCATTACTATTGAGAA GACTGGTGAATTTTCCGTCTGATCTATGATGTTAAAGGAAGATTTGCTGTGCACCGTATTACGAGC TGAAGAGGGCAAAATACAAGTTGTGTAAGTAAGGAGAGTCCAAACTGGTCCCAAAGGAATCCCAT TTTTGGTAACACATGATGGCAGAACCATTCGTTACCCTGACCCCAACATCAAAGTGAATGACACA ATTCAAATGGAAATTGCTACATCTAAAATTCTTGACTACATCAAATTTGAATCTGGCAACCTCTGC ATGATCACGGGGAGG
PC003	SEQ ID NO: 263 TCGGTCTTCTC GAAGACNTAYG TKAC	SEQ ID NO: 264 CCCTGGTTCTT CTTVRRRTTCT TCCTC	SEQ ID NO: 249 CCCTAGACGTCCCTATGAAAAGGCCCGTCTGGATCAGGAATTGAAAAATTATCGGCGCCTTTGGTT TACGAAACAAACGTGAAGTGTGGAGAGTAAAGTACACTTTGGCTAAAATCCGTAAAGCTGCTCGT GAACTGCTCACCCTAGAAGAAAAAGAGCCTAAAAGATTGTTGAAGGTAATGCACTTCTACGTCG TTTGGTGCGAATTGGTGTTCTGGATGAGAACAGGATGAAGCTTCAAATCTGGTCTGCAAAGTCAATT CATCATGCTAGAGTACTGATTAGGCAGGAGCACATCCGGGTGCGCAAGCAGGTGGTGAACATCC CCTCGTTCATCGTGCGGGTCGGACTCGGCAGAAGCACACTCGACTTCTCCCTGAAGTCGCCCCTTCGG GGGTGGCCGACCTGGCCCGTGTCAA
PC005	SEQ ID NO: 265 TGCGATGCGG CAARAARAAGG TBTGG	SEQ ID NO: 266 TCCTGCTTCTT SGYRGCRATW CGYTC	SEQ ID NO: 251 TGCGATGCGGCAAAAAGAAGGTGTGGTTGGATCCAAATGAAATCAACGAAATCGCCAACACCAA CTCAAGACAAAAACATCCGTAAGCTCATCAAGGATGGTCTTATCATCAAGAGGAAGAGCCAGTGGCAGTAC ACTCTAGGCCCGTGTACGCAAGGGTACGGCAAATGCCGTATGCCTCAAAAGGAACTGTGGGTCAGCGCATGC GAAAGGAAGGTACGGCAAATGCCGCAAGGAGGAACAGAAAATGACCGCCATCTTTACCA GCGTCCTGTACATGAAGCGAAGGCAGGTCAACGTGTTCAGGAACGAGAAGGTCCTTATGGAGTACATC CACAAGAAGAAGGCAGAAGGAGGCCAGGCAACGTAGGGAAGGCGTATCGCCACCAAGAAGCAGG TTGAAGGTGAAGTTGAAGCAGGCAGGGAAGCGTAGGGAAGGCGTATCGCCACCAAGAAGCAGG
PC010	SEQ ID NO: 267 CTCTCAAGGAT TCKYTRCARAT GTC	SEQ ID NO: 268 CGGCATTGGG CRATGGTYTCK CC	SEQ ID NO: 253 CTCTCAAGGATTCTTTGCAGATGTCGCTCAGCCTATTACCGCCCAACGCGTTGATTGATTGATC ACGTTCGGAAAAATGGTGCAAGTCCACGAACTGGGTACCGAAGGCTGCAGCAAGTCGTACGTGT TCTGTGGAACGAAAGATCTCACGCGCCAAGCAAGTCCAGGAGATGTTGGGCATTGGAAAAGGGTC ACCAAATCCCCAACAACAGCCAGGCAACCTGGGCGGGCCAGGGCAGAATCCCAAGCTGCCCC TGTACCACGGGGGAGCAGATTCTTGCAGCCGTGTCAAAATGGCCAAAGCTGAACTTGACAGATCTG ATCGGGGAGTTGCAGAAAGACCCTTGAGAAAGACCTATCCAGGCAAAAGACCTCTTAGATCCACAG GCGCAGCATTGTCCATGCGTCGGCCTCTTAGAATGCACCTATCCGAATACGGGTGGCAGAAT CATGATATTCTTAGGAGGACCATCATGACATACAAAGACAACAATGCCAAGTACTACGAGAAGCTATCAA CAGCCCCATCAGGTCCCATCATGACATACAAAGACAACAATGCCAAGTACTACGAGAAGGCTATCAA

			Sequence
			ACATTACGATCACTTGGCAATGCGAGCTGCCACCAACAGCCATTGCATCGACATTTACTCCTGCG CCCTGGATCAGACGGGACTGATGGAGATGAAGCAGTGCAATTCCACCGGAGGGCACATGG TCATGGGGATCCTTCAATTCCTCTATTCAAACAAACCTTCCAGCGAGTGTTCTCAAAAGACC CGAAGAACAGACCTCAAGATGCCATGGGGGCCATGGGGGCCCACCTTGGAGTGAAGCCCCTGCTTTCCGATACG AGTCCAAGGGGGCATGGGGAATACTGTGCAGTGGAAACTTTGCACGTTGGAGCCGAGCTCTACTGTGG GAACTAGGCACATGGGGAATACTGGTTAACCAGCATTCGGCGCGCCCATACCACAGGGAGGAGGCAGGGGCTGCA CGCTGTTCTTCGAGGTGGTTAACCAGTATCAGCAGCGACACGCGAGCGGCAAAGGAGGATCAGAGTGACCACGATTG TCCAGCTCATCACCCAGTATCGCCAACATCCAACCACCATTAGCGCTGGCTTCGACCAAGAAGC CTAGAAATTGGGCGGGACGCTACTGCCAACATGGCCGGTTACAGGCGTGTGCCAGAGGATGTTGATCAGCG GGCGGCAGTTGTGATGGGTGGACAGGATGTGGGGGAGAACTTCAGTGCTGTATCCTGATGAAACGTCGTTTATAGGCACATGC GCTCAGATGGTGGCGCAGTTTCTGCAGGTGTTCAATAATTCTCCTGATCATGATCCAGCCGATTTGTACAGTTACAGCTTCA ACGGTGCGCAGTTTCTGCAGGATTTGACTCAGTCTTGTTGGGACACAAGCTCTATTCAGCCGGATAGAATCCTGCTCAT TGATGCGTGGAGGCCTGTCTGTTGTTGGGACACAAGCTCTATTCAGCCGGATAGAATCCTGCTCAT GGACACTTTCTTCCAGATACTCATTTCCAGTGGAGAGACCATTGCCCAATGGCG
PC014	SEQ ID NO: 269 CGCAGATCAAR CAYATGATGGC	SEQ ID NO: 270 CGGATCTCGG GCASMARYTG C	SEQ ID NO: 255 CTGATGTTCAAAAACAAATCAAACACATGATGGCTTCATTGAACAAGAAGCCAATGAGAAAGCA GAAGAAATTGATGCCAAGGCAGGAGGAATTCAACATTGAAAAAGGGCGTTGGTCCAGCAAC AGAGACTCAAGATCATGGAGTACTACGAGAAAAAGGAGAAGCAAGTCGAACTTCAAAAGAAATT CAGTCCTCTAAATATGTTGAATCAGGCTCGTAAAAGTCTTGGTAAAGTCTTGGTGAAGTAACCAAAGACCAAGGAAAATACTCC AGCAGTCCTGGAGAGCCTAATCCTACAAGGACTGTTCCAGCTGTTCGAGAAGGAGGTGACGGTCC CAAATTTTGGAGAGCCTAATCCTACAAGGACTGTTCGAGAAGGAGGTGACGGTCC GGTGAGACGCAAGACCAGGACCTGGTCAGGTCCATCCTGACGATGAGTCGCACCTGTCTCAGGAGAT AGGACCGCACCGGCAAGATCAAGACAATCCTACTCAAGGTGGACGATGAGTCGCACCTGTCTCAGGAGAT CACCGGAGGCGTCGATTTGCTCGCTCAGAAGAACAAGATCAGCAACACGATGGAGGCT AGGTTGGATCTGATCGCTCA
PC016	SEQ ID NO: 271 GACTGTGTCTG GTGTRAACGG WCC	SEQ ID NO: 272 GGAATAGGAT GGGTRATRTC GTCG	SEQ ID NO: 257 GGAATAGGATGGGTGATGTCGTTGGGCCATAGTCAAGATGGGGGATCTGCGTGATGGAGCCG TTGGGCGCCCTCCACACGACCGCGCGCTGTAAATGGTGGCCAGATCGGTGTACATGTAACCG GGGAAACCCCTACGGCCGGGCACTTCTTCTCGAGCGGCAGACACCTCACGGTAGGCCAAGAATTCGG TACGACGACATGTCGGTCAAGATGACCAGCACGTGCTTCTCGACGTGTAGGCCAAGTTCA CGGCCCGTCAGAGCCAAACGGCGGCGTGATGATGGCGTCGATCGTTGGCCAAGTTCA AGAACAGACACACGGTACTTCTCCATGGACCGTTCTTCTTGAAGTGTCTGCTTGAAGAACCTGGCAGTT TCCATGTTGACACCCATAGCAACCAATAGCAAGTTGTCTTCATGGTCATCCAGCACAGA CTTGCCAGGTACTTTGACCAGCCAGCAACAATGCGAATCGGAATCTGGCCAATCTCATTGGTGGGGGC AGCCCAGCCGCGGCGGAAGATCGGAGAAGATCGGAGAAGATCGGAATCTTGGCGCTGGCGATAGAGTTCATCACGTCGATGGG

	Primer Forward 5'→3'	Primer Reverse 5'→3'	Sequence
			CCGTGATCCCAGTCTGGATCATTTCCTCGGGATAAAATACGGCGACCACGGGTTGATCGGCTGTCC TTGGATGTGAGGTAGTCCTCAGCCAGGATCGGGGGACCTTTATCAATGGGTTTTCCTGATCCAT TGAAGACAGTCCCAGCATATCTTGATACTGGAGTTCTTAGAATATCTCCAGTGAACTCACAC ACCGTGTTCTTAGCATCAATACCTGATGTGCCTTCAAATACCTGAACAACTGCCTTTGATCCACTG ACTTCCAAAACTTGTCCAGATCGTAGAGTTCCATCTGCCAATTTGAGCTGACAATTTCATTGAAT TTTGGAAACTTGACATCCTCAAGAATGACCAGTGGTCCGTTCACCAGACACAGTC
PC027	SEQ ID NO: 273 GGGCCAAGCA CWSYGAAATRC AG	SEQ ID NO: 274 TGTGCCACCC TAGTRCGRTG YTC	SEQ ID NO: 259 GGGCCAAGCACAGTGAAATACAGCAAGCTAACTTGAAAGCACTACCAGAAGGAGCTGAAATCAG AGATGGAGAACGTTTGCCAGTCACAGTAAAGGACCATGGGAGCATGCGAGATTTACCCACAAACA ATCCAACAACAACCCCAATGGGCGGTTTGTAGTGGTTTGTGGTGATGGAGAATACATAATATACAC GGCTATGGCCCCTTCGTAACAAAGCATTTGGTAGCGCTCAAGAATTTGGTAGCGCACAGGACTCC AGTGAATATGCCATCCGCGAATCCGGATCCACCATTCGAATCTTCAAGAATCTTCAAGAGAAAAAA GAATTCAAGTCCGACTTTGGTGCCGAAGGAATCTATGGTGGTTTTCTCTTGGGTGTGAAATCAG TGTCGGCTTAGCTTCTATGACTGGGACAAACGCTTGAGTTAGTAAGGCGCATTGAAATACAGCCT AGAGCTATCTACTGGTCAGATAGTGGCAAGTCCAGAAAGCTAGAGATAACAACCAAGTTGCCGAAGATGGAG ATTGTCCTATGACTCTGACCTTTGATGTCCTAGGTGAAATAAATGAATCAACTACTTTGTGGGTGTGAAC GACTGCTTCATTTACACAAACGCAGTCAACCGTATCAACTACTTTGTGGGTGGTTGGTAAC TATTGCACATCTGGACCGTCCTCTATATGTCTGGGCTATCAATTGCTATTATCTGTACTCGAATATCAGACTG CAGTCATGCGACGAGGAGACTTCCCAACGGCTGATCGAGTATTGCCTTCAATTCCAAAAGAACATCGC ACTAGGGTGGCACA

Table 2-EV

Target ID	Primer Forward 5'→3'	Primer Reverse 5'→3'	cDNA Sequence (sense strand) 5'→3'
EV005	SEQ ID NO: 523 TGCGATGCGG CAARAARAAGG TBTGG	SEQ ID NO: 524 TCCTGCTTCTT SGYRGCRATW CGYTC	SEQ ID NO: 513 TGCGATGCGGCAAGAAGAAGGTTTGGCTGGATCCTAATGAAATAACTGAAATTGCTAATACA AACTCTAGACAAAACATCCGCAACTGATTAAAGATGGTCTTATTATTAAAAGCCTGTCGCG GTGCATTCTCGTGCACGTGTACGGCAAAATACTGAAGCCCGGAAGTCGTCATTGTG GATTTGGTAAAGGAAAGGAAGGAACTGCAATGCTAGGATGCCCAGAAAGGAATTATGGATTCAA CGTATGAGAGTTCTCAGAGGTTATTGAAGAATATAGGGAAGCTAAGAAAATTGATAGGCA TTTATACCATGCTTTATATATGAAAGGAAATGTATTCAAGAATAAGGAGAGTAATGAT GGACTATATCCATAAAAAGAAGGCGGAGAAAGCACGTACAAAGAGTGCTAATGATCAAGCT GATGCAAGGAGGCTGAAAGTCAAGGAGTGAAGGCTGAAGAGCGTATCGCTACG

			AAGAAGCAGGA
EV009	SEQ ID NO: 525 GGGCCGTGGT CAGAAYATYWA YAAC	SEQ ID NO: 526 GCAGCCCACG CYYTGCACTC	SEQ ID NO: 515 CCAACTCTCGATCCAAGCATTCCAAAATACAGGACTGAAGAATCTATAATAGGAACAAACCC AGGAATGGGTTTAGGCCAATGCCCGACAACAACGAAGAAAGTACCCTGATTTGGTTACAG GGTTCTAATAAAACAAACTACGAAAAATGGAAAATGAATCTCTCTCATATTTAGACAAGTAT TACACTCCCGGAAAAATAGAAAAGGGAAATATTCCAGTAAAGGCGTGTTCATACGGAGAAAA ATTGATTAGGGGACAAGTATGTGATGTAGAGTGCCTTGTATATTCTGAAGCTGAACAGGATATGGA TGGGAACCGGAGTACTACAACGATCCAAATGACTCTTCCAGATGATACCGTGGGTAACATGC AGGACCATATACGTTATAATATCACCAATCCAGTGGAGAGAAATACCGTCTGGGTAACATGC GCAGGTGAAAATCCGGGTTACTATTTTCCATATTTGAATTCTGAAGGGTACCTAAGTCCATTATTGG CGGTACAATTCAAGAGACCGGTGTCTCGGTATTGTTATAAATATCGAGTGCAAAGCGTGGGCT GC
EV010	SEQ ID NO: 527 CGGCTGACGT GGAAYGTKTGG CC	SEQ ID NO: 528 CGGCCGTATTCT CCRAAYTTCTG GC	SEQ ID NO: 517 CTGGCGGCCACATGGTCATGGGTGATTCATTTAACTCTTCACTTTTCAAACAAACATTTCAAC GAGTATTTTCGAAAGATTCCAATGGAGACTTGAAGATGTCCTTCAACGCCATATTAGAAGTG AAGTGTTCTAGAGAACTTAAAGTACAAGGAGGTATAGGGTAACACAGTTCAGTGGAAACTGTGTA AAATCCTCTTGTTTCTGATTTAGAAATAGGCATGGGTAACAGTTCAGTGGAAACTGTGTA GCTTAAGTCCAAGCACTACGGTTGCCTTATTTTCGAAGTTGTTAATCAGCATGCAGCACCC ATTCCTCAAGGGGGACGTGGATGCATTCAGTTTATTACTCAATATCAGCATTCAAGTGGTCA GAAAAAATAAGGTAACTACAATAGCAAGAAATTGGGCGGATCGCCACTGCAAATATTCACC ATATTAGCCGCTGGCTTTGACGAACAAACTGCGGCTGTTTTAATGGCGAGGATCGCTGTATAT AGAGCAGAAACTGATGAGAGTTCAGATGTTCTCAGATGGTTGACAGAATGTTGATACGATT GTGTCAGAAATTTGGAGAATAATAACAAGATGACACCAACAGCTTCAGGCTCAGTGAAAACT TCAGCTTATATCCACAGTTTATGTATCATCTACGTCGTTCCCAATTTCTACAAGTGTTCAATAA TTCACCAGATGAAACTTCATTCTATAGGCACATGTTGATGAGGGAAGATCGCAATCAG
EV015	SEQ ID NO: 529 CGCTGTCGCAR GCRAARATGG	SEQ ID NO: 530 CGATCAAAGC GWCCRAAVCG ACG	SEQ ID NO: 519 CGGCCATCCGTCGCTGTCGTGTTCAAGGCGATCGGCGTTAAGCCTCCAAGGGGGTATTCTCCTTTACG CGGCCTCCCGGCACGGGGAAAACGCTGATCGCCAGGGCCGTTGCCAACGAAACTGGTGCGT TGTTCTTCCTCATCAATGGCCCGAGATTATGGCAGCAAGCTGGCCGGAGAATCCGAGAGCAA TCTTAGAAAGGCTTTGAAGAGGCTGATAAAAACTCTCCTGCAATCATCTTTATCGACGAATT AGAGCAATGCCTCCCAGCCGGAGAAGACTCATGGTGAGGTAGGAGACGCATCGTCTC CCAACTGTTGACTTTGACGTTGATGGACGGCATGAAGAAAGTTCCCATGTATCGTCGTGATGGCGGCC ACGAACAGGCCCAATTCCATCGACCCTGCCACTCAGAAGGTGAAGATTAGAAGTACTCAGAATACACCAAAAAC TCGACACATCGGTATCCCCGACGCTACTGGTGAAGATTAGAAGTACTCAGAATACACCAAAAAC

			ATGAAATTGGCTGACGATGTAGATTTGGAACAGATTGCGCGCAGAGACTCACGGTCATGTAG GTGCTGACTTGGCTCTTTGTGCTCAGAGGCTGCCTTGCAACACAATTAGAGAAAAATGGAC CTCATCGACTAGATGAGCAGCAGATCGATGCCGAGTCCTAAATTCTCTGCGCAGTTACCAT GGAGAACTTCCGTTACGCCCATGTCTAAGAGCAGTCCGAGCGCTTTGCGCGAAACCGTCGT
		SEQ ID NO: 532 CGGCATAGTC AGAATSGGRAT CTG	SEQ ID NO: 521 GACTGTGTCGTGGTGTGAACGGACCGTTGGTGATCCTTGATAGTGTTAAGTTTCCAAAATTTA ACGAAATTGTACAGCTCAAGTTATCAGATGGAACAGTTAGGTCTGGACAAGTTTTGGAAGTC AGTGGACAGAAGGCGGTTGTCTCCAAGTTTTTGAAGGCACCTCCAGTGTCTGAAGATATGTTGGGTCGT CTTTATGTGAATTTACAGGAGATATCTTAAGAACTCCAGTGTCTGATAAAGGCCGCCAATCTTAGCTGAAGATTTCT GTGTTTAATGGATCTGGAAAGCCTATCGATAAAGGCCGCCAATCTTAGCTGAAGATTTCT TGACATTCAAGGTCAACCTATAAATCCTTGGTCTCGTATCTATCCAGAAGAAAATGATCCAGA CTGGTATTTCTGCGATTGATGTGATGAAATTGCCAGAGGACAAAAGATTCCAATTTTCT CTGCAGCTGGTTTACCCCACAATCTGTCTTAGATGATCATGAAACAAATCTGTAGACAAGCTGGTCTTGTC AAATCCCAGGGAAATCTGTTGAAACAGCCAGATTCTTCAAGCAAGATTTGAAGAGAATGGCTCTA TATGGGTGTCAATATGAAACAGGCTGAATTTTTGAACTTGCCAATGATCGTCTACCATTGAAAGAATTATAACAC CCGTTTGACTTTAACAGGCGGCTGAATTTATGCATATCAATGTGAGAAGCATGTGTTAGTC ATATTGACTGACATGTCATCTTATGCTGAGGCTTTGCGTGAGGTATCTGCTGCT
EV016	SEQ ID NO: 531 GTTCACCGGC GAYATYCTGCG		

Table 2-AG

Target ID	Primer Forward 5'→3'	Primer Reverse 5'→3'	cDNA Sequence (sense strand) 5'→3'
AG001	SEQ ID NO: 611 CATTTGAAGCG TTTWRMYGCYC C	SEQ ID NO: 612 CGCTTGTCCC GCTCCTCNGC RAT	SEQ ID NO: 601 CATTTGAAGCGTTTTGCTGCCCCCAAAGCATGGATGTTGGACAAATTGGGGGGTGTGTTCGCCC CCAGGCCCTCCACCGGGCCACACAAGCTCAGGGAGTCCCTCCATTAGTGATTTTCTTGCCGTAA CAGGTTGAAGTACGCCCTGACAAACTGTGAGGTGACCAAGATCGTTATGCAGAGACTTATTAAG GTCGACGGCAAAGTCAGGACTGATCCTAACTATCCTGCTGATTCATGGATCGTGATCACCATTGA AAAAACTGGTAGAAGCAAAATACAAATTGTGCAAGTCCGCAAGGTGCAAACCGGACCAAAGGTATTC CATTCTTGGTCACCCACGATGGTAGGACCATTAGTACCCTGCAAAGTACCCAAATGATCAAGGTAAACGAC ACCATCCAACTGGAAATCGCCCACCTCAAAGATCCTGGACTTTATCAAATCCGGCAACTT GTGCATGATCACTGGTAGAGTGGGTAGAGTGGGAACGGCTAATGATCACGTGTTCGCCACTAGATTAA TCCGGGATCATTCGATATTGTCGTCATCGGTAAAGGAAGCAAAGCTTTCGTGTCTCTGCCAAGGGGCAAGGGAGT ACAACGTATTCGTCATCGGTAAAGGAAGCAAAGCTTTCGTGTCTCTGCCAAGGGGCAAGGGAGT GAAACTGTCCATCGCTG

	SEQ ID NO: 613 GGTCTGGTTGG ATCCHAATGAA ATCAAYGA	SEQ ID NO: 614 TCCTGCTTCTT SGYRGCRATW CGYTC	SEQ ID NO: 603 GGTCTGGTTGGATCCAAATGAAATCAATGAGATTGCCAACACCAACTCGAGGCAAAACATCCGTA AATTGATCAAGGATGGTTTGATCATTAAGAAAACCGGTGCAGTGCACTCTAGGGCTCGTGTCCGT AAAAACACAGAAGCTCGCAGGAGGGAAGGAAGCACTGCCGGTTTCGGTAAGAGGAAGGTACAGCG AACGGCTCGTATGCCTCAAAAGGAACTATGGATCCAAAGGATGCGTGTCTGAGCGGTCTCCTGA AAAAATACAGGGAAGCCAAAAAGATCCAAAAGAAGATCATCTGTACCACGCCCTGTACATGAAGGCCAA GGGTAACGTGTTCAAGAACAAGAAGAGTGTTGATGGAATACATCACCACAAGAAGAGGCTGAGAAG GCCCGTGCCAAGATGTTGGCCGACCAAGCTAACGCCAGAAGGCAAAAGGTGAAACAAGTCCCG TGAGAGGAGGGAAGAGCGTATCGCCGCGAAGAAGCAGGA
AG005			
AG010	SEQ ID NO: 615 CTGGCGGCCA CATGSTBATGG	SEQ ID NO: 616 CGCCATTGGG CRATGGTYTCK CC	SEQ ID NO: 605 CTGGCGGCCACATGCTTATGGGAGACTCTTCAATTCGTCGTTGTTCAAACAAACTTTCCAAAGG GTGTTCGCGAAGGACCAGAATGGACATTTGAAGATGGCTTCAACGGTACTTTGGAGGTGAAGT GCTCTAGGGAATTAAAAGTTCAAGGCGTATTGGCTCATGGCGTGTCGCTAAATGTAAAAAGTCCT TTGGTAGCGGACACGGAAATAGGCCATGGGAAACACCGTGCAATGGAAGATGTGCACCTTCAACC CTAGCACGACGATGGGCGCTGTTTTTCGAGGTGGTCAATCAGCACTCGAGTGGCCAAAGGAGGATAAGGG TGGTAGAGGGATGTATACAGTTTATTACACAATATCAGCACATCGGCGAATATTCACCACATCAGCGCGCGGGTTT CGATCAGGAACGTGCCGCGGTGATTATGGCCGGATAATGGCGTGTTTATAGAGCGGAGACCGATGA GAGTCCCGATGTTTTAAGATGGCGATGGTCGATCGTGATTCGTTGTGTCAAAGTTTGGAGAAT ATAACAAAGATGACCAGCATCCTTCAGATTAGGGAGGAAAATTTTAGCTTATACCCGCAATTCATGT ACCACTTAAGGCGATCCCAGTTTTTGCAAGTGTTCAACAATTCACCTGACGAAACGTCGTTTTACA GGCATATGCTTATGGGTCCTCCGGAAGATTTGACACAGTCCGTTTTTGTTGGACACCAGTCTTGTACAGT TACAGTTTTAATGGTCACGTTTTCCAGATATTGATTTTCCATGGAGAAACCATTGCCCAATGGCG TCTGCTTATGGACGGTTTATGGGAGCCGTTTTTCCAGATATTGATTTTCCATGGAGAAACCATTGCCCAATGGCG
AG014	SEQ ID NO: 617 CGCAGATCAAR CAYATGATGGC	SEQ ID NO: 618 GAACTTGCGG TTGABGTTSCG DCC	SEQ ID NO: 607 CGCAGATCAAGCATATGATGGCCTTCATTGAGCAAGAGGCTAATGCAAGAGGGAGGAAATTGA TGCCAAGGCGAAGAAGAATTAACATTGAAAAGGGCCGCCTTGTGCAACAAGATTGAAG ATCATGGAATACTATGAGAAGAAGGAGAAGCAAGTCGAACTACAAAAGAAATTCAATCCTCCAA CATGTGAACCAACCAGCCCGTCTTAAGGTTCTGAAAGTCCGGAAGCATGTTAGAGCTGTATTGG ATGAGGCTCGCAAGAAGCTTGGTGAAGTCACCAGGTCTTTCGAGGCAACCATGCAAATATGCCCGAGATTCTGGA ATCTTTGATCTTCCTTCAGGGACTCTACCAGCTTTGCTGCCAACCATGCAACCAAATACCGTGACGTCCGCCCA CAAGACAGAACCTTAGTCCAATCAGTGCTGCCCATCGATGACGAAACTCAACTGTCCGAATCCGCGGGAAT GCCGAGACTTTTGTGCAAACAAAACAAAATTAAGGTCTGCAACACCCTGGAGGCACGTTTGGACCTGA CGAACTTTTGTGCAAACAGTTGGTTCCGCAAATCCGTAACGCCTTGTTCGGACGCAACATCAACCGCAAGTTC TTTCGCAACAGTTGGTTCCGCAAATCCGTAACGCCTTGTTCGGACGCAACATCAACCGCAAGTTC
AG016	SEQ ID NO: 619	SEQ ID NO: 620	SEQ ID NO: 609

| GTGTCGGAGG ATATGYTGGGY CG | GGAATAGGAT GGGTRATRTC GTCG | GTGTCGGAGGATATGTTGGGCCGAGTGTTCAACGGATCAGGAGAAACCCATTGACAAGGTCCTC CAATCTTAGCCGAAGATTTCTTGGACATCCAAGGTCAACCCATCGACGTGCGGTATCTAC CCGGAAGAAATGATCCAGACCGGTATCTCCGGCCGGTTACCGCACAACGAAATCGCCGCCAAATCTGTAG CAAAAATCCCCATTTTCTCCGCGAAACTGCCGGGCAAATCGGTAATCGACGATCACGAGAGA ACAGGCCGGTTCGCCGCCATGGCGGGTGTCAACATGGAAACGCCCGTTTCTTCAAGCAGGACTTCGAAG ATCGTTCGCGCCGCCATGGAGGAACGTGTGTCTCTTCTTGAATTGGCCAACGATCCCACCATCGAGAGA AAAACGGTTCATGGAGAACGTGTGTCTCTTCTTGAATTTTGGCTTATCAATGCGAGAAACACGT ATCATCACGCCGCCCGTTTGGCTCTGACCGCCCGAATTTTGGCTTATCAATGCGAGAAACACGT GCTGGTTATCTTAACTATGATGTCGTCTTACGCTCGGTTCCCCGGTTACACTGTACACGTTCCCATCACCCCAGATTCCCATCTTGACTATGCCG AAGAAGTACCCGGACGTCGTGGGTTGAGGGGTAGAAAACGGTTCCATCACCCCATCTATTCCGACCATTACGA AACGACGACATCACCCCATCTATTCC |

Table 2-TC

Target ID	Primer Forward 5' → 3'	Primer Reverse 5' → 3'	cDNA Sequence (sense strand) 5' → 3'
TC001	SEQ ID NO: 803 GGCCCCAAGAA AGCATTTGAAG CG	SEQ ID NO: 804 CGCTTGTCCCC GCTCCTCNGC RAT	SEQ ID NO: 793 GGCCCCAAGAAGCATTTGAAGCGTCTCAATGCGCCCAAAGCATGGATGTTGGATAAACTG GGGGGTGTGTTTGCCCCTCGGCCTTCCACCGGCCCCCACAAGCTACGGGAGGTCGCTACC TTTGGTTATCTTCCTGCGAAACAGGCTGAAGTATGCCTTGACCAACTCAGAAGTGACGAA GATTGTTATGCAAAGATTGATTAAGTTGACGGAAAAGTTAGGACAGACCCCAACTACCCC GCGGGTTTCATGGATGTTGTGACTATTGAGAAAACTCCGGTTATTTATG ATGTTAAGGGAAGGTTCACAATCCATCGCATTACTGCTGGAGAAGAGGCCAAATATAAATTGTG CAAAGTGAAGAAGTACAGACAGGCCCCAAGGGCATTCCCTTCTTGGTGACCCGCGACG AGCCGACTATCAGATACCCAGAACCCATGATCAAAGTGAATGACACCATTCAATTGGAGAT TGCCCACTTCGAAAATTCTTGATTTTATCAAATTTGAGTCCGGTAATTTGTGTATGATTACTG GAGGTCGTAACTTGGGGGTGTCGGTGTACAGTGGTGAGCCGAGAACGTCACCCAGGTTCC TTCGACATCGTTCATATTAAGGATGCAAATGGGCACACC
TC002	SEQ ID NO: 805 CAGGAGTTCCT GGARRMBAAR ATMGA	SEQ ID NO: 806 GCAATGTCATC CATCAKRTCRT GTAC	SEQ ID NO: 795 CAGGAGTTCCTGGAGGCTAAAATCGACCAAGAGATCCTCACAGCGGAAGAAAACGGTC GAAAAACAAACGAGCGGGCCATCCAGGCCATCAAGAGGAAGAAACGCTACGAAAAGCAGC TCCAGCAGATCGATGCCACCCTCAGCACCATCGAGCACCATCGAGATGAAAAACGATGAAAAACGATGAAAAGCGGGGAGGGCCCTCGAGGG GGCCAACACCAACACAGCCGTACTCAAAACGATGAAAAACGCAGCGGACGCCCTCAAAAA TGCCCACCTCAACATGGATGTTGATGAGGTACATGACACATGATGACATTGC
TC010	SEQ ID NO: 807	SEQ ID NO: 808	SEQ ID NO: 797

	GCATTCTGCGC TGGGTCGATCG	AAAATTCGGGCGAATACAACAAAGACGACCCTAACAGTTTCCGTTTGAGTGAAAACTTCAGT CTCTATCCCCAATTCATGTACCATTTGGCGCCGCTCCAATTCCTCCAGTTTCAACAACT CCCAGACGAGACCTCGTTCTACCGCCACAGTTGTACAGTTATAGTTTCAACGGCCCCCTGAACCCGTCC TCCTCGACACTAGTTCCATTCAACCGATCGGATCCTTCTCATGGACACATTTTCCAAATT TTGATTTTCCACGGTGAGACAATCGCCCAATGGAGGAACCTCAGTACCAGGACGATGCCC GAATACGAGAACTTCCGGCA
TC014	SEQ ID NO: 809 GAGAAAGCCG ARGARATYGAT GC	SEQ ID NO: 810 GAACTTGCGG TTGABGTTSCG DCC
		SEQ ID NO: 799 GAGAAAGCCGAAGAAATCGATGCGAAAGCTGAGGAGGAGTTAACATTGAAAAAGGGCG CCTGGTCCAACAACAGCGCTTGAAGATCATGGAATATTACGAGAAGAAGGAGAAACCGGT GGAATTGCAGAAGAAAATTCAGTCGTCAAACATGTGCTGGATGACGCCCGAAACGTCTGGGCGA AAGTGCGTGAAGACCACGTCCACAATTCACAACTTTGGAGTCTCTTATCCTCCAGAGTCTC AATCACCAATGACCAGGCGAGATATTCACAACTTTGGAGAACAATATAGTGGTGAGAGTCAGG CAACAGGAGGAGTAATCACGGCATTCTCCCAGTTGTTGCCGACGAAATACAGGGAC GCCACTGGTAAAGACGTTCATCTTAAAATGCGCAAAAGGGTAAAATCAAGATTGACAACACCTTGAAC ACCGGAGGAGTGGTTTTGTATGCGCAACTTGTGCCAGAAAATTCGTACGGCCTTGTTTGGAC GCAACATCAACCGCAAGTTC
TC015	SEQ ID NO: 811 GGATGAACTAC AGCTBTTCCGH GG	SEQ ID NO: 812 CGATCAAAGC GWCCRAAVCG ACG
		GGATGAACTACAGCTGTTCCGTGGCGATACAGTGTTGCTGAAAGGGAGGCGGAAAG AGACCGTCTGCATTGTGCTGGCCGACGAAAACTGCCCCGATGAGAGATCGGATGAAC AGGATCGTCAGGAATAATCTACGGGTTAGGCTCTTGAGTCGTCTCTGGATCCAGCCCTGT CCCGACGTCAAATACGGGAAGAGGATCCACGTTTTGCCCATGCATGACACGTCGAAGG GCTCGTCGGGAAATCTCTTCGAGGTGTACTTAAAACCATACTTCCTCGAAGCTTATCGACCA ATCCACAAAGGCAACCGTCACCATATTGTATCGTCGGTGGTGGCATGGCCGTTGAATTCAAAGTG GTGGAAACGGAACGGATCAAACGAGAAGAGGAGGAAGCCTTGAACGCCGTCGGCTACGACGA TATCGGCGGTTGTCGCAAACAACTCGCACAAATCAAAGAAATGGTGCAATTACCTCTACG CCACCCGTCGCTCTTCAAGGCCATTGGCTGAAACCACGTGCCAACGAAACCGGTGCTTT ACCTCCAGGTACCGGTAAAACTTTAATCGCACGTGAGTAAATTAGCGCGGCACGTCGAAGG CTTCTTCTTAATCAACGGTCCCGAAATTATGGAGTAAAAACTCACGGGCTATTATTTCATCGATGAAT CTAAGGAAAGCGTTCGAAGAAGCCGATAAAAAACCCAGGCGAAGAAAAGCTCGCATGTTATCGTGATGGCG TCGCAATTGTTAACACTGATGGACGGCATGAAGAAAAGCTCGGATCCGAAGTTGTC GCCACAAATCGCCCGAACTCAATCGATCGGCGTTTGCGTGGTTCGGTCGCTTTGATCG

Table 2-MP

Target ID	Primer Forward 5'→3'	Primer Reverse 5'→3'	cDNA Sequence (sense strand) 5'→3'
MP001	SEQ ID NO: 898 GGCCCCAAGAAGCATTTGAAGCG	SEQ ID NO: 899 CGCTTGTCCCGCTCCTCNGCRAT	SEQ ID NO: 888 GGCCCCAAGAAGCATTTGAAGCGCACCCAAAGCATGGATGTTGGACAAATCGGGGGGTGTCTTCGCTCCACGTCCAAGCACCGGTCCACACAAACTTCGTGAATCACTACCGTTATTGATCTTCTTGCGTAATCGTTTGAAGTATGCACTTACTGGTGCGAAGTCACCAAGATTGTCATGCAAAGATTAATCAAGGTTGATGGCAAGTCCGTACCGACCCTAATTATCCAGCCGGTTTATGGATTGTTATATCATCCACAGAATTACTCCTGAAGAAGACCAGTGAGCACTTTAGATTGATCTATGATGTGAAGGTCGTTTCACCATCCACAGAATTACTCCTGAAGAAGCAAAATACAAGTTGTGTAAAGTAAAGAGGGTACAAACTGGACCCAAAGGTGTGCCCAAAGGTTAATGACACATTAGATACGATAACTGGAGGTCGCCGTACTATTCGCTACCCTGACCCTAACATCAAGGTTAATGGAAACTTGAAACTGGAAACTGGAGATATTGCATGCATCTAAAAATTTTGGATCATATCCGTTTTGAAACTGGAAACAGGGAAAGACATCCAGGATCGTCTTTGATATTGTTCACATTAAGGATGCAAATGAACATATTTTTGCTACCCGGAGTAAGGAGTAAGGGAGTTAAATTGACTATACATTTCTCTACCAAGGAGTAAGGGAGTTAAATTGACTAT
MP002	SEQ ID NO: 900 GAGTTCTTTAGTAAAGTATTCGGTGG	SEQ ID NO: 901 GCAATGTCATCCATCAKRTCRTGTAC	SEQ ID NO: 890 GAGTTTCTTTAGTAAAGTATTCGGTGGCAAAAAGGAAGGAAGAGAGAAGGGACCATCAACCGAAGATGCGATACAAAAGCTTCGATCCACTGAAGAGATGCTGATAAAGAAACAAGAATTTTAGAAAAAAAAATTGAACAAGAAGTAGCCGATAGCCAAAAAAAATGGTACAACTAATAAACGAGCTGCATTGCAAGCATTGAAGCGTAAGAAACGGTACGAACAACAATTAGCCCAAATTGATGGTACCATGTGTTAACTATTGAACAACAGCGGGAGGCATTAGAAGGTGCCAACACAAATACAGCAGTATTGACTACCATGAAAAACTGCAGCAGATGCCACTTAAATCAGCTCATCAAAACATGAATGTAGATGTGACATGATCTGATGGGATGACATTGC
MP010	SEQ ID NO: 902 GTGGCTGCATACAGTTCATTACGCAG	SEQ ID NO: 903 CGCGGCTGCTCCATGAAYASYTG	SEQ ID NO: 892 GTGGCTGCATACAGTTCATTACGCAGTATCAACATTCCAGTGGCTATAAACGAATTAGAGTCACCAACATTAGCTAGGAATTGGGCAGCACCCTGTTCAGAATATGCATGTTAGTGCTGCATTGATCAAGAAGCAATCTGCCGTTTAATGGCTCGTATGGTAGTGAACCGTGCTGAAACTGAGGATAGTCCAGATGTGATGCGTTGGGCTGATCGTGTCTTATACGCTTGTGTCAAAAATTGGTGATTATCAAAAAGATGATCCAAATAGTTTCCGATTGCCAGAAAACTTCAGTTTATATCCACAGTTCATGTATCATTTAAGAAGGTCTCAATTTTATACAAGTTTTAATAATAGTCCTGATGAAACATCATATTATAGGCACATGTTGATGCGTGAAGATGTTACCCAAAGTTTAATCATGATACAGCCAATTCTGTATAGCTATAGTTTTAATGGTACGTAGGCCAGAACCTGTACTTTTGGATACCAGTAGTATTCAACCTGATAAAATATTATTGATGGACACATTTTCCATATTTGATATTCCATGGAGAGACTATTGCTCAAT

			GGAGAGCAATGGATTATCAAAATAGACCAGAGTAGTAACCTCAAGCAGTTGCTTCAAGCCC CCGTTGATGATGCTCAGGAAATTCTCAAAACTGATTCCCAATGCCTCGGTATATTGACACAG AACAAGGTGGTAGTCAGGCAAGATTTTTACTATGCAAAGTAAACCCATCTCAAACACATAATAA TATGTATGCTTATGGAGGGTGATGGTGGAGCACCAGTTTTGACAGATGATGTAAGCTTGCAG CTGTTCAATGGAGCAGCCGCG
MP016	SEQ ID NO: 904 GTGTCGGAGG ATATGYTGGGY CG	SEQ ID NO: 905 GGAATAGGAT GGGTRATRTC GTCG	SEQ ID NO: 894 GTGTCGGAGGATATGTTGGGCCGGCGTTTTCAATGGCAGTGGAAAGCCGATAGATAAAGGACC TCCTATTTGGCTGAAGATTATTGGATATTGAAGGCCAACCTATTAATCCATACTCCAGAACA TATCCTCAAGAAATGATTCAAACTGGTATTCAGCTATTGATATCATGAACTCTATTGCTCGTG GACAAAAAATTCCAATATTTCAGCTGCCAGGTTACCACATAATGAGATTGCTGCTCAAATTTG TAGACAAGCTGGTCTCGTTAAAAAACCTGGTAAATCAGTTCTTGACGATCATGAAGACAATTTT GCTATAGTAGTATTTGCTGCTCGTGTTAATATGGGAGAATGTTGTTTGTTTCTTGAATTTAGCTAATGATCCTACTATTGA AGGAAAATGGTTCAATGGAGGAAGCTCTTGCTTTAACTGCTGCGAATTTTAGCTTACCAATGTGAAAAG GCGTATCATTACACCACGTCTTGCTTCCCTGGTCGTGTTCCCTGGTTACATGTACACCGATTTAGCTACAA TTTATGAACGTGCTGGGCGTGTAGAAGGAAGAAATGGTTCTATCACACAAATACCTATTTTAA CTATGCCTAACGACGACATCCACCCATCCTATTCC
MP027	SEQ ID NO: 906 CGCCGATTACC AAACAARACB TG	SEQ ID NO: 907 GGGGATACTGT CACAAYYTCDC CRCC	SEQ ID NO: 896 CGCCGATTACCAAAACAAGAAGACGTGTGTTCAGACATTAGAAGGCCATGCTCAAAAATATTTCTGC TCGTTTGTTCCATCCAGAACTTCCCATCGTGTTAACTGGCTCAGAAGATGGTACCGTCAGAA TTTGGCATTCTCGGTACTTATCGATTAGAATCATCATTAAACTATTAAACGTGTATGGAC AATCGTGTTACGGGGATCTAATAATGTAGCTCTAGGTTATGATGAAGGAGTATAATGGT TAAAGTTGGTCGTGAAGAGCCAGCCAGCAATGTCATGGATGTTCATGGGGGTAAAATTGTTTGGG CACGTCATAGTGAAGATGTGAACGTTTACCAATACAAGTTAAGACATGGTAGCTGTGAAATTTATCCAC AGTCAATATCTCATAATCCGAATGGTAGATTTTTAGTAGTATGTGGTGATGGGAGAGTATATTAT ATATACATCAATCAATGGCTTTGCGTAATAGAGAAAATTCTTCTACAATCAAAGTTTTAAAGAAAA AAAGTCTTTAAACCAGGGTGGCTTTATAATTTTGGCTTGAGAATGGTAACTTAGTTCGGAAGAATTGAGAA ATCTGTTACTGGGGTTGGCTTTATATTTGGCTCAATGTAAACTTAGTTCTTGCCACAGATGAAGC ACAACCTAAACATGTATTTTACGTTTGACGTCAATGTGCTTGAGATTTAGGAGCTGTCGCAAGAGCATCCAATTATGAAGCT ATACTTTATTTTACGTTTTGACGTCTGAAGATGCCTTTGAGATTTACACCACCAATGGAGTAAATCGTATCAACTATATG GCTAGTCCTGATGGGTTGGTGTGATTGCTTTATTTACACCACCAATGGAGTAAATCGTATCAACTATATG ACTGGTCTATGGGGTTGGTGTGATTGCTTTATTTACACCACCAATGGAGTAAATCGTATCAACTATATG TTGGGTGGTGAAGTTGTGACAGTATCCC

Table 2-NL

Target ID	Primer Forward 5' → 3'	Primer Reverse 5' → 3'	cDNA Sequence (sense strand) 5' → 3'
NL001	SEQ ID NO: 1117 GAAATCATGGAT GTTGGACAAATT GG	SEQ ID NO: 1118 ACTGAGCTTCACAC CCTTGCCC	SEQ ID NO: 1071 GAAATCATGGATGTTGGACAAATTGGGTGGTGTGTATGCACCCGACCCAGCACAGG TCCACACAAGCTGCGAGAATCTCTCCCACTTGTCATATTTTTGCGTAATCGGCTCAAG TACGCTTTAACTAACTGTGAAGTGAAGAAATTGTGATGCAGCGTCTCATCAAGGTTG ACGGCAAAGTGAGGACTGACCCCAACTATCCTGCAGGTTTTATGGACGTTTCAAAT CGAAAAGACAAACGAGTTCTTCCGTTTGATCTATGATGTTAAGGGACGTTCACCATC CACAGGATCACAGCTGAAGAAGCTAAGTACAAGCTGTGCAAAGTGAAGAGGGTTCAG ACAGGACCCAAGGGCATTCCATTTTTGACCACTCACGATGGACGCACCATCAGGTAT CCAGACCCCTTGGTAAAGTCAATGACACCATCCAATTGGACATTGCCACATCCAAAA TCATGGACTTCATCAGATTCGACTCTGTGTGAACAGGGAGGCGACACCCGGGGTCTTTCGACA TCGTGCACATCGGCAAGGGTAGTAAAGCATACGTGTCTCTGCCCAAGGGCAAGGGTGTGAA GCTCAGT
NL002	SEQ ID NO: 1119 GATGAAAAGGG CCCTACAACTG GC	SEQ ID NO: 1120 CTGATCCACATCCA TGTGTTGATGAG	SEQ ID NO: 1073 GATGAAAAGGGCCCTACAACTGGCGAAGCCATTCAGAAACTACGCGAAACAGAGGAA ATGCTGATAAGAAACAAGACTTTTAGAAAGAAAATTGAAGTTGAAGTTGGGAGTTGC CAGGAAGAATGGAACAAAAACAAAGAGCCGGATCCAGGCACTCAAAAGGAAGAA GAGTATGAAAGCAATTGCAGCAGATCGATGAACGTTATCAACAATTGAGATGCCA GAGAGAGGCCCCTGAGGAGCCAACAGAATACGGCCGTACTGCAAACTATGAAGA ACGCAGCAGATGCTCTCAAAGCGGCTCATCAACACATGGATGTGGATCAG
NL003	SEQ ID NO: 1121 TCCGCGTCGTC CTTACGAGAAG GC	SEQ ID NO: 1122 TTGACGCGGACCAG GTCGGCCAC	SEQ ID NO: 1075 TCCGCGTCGTCCTTACGAGAAGGCACGTCTCGAACAGGAGTTGAAGATCATCGGAGA GTATGGACTTCCGTAACAAGCGTGAGGTGTGGAGAGTCAAATACGCCCTGGCCAAGAT TCGTAAGGCCGCTCGTGAGCTGTTGACTCTGGAAGAGAAGGACCAGAAACGTTTGTT TGAAGGTAACGCCCTGCTGATTACGTCTTGGGGTTTAAAAATTGAAGATTTCCTTGAACGTGTCT ACAGACTCAGGTGTACAAACTCGGTTTGGCCAAGTCCATCCATCACGCCCGTGTACT CATCAGACAAAGACATATCGCAGAAGACTGCGCAAACAAGTAGTGAACATTGAACTTGTGT GTGCGCCTGGACCTCGCAGAAGCACACTTGACTTCTCGCTGAAGTCGCCGTTCGGCGG TGGCCGGACCTGGTCGCGTCAA
NL004	SEQ ID NO: 1123	SEQ ID NO: 1124	SEQ ID NO: 1077

ID	Forward primer	Reverse primer	Sequence
	TGAAGGTGGAGAARGGTTYGGMWCMAAG SEQ ID NO: 1125	GTCGTCTTCTCDGAHACRTAVAGACC SEQ ID NO: 1126	AAGGAGTTGGCTGCTGTGTAAGAACTGTCTGCTCTCACATCGAAAACATGCTGAAGGGA GTCACAAAGGGATTCCTGTACAAGATGCGTCCGTGCCGTGTACGCCCATTCCCATCAAC TGTGTGACGACCGAGAACAACTCTGTGATCGAGGTGCGTAACTTCCTGGGCGGAGAAG TACATCCGACGGGTGAGGATGGCGCCCGGCGTCACTGTTACCAACTCGACAAAGCA GAAGGACGAGCTCATCGTCGAAGGAAACAGCATAGAGGACGTGTCAAGATCAGCTG CCCTCATCCAACAGTCAACAACAGTGAAGAACAAGGATATTCGTAAATTCTTGGAC SEQ ID NO: 1079
NL005	SEQ ID NO: 1125 GGTCTGGTTGGATCCHAATGAAATCAAYGA	SEQ ID NO: 1126 TCCTGCTTCTTSGYRGCRATWCGYTC	TTGGATCCAATGAAATAAATGAAATCGCAAACACAAATTCACGTCAAAGCATCAGGA AGCTGATCAAGACGGTCTTATCATCAAGAAACCGGTTGCAGTACATTCACGTGCTCG CGTTCGTAAAAACACTGAGCCAGGAGAAGGCAGAGACATTGTGCTTGGTTAAGAG GAAAGGTACAGCCAACGCCCGTATGCCACAAAGGTTCTATGGGTGAATCGTATGCG TGTCTTGAGAAGACTGTTGAAAAATACAGACAAGATAAGAAAATCGACAGGCATCTG TACCATCACCTTTACATGAAAGGCTAAGGGTAACGTATTCAAGAACAAGCGTGTATTGA TGGAGTTCATTCATAAGAAGAAGGCCGAGAAAGCAAGAATGAAGATGTTGAACGACC AGGCTGAAGCTCGCAGACAAAAGGTCAAGGAGGCCAAGAAGCGAAGGGAA SEQ ID NO: 1081
NL006	SEQ ID NO: 1127 GGAGCGGAGACTACAACAAYKAYRGYTGGC	SEQ ID NO: 1128 GAGATCTTCTGCACRTTKACVGCATC	AAGTGCTTGTGTCAAGTGGTGGTGGTGGAGTACATTGACACCCTGGAGGAGGAGACG ACCATGATAGCGGATGTCGCCGGATGACCTGCGTCAGGACAAGGAGTATGCCTACTGT ACCACCTACACGCACTGCGAGATCCACAACCAAAGTCCCAGGAACACCTATCAGAGCGGCTATGG ATTATTCCCTTCCCCGATCACAACAGTCACCAACTTCCACGTGCGAATGGACACGCTG GGAAACAGGCGATGGCGTGTACCGCCACTGGTCACCACTCGCTCACCTCGTGGTGCCATCGCCTGCTAC CTGCGCTTCAGGGAGCTTCCTGCCGCACGTGTCAACTCTGTGGTGCCATCGCCTGCTAC ACTGGATACAACCAGGAGGACAGCGTGTCATTCATTCTCAAGGATGCAAGACTGAGCGTATTGGC ATTCTTCAGATCGTGGTTTCTTCCGATCTTACAAAGATGCAAGACGTGCAGGGAATGAGGAA GACCAAGAGGAGCAATTCGAGAAGCCCACAGACGAGTGTCAGGAATGAGGAA TGCCATTTATGACAAATTGGACGATGGCATCATTGTCCCGGTCTCTGAGAGTGTCT GGTGACGATGTGGTTATTGGCAAAACCATAACACTGCCCGATAATGATGACGAGCTG GAAGGTACAACAAAGAGGTTCACGAAGAGATGCCAGTACTTTCCTGCGTAACAGT GAGACGGGAATCGTGACCAAGTCATGTTAACCTTGAACTCTGAGGGTTACAAGTTC TGCAAAATTCGAGTCAGGTCTGTGCGTATCCGCAGATTGGCGATAAGTTCGCTTCC CGACATGGCCAAAAGGAATCGCACCGGATATTATCAATCCTCACGCTATCCCATCTCGTA TGACAATTGGCCATTTAATTGAATGTCTCCAAGGAAAGGTGTCGTCGAACAGGGGCG AGATAGGTGACGCGACGCCGTTCAAC SEQ ID NO: 1083
NL007	SEQ ID NO: 1129	SEQ ID NO: 1130	

	CGGTGTCCATTCACAGYTCCGG	CGATGCAAGTAGGTGTCKGARTCYTC	TTTCAGAGATTTCCTTCTGAAACCTGAAATTTGAGAGCAATCCTTGACTGTGGTTTG AACATCCATCTGAAGTACAACATGAATGCATTCCTCAAGCTGTACTTGGAATGGACAT ATTGTGTCAAGCGAAATCCGGTATGGGAAAAACTGCTGTATTTGTTGTTGGCGACATTA CAGCAAATTGAACCAACTGACAACCAGTCAGTGTATTGGTCATGTGTCATACCAGAG AGCTTGCATTCCAAATCAGCAAGAGTATGAACGATTTCGAAATGTATGCCAAATAT CAAGGTTGGAGTTTCTTCGGCGACTGTGGTTGGAACACCCGGACGAATTTTGGCGTTGGTACG ATTGAACTGTCCTCACATCGTGGTTGGAACACCCGGACACTTTGTCCTTGACGAATGTGACAAA CAACAAGAAGCTGGACCTCAAGCATCTCAAGGACATCTCAGGAAATATTCCGAAACACGCCG CACAGCAAAGTCATGATGTTCAGTGCAACTCTCAGTGAAGCTGTCCAGTCT GCAAGAAATTCATGCAGATCCGAGCAGCACTATGTCAAACTCAACCAGTTGAAGTCA CGCTTCACGGCCTGCAGCACATTGTGAATTACATATCTTGACATACTTGTTATATTGTGAAGTCA AGTTATTTGAATTACTTGACATACTTGAATTCAACCAGTTGTTATATTTGTGAAGTCA GTGCAGCGCTGCATGGCCCTATCGCAACAAGAACGATTGAAGAAATATCAAGAGTTCAAAG GCTATTCACCGTGGCATGAGCAATTTGGTAGCAACGAATCTGTTTGGGCAGAGGAATGATATTGA GAGAGTCAACATTGTATTCAACTATGACATGCCT
	SEQ ID NO: 1131 GTGGTGGATCACTTYAAYCGKAT G	SEQ ID NO: 1132 GCGCATTTGATCGTTBGTYTTCAC	SEQ ID NO: 1085
NL008			GGAAGGATAGAAAACCAGAAACGAGAGTTGTTGGTGTTCTTTGGGATGTGCTGGAGACCT GGAGGTGTATTAGATGTTTCAAACAGTTTGCAGTTCCATTTGATGAGGACGACAAAG AAAAGAAATGTTTGGTTCTTAGAGAAAAGGTTGTGGGTTGGTACCATAACATGGTCGGGATGTTCAA GAAAGTTAATGCTAGAGAAAAGGTTGTGGGTTGGTACCATACTGGACCCAAACTCCA CCAAAACGATGTTGCAATCAATGAGTTGATTCGTCGTTACTGTGTCCAAACTGTGTCTTA GTCATAATCGATGCCAAGCCTAAAGATTTGGGTGTCTACCTACACAGAGTC GTTGAAGAAAATCCATGATGAGAGGCTGAGGAGAGGCTGAGGAGATTGGCGTTGAACATCTGTTGAGAGAC ATCAAGAGATACAACAGTCGGGGTCACTTGCACAGCGCGTCACAAATCAGCTGATGGGC TTGAAGGGCTTGCATCTGCAATTACAGGATATGCGAGACTATTTGAATCAGGTTGTCG AGGAAAGTTGCCAATGAACCATCAAATGACCAAATTTTGTAGAGACTCGCTCTAC TCTACCCGATATCGGCCACGGCAATTTTGTAGAGACTCGCTCTAC
	SEQ ID NO: 1133 GGGCCGTGGTCAGAAYATYWAYA AC	SEQ ID NO: 1134 CCGCCAAAGGACTSARRTADCCCTC	SEQ ID NO: 1087
NL009			TGCGACTATGATCGACCGCCGGGACGCGGTCAGGTGTGCGACGTCAAGAA CTGGTTTCCCTGCACCTCTGAGAACAATTTCAACTACCATCAATCGAGCCCTTGTGTT TTTCTCAAACTGAACAAGATAATTGGTTGGCAACCGGAGTACTACAATGAGACTGAAG GCTTTCCAGATAATATGCCAGGTGACCTCAAGCGACACATTGCCCAACGAAGAGTA TCAACAAGCTGTTTATGCAACAATCTGGATAACTTGCCGAGGAGAGGGTCCTCTAGA

		CAAGGAGAATGCAGGGGAGATCCAGTACATCCCTAGACACAGGGGATTTCCGGGCTACTTCTACCCTTACACTAATGCC
NL010	SEQ ID NO: 1135 CGGCTGACGTGGAAYGTKTGGCC	SEQ ID NO: 1136 TGCCGGAAGTTCTCRTAYTCKGGC	SEQ ID NO: 1089 (amino terminus) GTCCAGTCGACTGGAAGCCACCAGGCTTGTTGTTCCGTTGGATGTCTGTATCAACCTTTGAAGGAGAGACCTGATCTACCGCCTGTACAGTACGATCCAGTTCTTGTACTAGGAATACTTGTCGTGCAATTCTGAATCCATTGTGCCAAGTCGACTATCGAGCCAAGCTATGGGTCTGCAACTTTGTTTCCAGAGGAATCCTTTCCCCCTCAAATGCAGCTATTTCGGAGCAGCATCAACCAGCAGAACTGATACCTTCATTTTCCACCATCGAATACATCATTACCAGAGCGCAAACGATGCCGCGCCGATGTTCGTGCTGGTGGTGGACACATGTCTGGACGACGAGGAGGCTGGGAGCTTTGAAGGACTCACTGCAGATGTCGCTGTGCTGCCGCCCAATGCACTCATCGGTCTCATCACGTTCGGCAAAATGGTGCAGGTGCACGAGCTTGGCTGCCGACGGCTGCTCGAAGAGCTACGTGTTCCGTGGCGTGAAGGACCTGACTGCCAAGCAGATCCAGGACATGTTGGCCATTGGCAAGATGGCCGCGCTCCACAGCCCATGCAACGCAGCATTCCCGGCGCCGTGTCCCTGCCACCTGTCAACAGATTTCTTCAGCCTGTCGGAAAGTGCGATATGAGTTTAACTGACTAGTGAGTTCAAGGGGAATTGCAAAGAGATCCATGGAATGTGTGGCTCAGGGCAAGGAACCCTCTCCGATCTACTACTGGGAGTTGCATTGTCCATTGCAGTTGGTGCTCGCTGAGTGCACA SEQ ID NO: 1115 (carboxy terminus) CGTTGAACGTGAAGGCTCGTGTCTGTGTCAGACACTGACATTGGCTTGGGCGGCCACCTCTCAATGGAAAATGTGCGCTTCACTCACTCCACAGCAACAACTTGTGCATTCTTCTTCGAAGTTGTCAACCAGCACGCAGCCCCAATCCCACAGCGGAAGAGGATGCATCATCATTACGCAATACCAACATTCCAGTGGCGCAGCACCAAACCTGCACACCACCATCGCTCGAAACTGGGCAGATGCGAGCAACCTGGCACACATCAGTGCCGGCTTCGACCAGGAGGCAGGAGCCGTGCTCATGGCCCGCATGGTCGTGCATCGCGCCGGAGACTGACGATGGACCTGACGTCATGCGCTGGGCTGACCCTAACAGTTTCCGTCTGCGATCCCAATTCTTGCAAGTGTTCAACAACAGATCCGCAGTTCATGTACCCATCTACTACAGGCACATCTTACTACAGCTACAGCCCGACACTTCAACCCGACAGAATCCTATTGCTCAATGGCACACATTTTGCTGCTCGACAAGCAGCAGTATTCAACCCGACAGAATCCTATTGCTCAATGGCACACATTTTCCAAATTCTCATTTTCCATGGCAGTACAGCACAGCTGGGCTACCAGGACAT
NL011	SEQ ID NO: 1137 CCCACTTTCAAGTGYGTRYTRGTCGG	SEQ ID NO: 1138 CGCTCTCTCTCGATCTGYDSCTGCC	SEQ ID NO: 1091 AGATGGTGGTACCGGCAAACTACATTGTCAAACGACATCTTACCGGAGAATTTGAAAAGAAGTATGTTGCCACCCTTGGAGTTGAAGTTCACCCCCTTGTATTTCACACAAACAGAGGTGTGATTAGGTTCAATGTGTGGGGACACAGCTGGCACAGCTGGGCCAGGAAAGTTCGGTGGA

			Sequence
			CTTCGTGATGGATATTACATTCAGGAGGACAATGCGCCATCATTATGTTTGACGTAACGT CAAGAGTCACCTACAAGAAACGTTCCCAACTGCCAACAAGTAGACATCAAGGACAGATTTAGTGAGGGTTTGCG AAAACATTCCCATTGTACTATGCGGCAACAAGTAGACATCAAGGACAGGAAAGTCAA GGCCAAGAGCATAGTCTTCCATAGGAAGAAGAACCTTCAGTACTACGACATCAGTGC GAAAAGCAACTACAACTTCGAGAAGGCCGTTCCTGTTGGTTGGCAAAGAAGCTGATCGG TGAACCCAACCTGGAGTTCGTCGCCATGCCGCCCTCCTCCCACCCGAGGTCACAAT GGACCCCCAAT
NL012	SEQ ID NO: 1139 GCAGGGCGCAGG TBGABGARGT	SEQ ID NO: 1140 GAATTCCTCTTSA GYTTBCCVGC	SEQ ID NO: 1093 GCAGCAGACGCAGGCAGGCACAGGTAGACGAGGTTGTCGATATAATGAAACAAACGTTGA GAAGTATTGGAGAGGGGATCAAAAACTATCAGAATTGGATGATCGAGCAGATGCTCTA CAGCAAGGCGCTTCACAGTTTGAACAGCAAGCTGGCAAACTCAAGAGGAATTC
NL013	SEQ ID NO: 1141 CAGATGCGCCC GTBGTDGAYAC	SEQ ID NO: 1142 GCCCTTGACAGAYT GDATVGGATC	SEQ ID NO: 1095 CGCAGAGCAAGTCTACATCTCTTCACTGGCCTTATTGAAAATGCTTAAGCACGGTCGC GCCGGGTGTTCCCATGGAAGTTATGGGCCTAATGTCTGGGCGAATTTGTAGACGACTAC ACTGTGCGTGTCATTGATGTATTCGCTATGCCACAGAGTGGAACGGGAGTGAGTGTG GAGGCTGTAGACCCGGTGTTCCAAGCGAAGATGTTGGACATGCTAAAGCAGACAGG ACGGCCCGAGATGGTGGTGGGCCTTGGTGGTACCACTCGCACCGGGCTTCGGCTGCTGG CTGTCGGGTGTCGACATCAACACGCAGGAGAGCTTCGAGCAACTATCCAAGAGAGC CGTTGCCGTCGTCGTC
NL014	SEQ ID NO: 1143 CGCAGATCAAR CAYATGATGGC	SEQ ID NO: 1144 GAACTTGCGGTTGA BGTTSCGDCC	SEQ ID NO: 1097 TTTCATTGAGCAAGAAGCCAATGAGAAAGCCGAAGAGAGATCGATGCCAAGGCCGAGGA AGAATTCAACATTGAAAAGGGAAGGCTCGTACAGCACCAGCGCCTTAAAATCATGGA GTACTATGACAGGAAGAGAGAAGCAGGTTGAGCTCCAGAAAAAATCCAATCGTCAAA CATGCTGAACCAGCGCGTCTGAAGGCACTGAAGGTGCGCGAAGATCACGTGAGAA GTGTGCTCGAAGAATCCAGAAAACGTCTTGGAGAAGTAACCAGAAACCCAGCCAAGT ACAAGGAAGTCCTCCCAGTATCTAATTGTCCAAGGACTCCTGCAGCGTGCTAGAATCAAA CGTAGTACTGCGCGTGCGCGAGGCGAAGATGACCGGCAAAGAGGTGGTGTGAAGCTGGCT CATGCCGCAGAGCAGTACGGCGCCGAAGATGACCCTCGAGTTGTTCGCGCCCGCAA GCTGACAACTTCCTGCGCAACATCCCAACACCCTCGAGTTGTTCGCGCCCGCAA GCCGCCGCATCAAGATCCCGAGATTAGAGTCGCGGCTCTTT ACTTGTGCCCGAGATTAGAGTCGCGGCTCTTT
NL015	SEQ ID NO: 1145 GCCGCAAGGAG ACBGTVTGC	SEQ ID NO: 1146 GTCCGTGGGAYTC RGCHGCAATC	SEQ ID NO: 1099 ATTGTGCTGTCTGACGAGACACATGTCCGTTCGAAAAGATCCGCATGAATCGAGTGGTC AGGAAGAATCTCGCGAGTGCGGCTTGTCCGACATTGTCTCGATCACAGCCTTGCCCAGAC GTCAAGTATGGAAAGCCGTATCCATTGTGCTGCCCATTGGCATGATGATACCGTTGAGGGTCTTA

		CAGGAAATCTGTTCGAAGTGTATTTGAAGCCATACTTCCTGGAAGCATACAGGCCAAT TCACAAGGATGATGCATTCATTGTTCGCGGAGGTATGAGAGCGGTCGAATTCAAGGT GGTTGAAACAGATCCATCGCCCTACTGCATTGTCGGCGCCAGACACCGTCATCCATTG TGAGGGAGACCCCATCAAACGTGAGGATGAAGAGACGCAGCAAACGCAGTCGGCT ACGACGACATTGGAGGTCAGAGAAAGCACTGGCGCGATCAAAGAGATGGTGGAG TTGCCGCTGAGACATCCCAGTCGTGTTCAAGGCGATCGCGTGAAGCCGCCACGAGG CATCCTGCTGTACGGACCACCGGGCGCCCTTCTTCCTCATCAACGGACCCGAGATTATGAGCAAAT CCAACGAAACGGGGCGCCCTTCTTCCTCATCAACGGACCCGAGATTATGAGCAAAT TGGCCGGCGAGTCGGGAGAGTAACCTGCGCAAAGCTTTCGAGGAAGCGGACAAAAAC GCACCGGCGCCATCATCTTCATCGATGAGCTGGACGCATCGTGTCGAGCTGTGATGGAC GACGCACGGCGAGGTGGAGCGACGCATCGTGTGCGCAGCTGTGATCGCGTGATGGAC GGTCTCAAGCAGAGCTCGCACGTGGCCTTAGGCGCTTGCCCGCTTTGATCGGCCATCG GATCGATGCGCCGCTTAGGCGTCTCTCGAGGTGCTGCGCCATCCACACCAAGAACATGAAGTT TCCGATGCCACCGGTCGTCTCGAGGTGCTGCGCCATCCACACCAAGAACATGAAGTT GGCTGATGACGTCGATTTGGAACA
NL016	SEQ ID NO: 1147 GTTCACCGGCG AYATYCTGCG	SEQ ID NO: 1148 CGGGCATAGTCAGA ATSGGRATCTG
		SEQ ID NO: 1101 GACGCCCAGTATCAGAAGACATGCTTGGTCGTGTATTCAACGGAAGTGGTAAGCCCAT CGACAAAGGACCTCCCATTCTTGCTGAGGATTATCTCGACATTCAAGGTCAACCCATC AATCCTTGGTCGCGTATCTCATCCCGAGGAAATGATCCAGACTGAATTCAGCCATCG ACGTCATGAACTCGATTGCTCGTGTGGCCAGAAATCCCCATCTTTTCAGCTGCCGGTCT ACCTCACAACGAAATTGCTGCTCAAATCTGTAGGACAACTTTGCTATTGTATTCGCAAACTGCCA GGAAAGTCAGTTCTCGATGACTCTCGAATTCTTCAAACAGGATTTCGAGGAGAACGGCTCTAT GAGTCAACATGGAAACTGCTCGTTCTTGAACCTGGCGAACGACCCGATCGAGCGTATCAT GGAGAACGTGTGCCTGTTCTTGACGGCGCGACATGAGCTCCTACCAGTGCGGAGAAGC ACGTGCTCGTCATCCTCACCGACATGAGCTCCTACCAGTGCGGAGAAGC TCCGCCGCCGGAGGAGGTGCCCGGCCGTGTGGTTCCCCGGTTACATGTACAC CGATCTGGCCACCATCTACGAGCGCCGGACGAGTCGAGGGTCGCAACGGCTCCA TCACG
NL018	SEQ ID NO: 1149 GCTCCGTCTACA THCARCCNGAR GG	SEQ ID NO: 1150 GTGCATCGGTACC AHSCHGCRTC
		SEQ ID NO: 1103 TATGCAAATGCCTGTCGCCACGCCCACAAATAGAAAGCACACAACAGTTTATTCGATCC GAGAAAACAACATACTCGAATGGATTCACCACCATTGAGGAGGACTTCAAAGTAGACA CTTTCGAATACCGTCTTCTGCGGGAGGTGTCGTTCGGCGAATCTCTGATCAGAAACTA CTTGCACGAGGGGACATGCAGATGTCGACGGTGGTGGACCGACATTGGGTCCCC CCTCGGCGCCCACACAGCAGGAAGCCGCGCAACTCAAAAATCCAGGAGGGGGGC GATGCCGTCTTTTCCATCAAGCTCAGGCTAGCCAGCCCCAAGCCTCGGCTGTCTGGTTC AAGAACGGTCAGCGCATCGGTCAGACGCGAGAAACACCAGGCCTCCTACTCCAATCAG

		SEQ ID NO: 1151 GTCCTGTCTGCT GCTVMGWTTYG C	SEQ ID NO: 1152 CCTTGATCTCHGC MGCCATBGTC	ACCGGCCACGCTCAAGGTCAACAAAGTCAGCGGCTCAAGACTCCGGCCACTACACGCT GCTTGCTGAAAATCCGCAGGATGTACTGTGTCTCAGCTTACCTAGCTGTGTGAATCA GCTGGCACTCAAGATACAGGATCAGTGAGCAATACAGCAGACAAGAGGTGGAGAC GACAGAGGCGGTGGACAGCGAGCGAAGGCAAGATGACGGCGGTTTGACTGCCGGTGCCGG CCGATCGCGACGCGGAGCGACGTGGCCTGGTTCATCAACGGCCAACAGGTGGCTGACGACG CCACGCACAAGATCCTCGTCAACGAGTCTGGCAACCACTCGCTCATGATCACCGGCG TCACTCGCTTGGACCACGGAGTGGTCGCGTATTGCCCGCAACAAGGCTGGCGAA ACCTCATTCCAGTGCAACTTGAATGTGATCGAGAAGAAGAACTGGTTGTGGCGCCGAAA TTTGTGGAGAGATTCGACACACCTGTTCAAGAGGTGAGCGGTTGTCGTGAG CGCACGCGTGTTGCGGACCGAGCGGTGAGTCGTGTTTGTGGACGGAGGTGCGACCAGCCTG GACATCCCGTACGCGAAGGCGTCG
NL019				SEQ ID NO: 1105 CGATGACACATACACAGAAAGTTACATCAGTACCATTGGTGTAGATTTTAAAATTAGAA CAATAGATCTCGATGGAAAAACCATAAAGCTTCAGATTTGGGACACGGCCGGCCAGG AGCGGTTCCGCACGATCACATCGAGCTACTACCGGGGCGCCCCACGGCATCATTGTG GTGTACGACGCTGACCGACCAGCAGGTCGTTCAACAACCTCAAACAGGTGCTGAGGA GATTGACGCCGCTACGCCTGTGATAATGTCAACAAACTGCTCGTGCGGCAACAAGTGTGA TCAGACCAACAAAAAGGTCGTCGGAGACGTCGGCGGAAGAACGCGACCAGCT GGGCATTCCGTTCCTGGAGACGTCGGCGACCAATGTGGGAGCAGGCGT TCAT
NL021		SEQ ID NO: 1153 CTCAATCAGAGC GTYCCHCCRTAY GG	SEQ ID NO: 1154 GGAATTGCCSAGV CGDGADCC	SEQ ID NO: 1107 CGTCAGTCAATTCTGTCACCGATATCAGCACCACGTTCATTCTCAAGCCACAAGAG AACGTGAAGATAAGCTTGAGGGCGCCACAGGCCTGTTTCATTTCACACGAACGACTT GTGATCTCACTGAAGGGAGGAGAACTCTATGTTCTAACTCTCTATTCCGATAGTATGC GCAGTGTGAGGAGTTTTCATCTGAGGAAAGCTGCTGCCAGTGTCTTGACTACTTGTAT CTGTGTTTGTGGAGGAGAACTATCTGTTCCTTGGTCCGTCTTCCGTCCGTCTGTTG CTCAGGTTTACTGAGAAGGAATTGAACCTGATTGAGCGGAGGGCCATCGAAAGCTCA CAGTCCCAGAATCCGGCCAAGAAGAAAAAGCTGGATACTTTGGGAGATTGGGATGGCA TCTGACGTCACTGAAATACGGGACCTGGATGAACTAGAAGTGTATGGCAGTGAAACA CAAACCTCTATGCAAATTGCATCCTACATATTC
NL022		SEQ ID NO: 1155 GCGTGCTCAAG TAYATGACBGAY GG	SEQ ID NO: 1156 CCAGTTCATGCTTR TANGCCCANGC	SEQ ID NO: 1109 TACATTGCACAGAGAATTCCTTTCCGAGCCAGATCTGCAATCTTACAGTGTTATGATA ATTGATGAAGCTCACGAGAGGACGTTGCACACTGATATACTGTTCGGTTTGGTGAAA GATGTCGCCCGATTCAGACCTGACTTGAAGCTTGCTCATATCAAGCGCCACACTGGAT

		GCTCAGAAATTCTCGGAGTTTTTGACGGATGCACCCATCTTCAGGATTCCGGGCCGT AGATTTCCGGTGGACATCTACTACACAAGGGCCGGAGGCTGACTACGTGGACGCA TGTGTCGTTTCGATCCTGCAGATCCACGCACCTCAGCCGTCTGGGAGACATCCTGGTC TTCCTCACCGGTCAGGAGGAGATCGAAACCTGCCAGGAGCTGCTGCAGGACAGAGT GCGCAGGCTTGGCGCCTCGTATCAAGGAGCTGTCTCCGCCACTCCATTCCAACCT ACCCAGTGATATGCAGGCAAAGATTTCCTGCCCACTCCACCAAATGCCTAGAAAGGTA GTATTGGCCACAAATATTGCAGAAACCTCATTGACCATCGACAATATAATCTACGTGA TTGATCCTGGTTTTTGTAAGCAGAATAACTTCAATTCAAGGACTGGAATCGCT TGTTGTAGTGCCTGTTTCAAAGGCATCGGCCAATCAGCGGAGCAGGGGCGGGGGAC GGGTGGCGGCCGGGCAAGTGCTTCCGTCTGTACACG
	SEQ ID NO: 1157 CCGGAGCTTCT CTCAGGAACGC	SEQ ID NO: 1111 CCGGAGCTTCTCTCAGGAACGCCAGCACGCAGGAAATGAAGGAATCCTCGGGTCGCA TGCATCACAGCGATCCTCTAATCGTCGAGACTCATAGCGGTCACGTGAGGAGGAATCT CGAAGACCGTCCTCGGACGGGAGGTCCACGTGTTTACCGGGATTCCGTTTGCGAAA CCTCCCATCGGTCCGTTGCGATTCCGTAAACCGGTTCCGACCCGTGGCACGG CGTTCTGGATGCGACCGCGCTTCCCAACAGCTGCTACCAGGAACGGTACGAGTATTT CCCGGGCTTCGAGGGAGGAGGAAATGTGGAATCGGTTGAGAATCGAATACGAATTGTCCGAGATTG TCTGTATTTGAACACATATGGGTGCCCGCCACCGGTGCCGAAGTGCCGGAGTGGATCTGATCTGGATTGTCCGAGAGCCAACAG CGAGGAGAATAAACCAAGAGCGAAGGTGCGAAGTGCCGGAGTGCGGCCGCC GTTACATGAGCGGCACAGCTACACTGGACGTGTACGAGCGTGTACGATGCTGACATGGTGACGCC ACGAGTGACGTCATCGTCGCCTCGAGCCTCCATGCAGTACCGAGTGGGTGCGTTCGGCTTCCTC TACCTCGCACAGGACTTGCCCTGCCATCCGCTGAGCGTCTTTGGCGAGTCGGCTGAGGGC TCTGGGACCCGGAACTCATGAGCGCCCTTGGCGAGTCCTAGCGGTTGGATCTGTAAG GGCGATCCGAACTCATGAGCGCCCTTGGCGAGTCCTAGCCGTTCGTGGCCATCATGCAGTC CATCCACTTGGTATCACCGATAACTCGGCGGCCTAGCCGTTCGTGGCCATCATGCAGTC AGGAACGATGAACGCACCGTGAACGACTGGGCCGCAACTCGTACGGCGACCGAAATCG CCAAGACGCTCATTGACGACTGCGGCGTCGCCTCCTCGACGACGCTCCC AGTCGCGTCATGTCCGTGTATGCGATCAGTCGGACTTCATCTCCGTGCAGCAA TGGAACAGTCACTCCGGCATTCTCGGCATTCTCGGATCTGCTCAAGGAAGGCGACTTTCAGGACACTGAA TTCCTGCCCAAACATCCCCTGCATCCCTGATCTGCTCAAGGAAGGGCGACTTTCAGGACACTGAA ATACTCATCGGCAGTAATCAGGATGAGGGTACCTACTTCATATTGTACGATTTCATCG ACTTCTTCCAAAAGAACGGGCCGAGTTTCTTGCAAAGAGATAAGTTCCTAGACATCAT CAACACAATTTCCAAAAGAACATGGGAGCATGGTATCTGAACCAGAAATGATCGGAGTGTG GTTGGTGATTACTTCTTCATCTGTCCGACAAATCATTCGCACAGGCATTCGCCACGGCAGAGC ATGAAAGAAGGTGTATTACTATTTCTTCACCCAGAACCAGTACAAGTTTATGGGG CGAGTGGGGAGTCAGTCATGCGAGTGATGGAGATGAAAATAGAATACGTTTTGTCATCCTCTC
NL023		

	Primer Forward	Primer Reverse	cDNA Sequence
NL027	SEQ ID NO: 1159 GCCGATCGTKYTVACKGGCTC	SEQ ID NO: 1160 GGTATAGATGAARCARTCDCCVACCCA	AACATGTCGCTGCAATTCAATGCTAGGAGGAAAGGGATCTCAGTCTGCGAATAATGCAA GCTTACTCTAGGTTTGCATTGACAGGTAAACCAGTGCCTGATGACGTGAATTGGCCTA TCTACTCCAAGGACCAGCCGCAGTATTACATTTTCAATGCGGAGACTTCGGCGCACAG GCAGAGGACCCAGAGCAACAGCGGTGTGCTTTC SEQ ID NO: 1113 AGAAGACGGCACGGTGCGTATTTGGCACTCGGGCACCTACAGGCTGGAGTCCTCGC TGAATTATGGCCTCGAAAGAGTGTGGACCATTTGCTGCTCGAGGATCCAACAATG TGGCTCTTGGCTACGACGAAGGCAGCAGCATAATGGTGAAGGTGGTCGGGAGGAGCCG GCCATCTCGATGGATGTGAACGGTGAGAGAGATTGTGTGGGCGGCCACTCGGAGAT ACAACAGGTCAACCTCAAGGCCATGCCGAGGGGCGTCGAAATCAAAGATGGCGAAC GACTGCCGGTCGCCGTTAAGGATATGGGCAGCTGTGAAATATATCCGCAGACCATCG CTCATAATCCCAACGGCAGATTCCTAGTCGTTTGTTGTGGAGATGGAGAGTACATAATTCA CACATCAATGGTGCTAAGAAATAAGGCGTTTGGCTCGGCCCAAGAGTTCATTGGGG ACAGGACTCGTCCGAGTATGCTATCAGAGAAGGAACATCCACTGTCAAAGTATTCAAA AACTTCAAAGAAAGAAATCATTCAAGCCAGAATTGGTGCTGAAGCATATTCGGCG GCTCACGTGCTGGTGCGTCGCATCGAGATCCAACCGAAACACGTTACTGGTCGGAGAGT TGGGAGCTGGTGCGTGGGGCCGCTGGCCCACTGATGACTCCTACTTTGTGCTCCGCTACGAGT GGGGGAGCTGGTGGTGGCTGCTGCGACGCGACCGGTGAGGT ACAGGCCGTGCTGCTCGCGCGCGACGCGACCGGTGAGGTGCACGCGCGGACGGC GTCGGAGGATGCATTCGAGGTCCTTGGTGAAGTGCACGAAACTGTAAAAACTGGATTG

Table 2-CS

Target ID	Primer Forward 5' → 3'	Primer Reverse 5' → 3'	cDNA Sequence (sense strand) 5' → 3'
CS001	SEQ ID NO: 1706 CATTTGAAGCGT TTWRMYGCYCC	SEQ ID NO: 1707 CTTCGTGCCCTT GCCRATKATRAA BACG	SEQ ID NO: 1682 TAAAGCATGGATGATGTTGGACAAACTGGGTGGCGGTACGCGCCGCCGTCGACCGG CCCCCACAAGTTGCGCGAGTGCCTGCCGCGTGGTGATCTTCCTCAGGAACGGGCTCAA GTACGGCGCTCACCGGAAATGAAGTGCTTAAGAGTGCTTAAGCAGCGACTTATCAAAGTTG ACGGCAAAGTCAGGACAGAGACCCCACATATCCCGCTGGATTTATGGATGTGTTTCCATT GAAAGACAAATGAGCTGTTCCGTCTTATATATGTCAAAGGCAGATTACTATTCAC CGTATTACTCCTGAGGAGCTAAATACAAGCTGTGACCACGACGTGCAAGGTGGGCGGTGGCGACG GGCCCCAAGAACGTGCCTTACCTGTGACCACGACTCCATCCAGCTGCGATACCCC GACCCCACTCATCAAGGTCAAGGACTCATCGGTAACCTATCGGTATGATCACGGGGAGCCGTAACTTG TGGACTTCATCAAGTTTGAATCTGGTAACCTATGGTAATCTATCACGGGGAGCCGTAACTTG GGGCGGCGTGGGCACCCATCGTGTCCCGCGAGCGACGCATCCCGGCGGTCCTTCGACATCGTG

CATATACGGGACTCCACCGGACATACCTTCGCTACCAGATTGAACAACGTGTTCATAATCGGCAAGGGCACGAAG

CS002	SEQ ID NO: 1708 GAGTTTCTTTAG TAAAGTATTCGG TGG	SEQ ID NO: 1709 GCAATGTCATCC ATCAKRTCRTGTA C	SEQ ID NO: 1684 GAGTTTCTTTAGTAAAGTATTCGGTGGCAAGAAGGAGGAGAAGGGTCCATCAACACACGAAGCTATACAGAAATTACGCGAAACGGAAGAGTTATTGCAGAAGAAACAAGAGTTTCTAGAGCGAAAGATCGACACTGAATTACAAACGGCGAGAAACATGGCACAAAGAATAAGAGAGTGCCATTGCGGGCACTGAGCGCAGAAGCGTTATGAAAGCAGCTTACCCAGATTGATGGCACGCTACCCAAATTGAGGCCCAAGGGAAGCGCTAGAAGGAGCTAACACCAATACACAGGTGCTTAACACTATGCGGAGATGCTGCTACCGCTATGAGACTCGCCCACAAGGATATCGATGTAGACAAGGTACACGATCTGATGGATGACATTGC
CS003	SEQ ID NO: 1710 CAGGAGTTGAR RATHATYGGHSA RTA	SEQ ID NO: 1711 CAGGTTCTTCCT CTTKACRCGDCC	SEQ ID NO: 1686 TGGTCTCCGCAACAAGCGTGAGGGTGTGGAGGGTGAAGTACACGCTGGCCAGGATCCGTAAGGCTGCCCGTGAGCTGCTCACACTCGAGGAGAAAGACCCTAAGAGGTTATTCGAAGGTAATGCTCTCTCCTTCGTGTCTGGTGAAGATTGAGCTTCTTGGATGAGAAGCAGATGAAGCTCGATTATGTACTCGGTCTGTCTAGCTAAGTCTATCATCATCGCCGTATTCTTATCAGACACAGGTGTTCAAGGCTGTGTCCGCAAGCAAGTTGTGAACATCCCTTCGTTCATCGTGCGGCTGGAGGCACATCCGTGTCCGCAAGCACATTGACTTCTCGCTGAAGTCTTCGGCGGCCGGCCG
CS006	SEQ ID NO: 1712 ACCTGCCAAGG AATGMGVAAYG C	SEQ ID NO: 1713 GAGATCTTCTGC ACRTTKACVGCAT C	SEQ ID NO: 1688 ACCTGCCAAGGAATGAGGAACGCTTTGTATGACAAATTGGATGATGATGTATAATTGCACCAGGGATTCGTGTATCTGGTGACGATGTAGTCATTGGAAAACTATAACTTTGCCAGAAAACGATGATGAGCTGGAAGGAACATCAAGACGATACAGTAAGAGATGCCTCTACATTCCTGCGAAACAGTGAAACTGGTATTGTTGACCAAGTTACACTTAACACGCGAAGGATACAAATTTGTAAAATACGTGTGAGATCTGTGAGAATCCCACAAATTGGAGACAAATTTGCTTCTCGTCTGTGAAGGATTGACACCAGATATTATCATCCACATGCTATCCCTCTCGTATGACAATTGGTCACTTGATTGAATGTATTCAAGGTAAGGTCTCCTCAAATAAGGTGAAATAGGTGATGCTACACCATTTAACGATGCTGTCAACGTGCAGAAGATCTC
CS007	SEQ ID NO: 1714 CGGTGTCCATTC CGGG	SEQ ID NO: 1715 CGATGCAAGTAG GTGTCKGARTCY TC	SEQ ID NO: 1690 TTTCAGAGATTTCTTGTTGGAACCAGAGATTTTGGGGGCTATCGTCGATTGCGGTTTCGAGCACCCTTCAGAAGTTCAACATGAAGTGTATTCCCCAAGCTGTTTTGGGAATGGATATTCTTTGTCAAAGCTAAATCCGGAATGGGAAAAACCGCCTATTTGTTTTAGCAACACTGCAACAGCTAGAACCTTCAAATAAGCAAGGAATATGAGAGGTTCTCTAAATATGGCTGTGGTTAGCTCGCTTTCCAAATAAGCAAGAGGAATCAAATGTTACGTATTAGTAATGTGCCATACAAGGGAAAGTATCTGTATTCTTTGGTGGGATGCCAATTCAGAAGATGAAGAAGTATTGAGAGACAG

		CCTGCCCGCACATCGTTGTTGGTACTCCTGGCAGAATATTAGCATTGGTTAACAACAAGAAACTGAATTAAAACACCTGAAACACTTCATCCTGGATGAATGTGACAAAATGCTTGAATCTCTAGACATGAGACGTGATGTGCAGGAAATATTCAGGAACATTGAGTAAGGAGATCAGAACCAGTCTGTAAGAAATTTAGGTCATGATGTTTTCTGCAACATTGATGTGGATGAAGCTAAACTTACATTGCACGGTTTATGCAAGATCCTATGGAAGTTTAAACTCAAGGAAAATGAAAGAATAAGAAGTTATTTGAACTTTTGCAGCAACAATATGTTAAACTCAAGGAAAATGAAAGAATAAGAAGTTATTTGAACTTTGGATGTACTGGAGTTCAACCAAGTTGTCATATTTGTAAAGTCAGTGCAGCGCTGCATAGCTCTGCCACAGTCTGCTGCAGACAACAAACTTCCAGCTATTGGTATACACCGAAAATATGACTCAAGATGAGCGTCTCTCCCGCCATCAGCAGCTTCAAAGATTCAAAGGATCCTTGTTGCGACAAAATCTTTTTGGACAGGGGGTATGGACGTTGAAGAGTCAACACATAGTCTTCAATTATGACATGCCG
CS009	SEQ ID NO: 1716 CCTCGTTGCCAT YTGYWTKTGG	SEQ ID NO: 1717 CTGGATTCTCTC CCTCGCCAMGAHA CC	SEQ ID NO: 1692 CCTCGTTGCCATTTGTATTTGGACGTTTCTGCAGCGGCGGCTGGACTCACGGGGAGCCCATGTGGCAGCTGGACGAGACGCATCATCGGCACCAACCCGGGCTTCCGGCCCACGCCGCCAGAGGTCGCCAGCAGCGTCATCGGTCATTGGTATAAAGGCAACGACCCAACAGCCAACAATTCTGGGTGCAAGAAACCTCCAACTTCTAACCGGTACAAACGAGACGGTAAGAAGCAGGAGCAGGCCAGAACCATCAACAACTGTGATTTCAACTGCCTCCTCCGGCCGGTAAGGTGTGCGACGTGGACATCAGCGCCCTGCATCTTCCTCAAACTCAACAAGACCTTCGGCTGGAGGATACCACAAGTCCACGCGCCCTGCATCTTCCTCAACAAGACCTTCGGCTGGAGGCGCGCACTTCTACAACAGCAGGAATATGACAGCGTACGGTACGCGTACGATAAGAATTATCTAAACATGGTATGGGTGTCTTGCGAGGGAGAATCCAG
CS011	SEQ ID NO: 1718 GGCTCCGGCCAA GACVACMTTYGT C	SEQ ID NO: 1719 GTGGAAGCAGGG CWGGCATKGCRA C	SEQ ID NO: 1694 GGCTCCGGCCAAGACGACCTTTGTCAAACGACACTTGACTGGAGAGTTCGAGAAAAGATATGTCGCCACACATTAGGTGTCGAGGTGCATCCCTTAGTATTCCACACAAATAGAGCCCCTATAAGGTTTAATGTATGGGATACTGCTGCGCCAAGAAAAGTTTGGTGGTCTCCGAGATGGTTACTATATCCAAGGTCAAGTGCCATCATCATGTTGCGATGGTTAGTGCGAGTCTGTGAAGGCATTCCAATTGTTCTTTGTGGCAACAAGTAGATATCAAGGACAGAAAGTCAAAGCAAAACTATTGTTTTCCACAGAAAACCCTTCCTCTGGTTAGCGGAGAAGTTGATCGGTGATGGTAACCTAGAGTTTGTCGCCCATGCAGCCCTGCTTCCAC
CS013	SEQ ID NO: 1720 GGATCGTCTGC TAMGWYTWGGA GG	SEQ ID NO: 1721 CTATGGTGTCCA GCATSGCGC	SEQ ID NO: 1696 CAGATGCGCCCGTTGTTGATACTGCCGAACAGGTATACATCTCGTCTTTGGCCCTGTTGAAGATGTTAAAACACGGCGGCCGGTGTTCCAATGGAAGTTATGGGACTTATGTTAGGTGAATTTGTTGGTGATGATTACACGGTGCGTGTCATAGACGACTGATATTTGCCATGCCTCCAAAC

CS014	SEQ ID NO: 1722 ATGGCACTGAG CGAYGCHGATG	SEQ ID NO: 1723 GAACTTGCGGTT GABGTTSCGDCC
		SEQ ID NO: 1698 TTCAAAAGCAGATCAAGCATATGATGGCCTTCATCGAACAAGAGGGCTAATGAAAAGGCC GAGGAAATCGATGCAAAGGCCGAAGAGGAGTTCAACATTGAAAAGGCCGCTGGTG CAGCAGCAGCGGCTCAGATCATGGAACATCTACGAAAGAAAGAGAAACAAGTGGAAC TCCAGAAAAGATCCAATCTTCGAACATGCTGAATCAAGCCGTCTGAATCAAGCCGTCTGAAGGTGCTCAAA GTGCGTGAGGACCACGTACGCAACGTTCTCGACAGATCTGCTGGTCAACGCCGTCGAG GTGCCCAAAGACGTGAAACTTTACACAGATCTGCTGGTCAACGCCGTCGAG TATTCCAGCTCATGGAACCCCACAGTAACAGTTCGCGTTAGGCAGGCGACGTCTCCTT AGTACAGTCCATATTGGGCAAGGCACCAGCAGGATTACAAAGCAAAGATCAAGAAGGAC GTTCAATTGAAGATCGACACAAGGGCTATTAAGATCAGCAACACTCTGGAGTCTCGTGGA GCTGATAGCCCAACAACTGTTGCCCGAAATACGTACCGCATTGTTC
CS015	SEQ ID NO: 1724 GCCGCAAGGAG ACBGTVTGC	SEQ ID NO: 1725 CGATCAAAGCGW CCRAAVCGACG
		SEQ ID NO: 1700 ATCGTGCTTTCAGACGATAACTGCCCCGATGAGAAGATCCGCATGAACCGCGTCGTGC GAAACAACTTGCGTGTACGGCCTGTCAGACATAGTCTCCATAGCGCCCTTGTCCATCGGT CAAATATGGGAAACGGGTACATATATTGCCCATTGATGATTCTGTCGAGGGTTTGACTG GAAATTTATTCGAAGTCTACTTGAAACCATACTTCATGGAAGCTTATCGGCCTATCCATC GCGATGACACATTCATGGTTCGCGGGCATGAGGGGCTGTTGAATTCAAGTGGTGGA GACTGATAGTCGTCGCCGTATTGCATCGTCCCGACAACAGTGATACACTGCCGAAGGA GACCCTATCAAACGAGGAAGGAAGAAGAAGCCCTAAACGGCTAGGGTACGAGGTACGGAAGAC ATCGGTGGCTGTCGCTGTTCAAGGCAATTGGTGTGAAGCCGCCACGTGGAATCCTCATGTA GGCATCGTCCGTCGCTGGTACCGGCAAAACTCTCATTGCTCGGCGAGATCATGTCCAAACTCGGCGGGAGTCCG TGGGCCGCGCCTGGTACCGGCAAAACTCTCATTGCTCGGCGAGATCATGTCCAAACTGGT GCATTCTTCTTTCTGCAAGGCATTCGAGGAAGCGGACAAGAACTCCCGCGCTATAATCTT AATCGAACCTTGCGTATTGTGTCGCAACTACTTACTCTTATGGATGGAATGAAGAGTCATCGCACG GCGTCGTATTGTGTCGCAACTACTTACTCTTATGGATGGAATGAAGAGTCATCGCACG TGATCGTAATGGCCGCGCCACCAACCGTCCGAATTCGATCGACCCGGCGCTA
CS016	SEQ ID NO: 1726 GTTCACCGGCG AYATYCTGCG	SEQ ID NO: 1727 GTCGCGCAGGTA GAAYTCKGC
		SEQ ID NO: 1702 AGGATGGAAGCGGGGATACGTTTGAGCATCCTTGGGAAGATACGGAGCAGCTGC CAGCCGATGTCCAGCGACTCGAATACTGTGCGGTTCTCGTAGTTGCCCTGTGTGATGA AGTTCTTCTCGAACTTGGTGAGGAACTGGAGGTAGAGCAGATCGTCGGGTGTCAGGGC

| CS018 | SEQ ID NO: 1728 GCTCCGTCTACA THCARCCNGAR GG | SEQ ID NO: 1729 GTGCATCGGCGTAC CAHSCHGCRTC | TTCCTCACCGACGACAGCAGCCTTCATGGCCTGCACGTCCTTACCGATGGCGTAGCAGGCG TACAGCTGGTTGGAAACATCAGAGTGGTTCCTTGCGGGTCATTCCCTCACCGATGGCAG ACTTCATGAGACGAGACAGGGAAGGCAGCACGTTACAGGCGGGTAGATCTGTCTGTT GTGGAGCTGACGGTCTACGGTAGATCTGTCCTCAGTGATGTAGCCCGTTAAATCGGGA ATAGGATGGGTGATGTCGTCGTTGGGCATAGTCAAGATGGGGATCTGCGTGATGGATC CGTTTCTACCCTCTACACGCCCGGCTCTCTCGTAGATGGTGGCCAAATCGGTGTACAT GTAACCTGGGAAACCACGTCCGGGCACCTCCTCACGGCGGCGGACACTTCACG CAGAGCCTCCGCGTACGAAGACATGTCAGTCAAGATTACCAGCACGTGTTTCTCACAC TGGTAGGCCAAGAACTCAGCAGCAGTCAAGGCCAAACGTGGTGTGATGATTCTCTCAA TAGTGGGATCGTTGGCCAGATTCAAGAACAGGCACACGTTCTCCATGAGCCGTTCTC CTCGAAGTCCTGCTTGAAGACCGGCCGTTCTCCATGTTCACACCCATGGCGGGCGAAC ACGATGGCAAAGTTGTCCTCGTGTCGTCCAGCACAGATTTGCGGGGATCTTTACAA GACCGGCTTGCCTACAGATCTTTGCCCGCGGCAATTTCGTTGTGTGGCAGACCGGCAGCCG AGAAAATGGGGATCTTTTGCCCGCGAGCAATGGAGTTCATCACGTCGATAGCGGAGAT ACCAGTCTGATCATTCCTCAGCAAGGTAGATACGGGACCAGGGGTTGATGGGCTGTCCC TGGATGTCCAAAAGTCTTCAGCAAGATTGGGGGACCTTTGTCAATGGGTTTTCCAGA GCCGTTGAATACGGCGACCCAACATGTCTCGGAGACAGGGGTGC | SEQ ID NO: 1704 GCTCCGTCTACATTCAGCCGGAAGGCGTCCCGTACCTGCTCAGCAATCCCAACAGCA GCAGAGTTACCGCCACGTCAGCGGAGAGCGTCGAACACAAATCCTACGGCACGCAAGG GTACACCACTTCGGAACAGACCAAGCAGACAGAGAAGGTGGCGTACACCAACGGTTCC GACTACTCTTCCACGGACGACTTTAAGTGGATACGTTCGAATACAGACTCCTCCGAG AAGTTTCGTTCAGGGAGTCGACAAGTCTCTCGTGTGGTGACCCCTCCTAAGATAGCACAAAAG CAGCACGGAGGTCGACAAGCTGCAGGAGGAGCCGACGCTCAGTTTCAAGTTTCAGAGAGAT CCTAGGAATTCCAAGCTGCAGGAGGAGCCGACGCTCAGTTTCAAGTTTCAGTTTCAGCTGTCG GGTAACCCGCGGCCACGGGTGTCATGGTTCAAGAACGGGCAGAGGATAGTCAACTCG AACAAACACGAAATCGTCACGACACATAATCAAACAATACTTAGGGTAAGAAACACACA AAAGTCTGATACTGGCAACTACACGTTGTTGGCTGAAAATCCTAACGGATGCGTCGTCA CATCGGCATACATAATGGACAATCAGCAAACAGCTGTAGAAGAAAGAGTAGAAGTTAATGAAA AAGCTCTCGCTCCGCAATTCGTAAGAGTCTGCCAAGAGGCCGATGTAACGGAGGGGAA AATGACGCGATTGCCGCGGTCACCGGCGAGACCTTACCCAGAAGTCACGTGGTTC ATTAACGATAGACAAATTCGAGACGATTATWATCATGAGATATTAGTAAACGAATCGTGT AATCATGCACCTTATGATTACAAACGTCGATCTCAGTGAGTCAGTCTAGTATCATGTATA GCACGCAACAAGACCGGCGAAACTTCGTTGGAGCGGTTCAGCACGTCAACGTGCGAGG AGCAAGTGGTCGCTCCCAAATTCGTGGAGCGGTTCAGCGCTCAACGTGCGAGG GCGAGCCCGTGCAGCTGCAGCTGCGCCGCTGCGGCGCGCCGCCGTACGCCGCCGCACCATCACA |

TGGCAGAAGGACGGCGGCGTTCAAGTTATACCCAATCCAGAGCTACGAATAAATACCGAAG
GTGGGGCCTCGACGCTGGACATCCCTGAGCCAAGGCGTCGGACGCGGGATGGTAC
CGATGCAC

Table 2-PX

Target ID	Primer Forward 5' → 3'	Primer Reverse 5' → 3'	cDNA Sequence (sense strand) 5' → 3'
PX001	SEQ ID NO: 2110 GGCCCCAAGAAG CATTTGAAGCG	SEQ ID NO: 2111 CTTCGTGCCCCTTGC CRATKATRAABACG	SEQ ID NO: 2100 GGCCCCAAGAAGCATTTGAAGCGGCCTGAACGGCGCCGCGGCCATGGATGCTGGA CAAGCTCGGCGGCGTGTACGCGCCGCGGCCCAGCACAGCGGCCCGCCACAGCTG CGGCGAGTGCCTGCCGCTCGTCATCTTCCTGCAACCGCCTCAGTACGGCGCTCAG CGGCAACGAGGTGCTGAAGATCGTGAAGCAGCGCCTCATCAAGGTGGACGGCA AGGTCCGCACGACCACCTACCCGGCTGGATCTACGATGTGTGTCGATTG AAAGACCAATGAGCTGTTCCGTCTGATCTACGATGTGAAGGGACGCTTCACCAT CCACCGCCATCCTCCCGAGGAGCCAAGGTACAAGCTGTCGCAAGGTGAAGCGCG TGGCAGCGGGCCCCAAGAACGCTCATCAAGGTCAACGACTCATCCAGCTCGACATC CTGCGGCTACCCCGACCCGGCTCATCAAGGTCAACGACTCATCCAGCTCGACATC GCCACCTGCAAGATCATGGACATCAAGTTCGACTCAGGTAACCTGTGCATGA TCACGGGAGGGCGTAACTTGGGCGAGTGGGCCACCATCGTGTCCCGCGAGAGG CACCCCGGGAGCTTCGACATCGTTCAACATCAAGAGCACCACCGGACACACCTTC GCCACCAGGTTGAACAACGTGTTCATCATCGGCAAGGGCACGAAG
PX009	SEQ ID NO: 2112 GCACGTTGATCTG GTACARRGGMAC C	SEQ ID NO: 2113 GCAGCCCACGCYYT GCACTC	SEQ ID NO: 2102 GCACGTTGATCTGGTACAAAGGAACCGGTTACGACAGCTACAAGTATTGGGAGA ACCAGCTCATTGACTTTTGTCAGTATACAGAGAAGAAGGTCAGACAGGCGGGTGC TGGTCAGAACATCTTCAACTGTGACTTCCGCAACCCGCCCACACGCAAGGT GTGCGACGTGGACATCCGGCCTGCGATCTCTTGAAGCTGAATAAGATCTACGGCTGG TTTCCACAAGTCTTCGCGTCTTCTTACAACGACACGGCTAACCTGCCTGAAGCCATGCCCGTGGAC TTGCAGACCCACCACATTCGTAACATTACTGCCTTCAACAGAGACTATGCGAACATGG TGTGGGTGTCGTGCCACGGCGAGACGGCGGCGGCGGAGAACATCGGGCC GGTGCGCTACCTGCCCACCGGCGGCTTCCCCGGGTATCTGAGCCCGTGGTCGCCGTGCATTTGGAGAGGCCGAGGA CGCCGAGGGGTATCTGAGCCCGTGGTCGCCGTGCATTTGGAGAGGCCGAGGA CCGGCATAGTGATCAACATCGAGTGCAAGCGTGGGCTGC
PX010	SEQ ID NO: 2114 GTGGCTGCATACA	SEQ ID NO: 2115 CGCGGCTGCTCCAT	SEQ ID NO: 2104 GTGGCTGCATACAGTTCATTACGCAGCACTCTAGTGGACAACGTCGCG

	GTTCATTACGCAG	GAAYASYTG	TTCGGGTCACCACTGTCGCGCGCAATTGGGGCGGCGACGCAGCCGCCAACTTACAC CACATATCGGCGGCCTTCGACCAGGAGCAGGAGGACGGCCGCGGCGGTGGTGATGGCCGCGGC TGGTGGTGTACCGGCCGGGACGGCTGTGCCAGAAGTTCGGCGAGTACGGCGAAGGACG ACCCGAAACAGCTTCCGTCGCCGCTCGCGTCTGTCGGAGAACTTCAGCCTGTACCCGCAGTTCATGT ACCACCTGCGCGCCGTTCCTGCGCAGTTCCTGCGAGGCGGCAAGAACCTGACCCCGACGAGA CCACCTTCTACAGACACATGCTGATGCGGCGAAGAACCTGACCCAATCCTCATCAT GATCCAGCGGATCCTCTACTGTACAGCTTCGTGAGGCGGCAAGACCTTCGGAGGCGGCATCCTGCTCATGGCAACCGTGCT GTTAGACACCAGCTCCATCCAGCCGCACGGCCATCCTGCTCATGGCAACCTCTT CCAGATCCTCATCTACCATGGAGGAGAACTTCAAGCAGCTGCTCGGAGCGCCCCGTA CCAAGACATGGCTGAGTACGGAGATCCTGCAGACCAGGTTCCCGTGCTGCGGCGCCCGTG ACGAGCGCAGGAGATCCTGCGAGACCAGGCCCGGTTCCCGTGCGGGGCGTACATTGATA CAGAGCACGGCGGCTCACAGGCCCGGTTCTTGCTTTCCAAAGTGAATCCCTCTC AGACTCACAACAACATGTACGCGATGCCGATATGGGGGGCGATGCCGATACCATCAGCGG ACGGTGGCGCCCCGTGTTGACGGATGACGTTCGCGCTGCAAGTGTTCATGGAG CAGCCGCG SEQ ID NO: 2106
PX015	SEQ ID NO: 2116 GCCGCAAGGAGA CBGTVTGC	SEQ ID NO: 2117 GCAATGGCATCAAK YTCRTCRATG	GCCGCAAGGACCGTGTGCATTGTGTCTGCCGACGACAACTGCCCCGACGAG AAGATCCGCATGAACGCGGTCGTCCGGAACAACCTGCGAGTGCGCCTGTCGAGAC ATTGTGTCCATGCCATGCCGGAAACCTGAAGTACGGCAAGAGAGTTCATATTC TGCCCATTGATGACTCTGTTGAGGGTTTGACTGGAAACCTGTTCGAAGTCTACCT GAAGCCGTACTTCATGGAGGCGTACCGGCCGTCGAGTTCAAGGTGGTGGAGACCACCCT GGTGCGCGGGCATGCCGCCGTCGAGTTCAAGGTTCAAGGTGTGGAGACCGACCCT CGCCCTACTGCATGCGTCGTGCCCCGACACGGTCTCAACGCCGTCGGCTACGACGACATC TTAAACGCGAGGAAGAGAGGAGCTGGCCGCAGATCAAGGAGATGGTGAGCGCCGGGGATAC GGCGGGTGCCGCCAACCCCTGCTGTTCAAGGCCATCGGGGCAAGACCTTGATCGTCGCT GCGCCACCCCTCGCTGTTCAAGGCCGAGAAGACCTTGATCGTCGCT TGATGTACGGGCGCCCCCGGCATTCTTCTTCCTCATCAACGCCCCGAGATCATGTCGAAA AATGAGACGACGGGCGCATTCGAGTCGAATCGAACCTGCGCAAGGCGTTCGAGGAGGGACAA CTCGCCCGGTGAATCGGCCATCATCCTCATTGATGAACTTCATTGATGAACTTCATTGC GAACTCTCGGGCCCATCATCCTCATTGATGAACTTGATGAACTTGATGGCCATTGC SEQ ID NO: 2108
PX016	SEQ ID NO: 2118 GTTCACCGGCGAY ATYCTGCG	SEQ ID NO: 2119 CATCTCCTTGGGGA AGATACGCAGC	GTTCACCGGCGGATATTCTGCGCACGCCCGTCTCTGAGGACATGCTGGGTCGTAT TTCAACGGCTCCGGCAAGCCCATCGACAGGGCCCCGATCCTGGCCGAGG AGTACCTGGACATCCAGGGCAGCCCATCAACCCGTGGTCCCGTATCTACCCGG AGGAGATGATCCAGACTGGTATCTCCGTATCGACGTGATGAACTCCATCGCCC GTGGTCAGAAGAATCCCCATCTTCTCCGCGCCGGTCTGCGCCCCCACCAACGAGATTG

CTGCTCAGATCTGTAGGCAGGCTGGTCTTGTCAAGGTCCCCGGAAAATCCGTGT TGGACGACCACGAAGACAACTTGCCATCGTGTTCGCCGGCCATGGGAGTCAACA TGGAGACCGCCAGGTTCTTCAAGCAGGACTTCGAGGAGAACGGTTCCATGGAGA ACGTCTGTCGTTCTTGAACTTGGCCAATGACCCGACCATTGAGAGGATTATCAC GCCGAGGTTGGCGCTGACTGCTGCCGAGTTCTTGGCCTACGGCGAGGTCTTCGTGAAGTG TCAGCCGCCCGTGAGGAGGTGCCCGGACGACGTGGTTTCCCAGGTTACATGTA CACGGATTTGGCCACAATCTACGAGCCGGCGCCGGGCGAGTCGAGGCGCAACG GCTCCATCACGACGAGATCCCATCCTGACCATCGCCAACGACGACATCACCCACC CCAATCCCCGACTTGACCGGGTACATCACTGAGGGACAGAGATCTACGTGGACCGGTC AGCTGCACAACAGGCAGATCTACCCGCGCGGTGAATGTGCTCCCGTCGCTATCTC GTCTCATGAAGTCCGCCATCGGAGAGGGGCATGACCAGGAGGACCACTCCGAC GTGTCCAACCAACTGTACGCGTGCTACGCCCATCGGCAGGACGGTGCAGGCGAT GAAGGCGGTGGTGGGCGGAGGAGGCGGCTCACGCCCGACGACCTGCTCTCACCTCG AGTTCCTCACCAAGTTCGAGAGAAGAACTTCATCACACAGGAGCTACGAGAACC GCACAGTGTTCGAGTCGCTGGACATCGGCTGGCAGCCCCTGCGTATCTTCCCCA AGGAGATG

Table 2-AD

Target ID	Primer Forward 5'→3'	Primer Reverse 5'→3'	cDNA Sequence (sense strand) 5'→3'
AD001	SEQ ID NO: 2374 GGCCCCAAGAAGCA TTTGAAGCG	SEQ ID NO: 2375 CGCTTGTCCCG CTCCTCNGCRA T	SEQ ID NO: 2364 GGCCCCAAGAAGCATTTGAAGCGGTTTAAATGCTCCTAAAGCATGGATGTTGGACAA ACTCGGAGGAGTATTCGCTCCTCCGCCCCCAGTACTGGCCCCCACAAATTGCGTGAA TGTTTACCTTTGGTGATTTTTCTTCGCAATCGGCTCAAGTATGCTCTGACGAACTGT GAAGTAACGAAGATTGTTATGCAGCGACTTATCAAAGTTGACGGCAAGGTGCGAAC CGATCCGAATTATCCCGCTGGTTTCATGGATGTTGTCACCATTGAGAAGACTGGAG AGTTCTTCAGGCTGGTGTATGATGTGAAAGGCCGTTTCACAATTCACAGAATTAGT GCAGAAGAAGCCAAGTACAAGCCTCGAGGCCGCTACCATCCGTATCCTCGCCCAA AAGGTATTCCATTCTTGGTGACCCATGGCCGGCTACTATCCGTATATCATCATGAC CACATCAGATTGAATCTGGCAACCTGTGTATGATTACTGGTGGACGTAACTTGGG TCGAGTGGGGACTGTTGTGAGTCGAGAACGTCACCCAGGCTCGTTTGATATTGTT CATATCAAGGATACCCAAGGACATACTTTTGCCACAAGATTGAATAATGTATTCATC ATTGGAAAAGCTACAAAGCCTTACATTTCATTGCCAAAGGGTAAGGGTGTGAAATT GAGTATCGCCGAGAGGGAGGGGACAAGCG

AD002	SEQ ID NO: 2376 GAGTTTCTTTAGTAA AGTATTCGGTGG	SEQ ID NO: 2377 GCAATGTCATCC ATCAKRTCRTGT AC	SEQ ID NO: 2366 GAGTTTCTTTAGTAAAGTATTCGGTGGGAAGAAGAAAGATGGAAAGGCTCCGACCACTG GTGAGGCCATTCAGAAGAACTCAGAGAACAAGAAGAAATGTTAATCAAAAGCAGGAA TTTTTAGAGAAGAAGAAAATCGAACAAGAGAATCAATGTTGCAAAGAUAAAATGGAACGAAA AATAAGCGAGCTGCTATTCAGGCTCTGAAAAGGAAAAAGAGAGGTATGAAAAACAATT GCAGCAAATTGATGGCACCTTATCCACAATGAAATCGAAAGAGAAGAGCTTTGGAGG GTGCTAATACTAATACACGCTGTATTACAAACAATGAAATCAGCAGCAGATGCCCTTA AAGCAGCTCATCAGCACATGGACAAGGTACATGACCTGATGGATGACATT GC
AD009	SEQ ID NO: 2378 GAGTCCTAGCCGCGCV YTSGTKGC	SEQ ID NO: 2379 CTGGATTCTCTC CCTCGCAMGAH ACC	SEQ ID NO: 2368 GAGTCCTAGCCGCCTTGGTTGCAGTATGTTTATGGGTCTTCTTCCAGACACTGGAT CCTCGTATTCCCACCTGGCAGTTAGATTCTTCTATCATTGGCACATCTCTGGCCT AGGTTTCCGGCCAATGCCAGAAGATAGCAATGTAGAGTCAATGTCTCATCTGGTACC GTGGAACAGATCGTGATGACTCCGTCTGCTGACCCCTGGTCGAGGTCAGAACATCCACAACT GTGTGTACAAGACTCCTGGTCTGCTGACCCCTGGTCGAGGTCAGAACATCCACAACT GTGACTATGATAAGCCGCCAAAGAAAGGCCAAGTTGCAATGTGGACATCCAAGAAT TGGCATCCCTGCCATTCAACAAGAATCTACAAGATCCCTGAATACTACAATGAGAGTAC ATTCATCAAGCTCAACAAGATCTACAACAATTGGATCCCTGAAGCAGTTGCCATGCAT GAATTTGCCTGAGCAGATGCCAGAAGAACCTGAAGCAGTACATCCACAACCTGGAG AGTAACAACTCGAGGGAGGATGAACACGGTGTGGGTGTGCGTGCGGGAGGAGAAT CCAG
AD015	SEQ ID NO: 2380 GGATGAACTACAGC TBTTCCGHGG	SEQ ID NO: 2381 GTCCGTGGGAY TCRGCHGCAAT C	SEQ ID NO: 2370 GGATGAACTACAGCTTTTCCGAGGAGGAGATACAGTTCTTCTTAAAGGAAAAAGGGAGGA AAGAAACTGTATGCAGTATCATAGTGTTATCAGTGATACATGTCCTGATGGAAAATAAGAA TGAATAGAGTTGTACGCAACAATTTACGTGTTCGTTTGTCAGATGTTGTATCTGTAC AACCTTGTCCTGATGTTAAGTATGGAAAAAGGATACACATTGACTACCAATTGATGATA CAGTTGAAGGACTAACCGGGAATTTGTTTGAGGTGTACTTAAAACCGTACTTTCTC GAAGCATACGACCCATTCACAAGAGTAGTGAAACAGATGATGCGTTTATTGTTCGTGGTGGTATGCG AGCAGTAGAATTCAAGTAGTGAAACAGATCCTTCACCATATTGTATTGTTGCTCC TGATACTGTTATTCACTGTGAAGGTGATCCAATAAACGTGAAGAGGAAGAAGAAG CATTAAATGCTCGTTGGTTATGATGACATTGGCCATTGGTGCAAAACAGCTAGCACAG ATCAAGGAAATGGTGACCGAGGGGAATACTGCTGTATGACCCCCTGGAACTGGTAAAACC TGTTAAGCCACCAGGGCTGTGGCTAATGAAACTGGTGCATTCTCTTTTAATAAATGGT CTCATTGCCAGGTGGTGTGGCTAATGAAACTTACGTAAGGCATT CCTGAAATTATGAGCAAGCTTGCTGGTGAATCTGAAAGCAACTTACGTAAGGCAAT TGAAGAAGCTGATAAGAAGAATGCTCCGGCAATTATATTTATTGATGAACTAGATGCAAT

		TGCCCCTAAAAGAGAGAAAAACTCATGGAGAGGTGGAACGTCGCATAGTTCACAAC TACTAACTTAATGGATGGTCTGAAGCAAAGTTCACATGTTATTGTTATGGCTGCCA CAAATAGACCCAACTCTATTGATGGTGCCTTGCGCCGCTTGCCAGATTGATAGG GAAATTGATATTGGTATACCAGATGCCACTGGTCGCCTTGAAATTCTTCGTATCCAT ACTAAGAATATGAAGTTAGCTGATGTTGATTGGAACAGATTGCAGCCGAATC CCACGGAC
AD016	SEQ ID NO: 2382 GTTCACCGGCGGAYA TYCTGCG	SEQ ID NO: 2383 GGAATAGGATG GGTRATRTCGT CG
		SEQ ID NO: 2372 GTTCACCGGCGGATATTCTGCGCGTGCCCGTGTCCGAGGACATGCTGGCCGCAC CTTCAACGGCAGCGGCATCCCCATGCACGGGCCCGCCCATCGTCGCAGAGAC CTACCTCGACGTCCAGGCATGCCGATTAATCCTCAAACGCGCATCTACCCGGAA GAAATGATCCAGACGGGGGATCTCGACCATCGAGCGTGATGACGTCCATCGCGCGAG GGCAGAAGATCCCCATCTTCTCGGGCGCGGGGCTGGTGCGCACAAGGAGACAACAAGGACGACT CGCAGATCTGCCGACAGGCGGGGCGATGGGCGTCAACATGGAGACGGCGCCTTCTTCAA GCGGCGAGTTCGGCGAGACGGGCGGTGGTGCTGTTCCTCAACCTGGC CAACGACCCCACCATCGAGCGCATCATCACCCCGGCAGTGTCGTCGTCATCATGACGACATG CGAGTTCCTGGCCTACCAGTGCAACAAGCACGTGCTGCTGCGGGCGGAGGTTCC TGGGCGAAGAGGCTTCCAGGCTACAGTTACACCGATCTCTCCACCATCTACGAG CGCGCTGGCCGTGTGCAAGGCCGCCCGGCTCCATCACTCAGATCCCATCCTG ACGATGCCCAACGAGCGACATCACCCCTATTC

Table 3-LD

Target ID	cDNA SEQ ID NO	Corresponding amino acid sequence of cDNA clone
LD001	1	SEQ ID NO: 2 (frame +1) GPKKHLKRLNAPKAWMLDKLGGVFAPRPSTGPHKLRESLPLVIFLRNRLKYALTNSEVTKIVMQRLIKVDGKVRTD SNYPAGFMDVITIEKTGEFFRLIYDVKGRFAVHRITAEEAKYKLCKVRRMQTGPKGIPFIVTHDGRTIR
LD002	3	SEQ ID NO: 4 (frame -3) AMQALKRKKRLEKNQLQIDGTLTTIELQREALEGASTNTTVLESMKNAAEALKKAHKNLDVDNVHDMMDDI
LD003	5	SEQ ID NO: 6 (frame -2) PRRPYEKARLDQELKIIGEYGLRNKREVWRVKYTLAKIRKAARELLTLEEKDQRRLFEGNALLRRLVRIGVLDETRM KLDYVLGLKIEDFLERRLQTQVFKLGLAKSIHHARVLVRQRHIRVRKQVVNIPSFIVRLDSQKHIDFSLKSPFGGGRP GRVKRKNL

LD006	7	SEQ ID NO: 8 (frame +1) HNYGWQVLVASGVVEYIDTLEEETVMIAMNPEDLRQDKEYAYCTTYTHCEIHPAMILGVCASIIPFPDHNQSPRNT YQSAMGKQAMGVYITNFHVRMDTLAHVLYYPHKPLVTTRSMEYLRFRELPAGINSIVAIACYTGYNQEDSVILNAS AVERGFFRSVFYRSYKDAESKRIGDQEEQFE
LD007	9	SEQ ID NO: 10 (frame +1) PKKDVKGTYVSIHSSGFRDFLLKPEILRAIVDCGFEHPSEVQHECIPQAVIGMDILCQAKSGMGKTAVFVLATLQQL EPADNVVYLVMCHTRELAFQISKEYERFSKYMPSVKGVFFGGMPIANDEEVLKNKCPHIVVGTPGRILALVKSR KLVLNLKHFILDECDKMLELLDMRRDVQEIYRNTPHTKQVMMFSATLSKEIRPVCKKFMQDPMEVVVDDEAKLTL HGLQQHYVKLKENENKNKLLFELLDVLEFNQVIFVKSVQRCVALAQLLTEQNFPAIGIHRGMDQKERLSRYEQFKD FQKRILVATNLFGRGMDIERVNIVFNYDMPEDSDTYLH
LD010	11	SEQ ID NO: 12 (frame +1) VKCSRELKIQGGIGSCVSLNVKNPLVSDTEIGMGNTVQWKMCTVTPSTTMALFFEVVNQHSAPIPQGGRGCIQFIT QYQHASGQKRIRVTVARNWADASANIHHVSAGFDQEAAAVIMARMAVYRAESDDSPDVLRWVDRMLIRLCQKF GEYNKDDPNSFRLGENFSLYPQFMYHLRRSQFLQVFNNSPDETSFYRHMLMREDLTQSLIMIQPILYSYSFNGPP EPVLLDTSSIQPDRILLMDTFFQILIFHGETIAQW
LD011	13	SEQ ID NO: 14 (frame -1) PTFKCVLVGDGGTGKTTFVKRHMTGEFEKRYVATLGVEVHPLVFHTNRGPIRFNWWDTAGQEKFGGLRDGYYIQ GQCAIIMFDVTSRVTYKNVPNWHRDLVRVCENIPIVLCGNKVDIKDRKVKAKSIVFHRKKNLQYYDISAKSNYNFEK PFLWLARKLIGDPNLEFVAMPALLP
LD014	15	SEQ ID NO: 16 (frame +3) QIKHMMAFIEQEANEKAEEIDAKAEEEFNIEKGRLVQQQRLKIMEYYEKKEKQVELQKKIQSSNMLNQARLKVLKV REDHVRTVLEEARKRLGQVTNDQGKYSQILESLILQGLYQLFEKDVTIRVRPQDRELVKSIIPTVTNKYKDATGKDI HLKIDDEIHLSQETTGGIDLLAQKNKIKISNTMEARLELISQQLLPEI
LD015	17	SEQ ID NO: 18 (frame -1) RHPSLFKAIGVKPPRGILLYGPPGTGKTLIARAVANETGAFFFLINGPEIMSKLAGESESNLRKAFEEADKNSPAIIFI DELDAI
LD016	19	SEQ ID NO: 20 (frame -2) TVSGVNGPLVILEDVKFPKYNEIVQLKLADGTIRSGQVLEVSGSKAVVQVFEGTSGIDAKNTACEFTGDILRTPVSE DMLGRVFNGSGKPIDKGPPILAEDFLDIQGQPINPWSRIYPEEMIQTGITAIDVMNSIARGQKIPIFSAAGLPHNEIAA QICRQAGLVKIPGKSVLDDHEDNFAIVFAAMGVNMETARFFKQDFEENGSMENVCLFLNLANDPTIERIITPRLALT AAEFLAYQCEKHVLVILTDMSSYAEALREVSAAREEVPGRRGFPGMYTDLATIYERAGRVEGRNGSITQIPILTMP NDDITHPI

| LD018 | 21 | SEQ ID NO: 22 (frame +2)

TWFKDGQRITESQKYESTFSNNQASLRVKQAQSEDSGHYTLLAENPQGCIVSSAYLAIEPVTTQEGLIHESTFKQQ QTEMEQIDTSKTLAPNFVRVCGDRDVTEGKMTRFDCRVTGRPYPDVTWYINGRQVTDDHNHKILVNESGNHALM ITTVSRNDSGVVTCVARNKTGETSFQCNLNVIEKEQVAPKFVERFTTVNVAEGEPVSLRARAVGTPVPRITWQR DGAPLASGPDVRIAIDGGASTLNISRAKASDAAWYRC |
| LD027 | 23 | SEQ ID NO: 24 (frame +1)

HGGDKPYLISGADDRLVKIWDYQNKTCVQTLEGHAQNVTAVCFHPELPVALTGSEDGTVRVWHTNTHRLENCLN YGFERVWTICCLKGSNNVSLGYDEGSILVKVGREEPAVSMDASGGKIIWARHSELQQANLKALPEGGEIRDGERL PVSVKDMGACEIYPQTIQHNPNGRFVVVCGDGEYIIYTAMALRNKAFGSAQEFVWAQDSSEYAIRESGSTIRIFKN FKERKNFKSDFSAEGIYGGFLLGIKSVSGLTFYDWETLDLVRRIEIQPRAVYWSDSGKLVCLATEDSYFILSYDSEQ VQKARENNQVAEDGVEAAFDVLGEMNESVRTGLWVGDCFIYT |

Table 3-PC

Target ID	cDNA SEQ ID NO	Corresponding amino acid sequence of cDNA clone
PC001	247	SEQ ID NO: 248 (frame +1) AWMLDKLGGVFAPRPSTGPHKLRESLPLVIFLRNRLKYALTNSEVTKIVMQRLIKVDGKVRTDSNYPAGFMDVITIE KTGEFFRLIYDVKGRFAVHRITAEEAKYKLCKVRRVQTGPKGIPFLVTHDGRTIRYPDPNIKVNDTIQMEIATSKILDY IKFES
PC003	249	SEQ ID NO: 250 (frame: +2) PRRPYEKARLDQELKIIGAFGLRNKREVWRVKYTLAKIRKAARELLTLEEKEPKRLFEGNALLRRLVRIGVLDENRM KLDYVLGLKIEDFLERRLQTQVFKSGLAKSIHARVLIRQRHIRVRKQVVNIPSFIVRLDSQKHIDFSLKSPFGGGRP GRV
PC005	251	SEQ ID NO: 252 (frame +3) PNEINEIANTNSRQNIRKLIKDGLIIKKPVAVHSRARVRKNTEARRKGRHCGFGKRKGTANARMPQKELWVQRMR VLRRLLKKYREAKKIDRHLYHALYMKAKGNVFRNKRVLMEYIHKKKAEKARAKMLSDQANARRLKVKQARERRE
PC010	253	SEQ ID NO: 254 (frame +3) LKDSLQMSLSLLPPNALIGLITFGKMVQVHELGTEGCSKSYVFCGTKDLTAKQVQEMLGIGKGSPNPQQOPGQPG RPGQNPQAAPVPPGSRFLQPVSKCDMNLTDLIGELQKDPWPVHQGKRPLRSTGAALSIAVGLLECTYPNTGGRI MIFLGGPCSQGPGQVLNDDLKOPIRSHHDIHKDNAKYMKKAIKHYDHLAMRAATNSHCIDIYSCALDQTGLMEMK QCCNSTGGHMVMGDSFNSSLFKQTFQRVFSKDPKNDLKMAFNATLEVKCSRELKVQGGIGSCVSLNVKSPLVSD TELGMGNTVQWKLCTLAPSSTVALFFEVVNQHSAPIPQGGRGCIQLITQYOHASGQRRIRVTTIARNWADATANIH HISAGFDQEAAAVVMARMAGYKAESDETPDVLRWVDRMLIRLCQKFGEYNKDDPNSFRLGENFSLYPQFMYHLR

		RSQFLQVFNNSPDETSFYRHMLMREDLTQSLIMIQPILYSYSFNGPPPEPVLLDTSSIQPDRILLMDTFFQILIFHGETIAQW
PC014	255	SEQ ID NO: 256 (frame +3) DVQKQIKHMMAFIEQEANEKAEEIDAKAEEEFNIEKGRLVQQORLKIMEYYEKKEKQVELQKKIQSSNMLNQARLKVLKVREDHVRAVLEDARKSLGEVTKDQGKYSQILESLILQGLFQLFEKEVTVRVRPQDRDLVRSILPNVAAKYKDATGKDILLKVDDESHLSQEITGGVDLLAQKNKIKISNTMEARLDLIA
PC016	257	SEQ ID NO: 258 (frame +2) LVILEDVKFPKFNEIVQLKLADGTLRSGQVLEVSGSKAVVQVFEGTSGIDAKNTVCEFTGDILRTPVSEDMLGRVFNGSGKPIDKGPPILAEDYLDIQGQPINPWSRIYPEEMIQTGITAIDVMNSIARGQKIPIFSAAGLPHNEIAAQICRQAGLVKVPGKSVLDDHEDNFAIVFAAMGVNMETARFFKQDFEENGSMENVCLFLNLANDPTIERIITPRLALTAAEFFLAYQCEKHVLVILTDMSSYAEALREVSAAREEVPGRRGFPGYMYTDLATIYERAGRVEGRNGSITQIPILTMP
PC027.	259	SEQ ID NO: 260 (frame +1) QANLKVLPEGAEIRDGERLPVTVKDMGACEIYPQTIQHNPNGRFVVVCGDGEYIIYTAMALRNKAFGSAQEFVWAQDSSEYAIRESGSTIRIFKNFKEKKNFKSDFGAEGIYGGFLLGVKSVSGLAFYDWETLELVRRIEIQPRAIYWSDSGKLVCLATEDSYFILSYDSDQVQKARDNNQVAEDGVEAAFDVLGEINESVRTGLWVGDCFIYTNAVNRINYFVGGELVTIAHLDRPLYVLGYVPRDDRLYLVDKELGVVSYXIAIICTRISDCSHATRLPNG*SSIAFNSK

Table 3-EV

Target ID	cDNA SEQ ID NO	Corresponding amino acid sequence of cDNA clone
EV005	513	SEQ ID NO: 514 (frame +3) RCGKKKVVWLDPNEITEIANTNSRQNIRKLIKDGLIIKKPVAVHSRARVRKNTEARRKGRHCGFGKRKGTANARMPRKELWIQRMRVLRRLLKKYREAKKIDRHLYHALYMKAKGNVFKNKRVMMDYIHKKAEKARTKMLNDQADARRLKVKEARKRREERIATKKQ
EV009	515	SEQ ID NO: 516 (frame +1) PTLDPSIPKYRTEESIIGTNPGMGFRPMPDNNEESTLIWLQGSNKTNYEKWKMNLLSYLDKYYTPGKIEKGNIPVKRCSYGEKLIRGQVCDVDVRKWEPCTPENHFDYLRNAPCIFLKLNRIYGWEPEYYNDPNDLPDDMPQQLKDHIRYNITNPVERNTVWVTCAGENPADVEYLGPVKYYPSFQGFPGYYFPYLNSEGYLSPLLAVQFKRPVSGIVINIECKAWA
EV010	517	SEQ ID NO: 518 (frame +3) GGHMVMGDSFNSSLFKQTFQRVFSKDSNGDLKMSFNAILEVKCSRELKVQGGIGPCVSLNVKNPLVSDLEIGMGNTVQWKLCSLSPSTTVALFFEVVNQHAAPIPQGGRGCIQFITQYQHSSGQKKIRVTTIARNWADATANIHHISAGFDEQTAAVLMARIAVVRAETDESSDVLRWVDRMLIRLCQKFGEYNKDDTNSFRLSENFSLYPQFMYHLRRSQFLQVFNNSPDETSFYRHMLMREDRNQ

EV015	519	SEQ ID NO: 520 (frame +1) RHPSLFKAIGVKPPRGILLYGPPGTGKTLIARAVANETGAFFFLINGPEIMSKLAGESESNLRKAFEEADKNSPAIIFIDE LDAIAPKREKTHGEVERRIVSQLLTLMDGMKKSSHVIVMAATNRPNSIDPALRRFGRFDREIDIGIPDATGRLEVLRIHT KNMKLADDVDLEQIAAETHGHVGADLASLCSEAALQQIREKMDLIDLDDEQIDAEVLNSLAVTMENFRYAMSKSSPSA LRETV
EV016	521	SEQ ID NO: 522 (frame +2) TVSGVNGPLVILDSVKFPKFNEIVQLKLSDGTVRSGQVLEVSGQKAVVQVFEGTSGIDAKNTLCEFTGDILRTPVSED MLGRVFNGSGKPIDKGPPILAEDFLDIQGQPINPWSRIYPEEMIQTGISAIDVMNSIARGQKIPFSAAGLPHNEIAAQIC RQAGLVKIPGKSVLDDHEDNFAIVFAAMGVNMETARFFKQDFEENGSMENVCLFLNLANDPTIERIITPRLTAAEFM AYQCEKHVLVILTDMSSYAEALREVSAA

Table 3-AG

Target ID	cDNA SEQ ID NO	Corresponding amino acid sequence of cDNA clone
AG001	601	SEQ ID NO: 602 (frame +1) HLKRFAAPKAWMLDKLGGVFAPRPSTGPHKLRESLPLVIFLRNRLKYALTNCEVTKIVMQRLIKVDGKVRTDPNYPAG FMDVITIEKTGEFFRLIYDVKGRFTIHRITAEEAKYKLCKVRKVQTGPKGIPFLVTHDGRTIRYPDPMIKVNDTIQLEIATS KILDFIKFESSGNLCMITGGRNLGRVGTVVNRERHPGSFDIVHIRDANDHVFATRLNNVFVIGKGSKAFVSLPRGKGVK LSIA
AG005	603	SEQ ID NO: 604 (frame +2) VWLDPNEINEIANTNSRQNIRKLIKDGLIIKKPVAVHSRARVRKNTEARRKGRHCGFGKRKGTANARMPQKELWIQR MRVLRRLLKKYREAKKIDRHLYHALYMKAKGNVFKNKRVLMEYIHKKAEKARAKMLADQANARRQKVKQVP*EEG RAYRREEAG
AG010	605	SEQ ID NO: 606 (frame +3) GGHMLMGDSFNSSLFKQTFQRVFAKDQNGHLKMAFNGTLEVKCSRELKVQGGIGSCVSLNVKSPLVADTEIGMGN TVQWKMCTFNPSTTMALFFEVVNQHSAPIPQGGRGCIQFITQYQHSSGQRRIRVTTIARNWADASANIHHISAGFDQ ERAAVIMARMAVYRAETDESPDVLRWVDRMLIRLCQKFGEYNKDDQASFRLGENFSLYPQFMYHLRRSQFLQVFNN SPDETSFYRHMLMREDLTQSLIMIQPILYSYSFNGPPEPVLLDTSSIQPDRILLMDTFFQILIFHGETIAQW
AG014	607	SEQ ID NO: 608 (frame +3) QIKHMMAFIEQEANEKAEEIDAKAEEEFNIEKGRLVQQQRLKIMEYYEKEKQVELQKKIQSSNMLNQARLKVLVRE DHVRAVLDEARKKLGEVTRDQGKYAQILESLILQGLYQLFEANVTVRVRPQDRTLVQSVLPTIATKYRDVTGRDVHLS IDDETQLSESVTGGIELLCKQNKIKVCNTLEARLDLISQQLVPQIRNALFGRNINRKF
AG016	609	SEQ ID NO: 610 (frame +1)

VSEDMLGRVFNGSGKPIDKGPPILAEDFLDIQGQPINPWSRIYPEEMIQTGISAIDVMNSIARGQKIPIFSAAGLPHNEIA
AQICRQAGLVKLPGKSVIDDHEDNFAIVFAAMGVNMETARFFKQDFEENGSMENVCLFLNLANDPTIERIITPRLALTA
AEFLAYQCEKHVLVILTDMSSYAEALREVSAAREEVPGRRGFPGYMYTDLATIYERAGRVEGRNGSITQIPILTMPND
DITHPI

Table 3-TC

Target ID	cDNA SEQ ID NO	Corresponding amino acid sequence of cDNA clone
TC001	793	SEQ ID NO: 794 (frame +1) GPKKHLKRLNAPKAWMLDKLGGVFAPRPSTGPHKLRESLPLVIFLRNRLKYALTNSEVTKIVMQRLIKVDGKVRTD PNYPAGFMDVVTIEKTGEFFRLIYDVKGRFTIHRITGEEAKYKLCKVKKVQTGPKGIPFLVTRDGRTIRYPDPMIKVN DTIQLEIATSKILDFIKFESGNLCMITGGRNLGRVGTVVSRERHPGSFDIVHIKDANGHTFATRLNNVFIIGKGSKPYV SLPRGKGVKLSI
TC002	795	SEQ ID NO: 796 (frame +1) QEFLEAKIDQEILTAKKNASKNKRAAIQAIKRKKRYEKQLQQIDGTLSTIEMQREALEGANTNTAVLKTMKNAADAL KNAHLNMDVDEVHDMMDDI
TC010	797	SEQ ID NO: 798 (frame +3) PEVLVFGHVLVLEVPPLGDCLTVENQNLEKCVHEKDPIGLNGTSVEEDGFRGAVETITVQNRLDHNETLGEVLPH QHVAVERGLVWGVVENLEELGAAQMVHELGIETEVFTQTETVRVVFVVFAEF
TC014	799	SEQ ID NO: 800 (frame +1) EKAEEIDAKAEEEFNIEKGRLVQQQRLKIMEYYEKKEKPVELQKKIQSSNMLNQARLKVLKVREDHVHNVLDDARK RLGEITNDQARYSQLLESLILQSLYQYLGISDELFENNIVVRVRQQDRSIIQGILPVVATKYRDATGKDVHLKIDDES HLPSETTGGVVLYAQKGKIKIDNTLEARLDLIAQQLVPEIRTALFGRNINRKF
TC015	801	SEQ ID NO: 802 (frame +2) DELQLFRGDTVLLKGKRRKETVCIVLADENCPDEKIRMNRIVRNNLRVRLSDVVWIQPCPDVKYGKRIHVLPIDDTV EGLVGNLFEVYLKPYFLEAYRPIHKGDVFIVRGGMRAVEFKVVETEPSPYCIVAPDTVIHCDGDPIKREEEEALNA VGYDDIGGCRKQLAQIKEMVELPLRHPSLFKAIGVKPPRGILLYGPPGTGKTLIARAVANETGAFFLINGPEIMSKL AGESESNLRKAFEEADKNSPAIIFIDELDAIAPKREKTHGEVERRIVSQLLTLMDGMKKSSHVIVMAATNRPNSIDPA LRRFGRFD

Table 3-MP

Target ID	cDNA SEQ ID NO	Corresponding amino acid sequence of cDNA clone
MP001	888	SEQ ID NO: 889 (frame +1) GPKKHLKRLNAPKAWMLDKSGGVFAPRPSTGPHKLRESLPLLIFLRNRLKYALTGAEVTKIVMQRLIKVDGKVRTDPN YPAGFMDVISIQKTSEHFRLIYDVKGRFTIHRITPEEAKYKLCKVKRVQTGPKGVPFLTTHDGRTIRYPDPNIKVNDTIR YDIASSKILDHIRFETGNLCMITGGRNLGRVGIVTNRERHPGSFDIVHIKDANEHIFATRMNNVFIIGKGQKNYISLPRSK GVKLT
MP002	890	SEQ ID NO: 891 (frame +2) SFFSKVFGGKKEEKGPSTEDAIQKLRSTEEMLIKKQEFLEKKIEQEVAIAKKNGTTNKRAALQALKRKKRYEQQLAQID GTMLTIEQQREALEGANTNTAVLTMKTAADALKSAHQNMNVDDVHDLMDDI
MP010	892	SEQ ID NO: 893 (frame +3) GCIQFITQYQHSSGYKRIRVTTLARNWADPVQNMMHVSAAFDQEASAVLMARMVVNRAETEDSPDVMRWADRTLI RLCQKFGDYQKDDPNSFRLPENFSLYPQFMYHLRRSQFLQVFNNSPDETSYYRHMLMREDVTQSLIMIQPILYSYSF NGRPEPVLLDTSSIQPDKILLMDTFFHILIFHGETIAQWRAMDYQNRPEYSNLKQLLQAPVDDAQEILKTRFPMPRYID TEQGGSQARFLLCKVNPSQTHNNMYAYGG*WWSTSFDR*CKLAAVHGAAA
MP016	894	SEQ ID NO: 895 (frame +1) VSEDMLGRVFNGSGKPIDKGPPILAEDYLDIEGQPINPYSRTYPQEMIQTGISAIDIMNSIARGQKIPIFSAAGLPHNEIA AQICRQAGLVKKPGKSVLDDHEDNFAIVFAAMGVNMETARFFKQDFEENGSMENVCLFLNLANDPTIERIITPRLALT AAEFLAYQCEKHVLVILTDMSSYAEALREVSAAREEVPGRRGFPGYMYTDLATIYERAGRVEGRNGSITQIPILTMPN DDITHPI
MP027	896	SEQ ID NO: 897 (frame +3) PITKTRRVFRH*KAMLKIFLLVCFHPELPIVLTGSEDGTVRIWHSGTYRLESSLNYGLERVWTICCLRGSNNVALGYDE GSIMVKVGREEPAMSMDVHGGKIVWARHSEIQQANLKAMLQAEGAEIKDGERLPIQVKDMGSSCEIYPQSISHNPNG RFLVVCGDGEYIIYTSMALRNKAFGSAQDFVWSSDSEYAIRENSSTIKVFKNFKEKKSFKPEGGADGIFGGYLLGVKS VTGLALYDWENGNLVRRIETQPKHVFWSESGELVCLATDEAYFILRFDVNVLSAARASNYEAASPDGLEDAFEILGEV QEVVKTGLWVGDCFIYTNGVNRINYYVGGEVVTVS

Table 3-NL

Target ID	cDNA SEQ ID NO	Corresponding amino acid sequence of cDNA clone
NL001	1071	SEQ ID NO: 1072 (frame +2) KSWMLDKLGGVYAPRPSTGPHKLRESLPLVIFLRNRLKYALTNCEVKKIVMQRLIKVDGKVRTDPNYPAGFMDVVQIEK TNEFFRLIYDVKGRFTIHRITAEEAKYKLCKVKRVQTGPKGIPFLTTHDGRTIRYPDPLVKVNDTIQLDIATSKIMDFIRFDS GNLCMITGGRNLGRVGTVVNRERHPGSFDIVHIKDVLGHTFATRLNNVFIIGKGSKAYVSLPKGKGVKLS
NL002	1073	SEQ ID NO: 1074 (frame +1) DEKGPTTGEAIQKLRETEEMLIKKQDFLEKKIEVEIGVARKNGTKNKRAAIQALKRKKRYEKQLQOIDGTLSTIEMQREAL EGANTNTAVLQTMKNAADALKAAHQHMDVDQ
NL003	1075	SEQ ID NO: 1076 (frame +2) PRRPYEKARLEQELKIIGEYGLRNKREVWRVKYALAKIRKAARELLTLEEKDQKRLFEGNALLRRLVRIGVLDEGRMKLD YVLGLKIEDFLERRLQTQVYKLGLAKSIHHARVLIRQRHI RVRKQVVNIPSFVVRLDSQKHIDFSLKSPFGGGRPGRV
NL004	1077	SEQ ID NO: 1078 (frame +1) KELAAVRTVCSHIENMLKGVTKGFLYKMRAVYAHFPINCVTTENNSVIEVRNFLGEKYIRRVRMAPGVTVTNSTKQKDEL IVEGNSIEDVSRSAALIQOSTTVKNKDIRKFLD
NL005	1079	SEQ ID NO: 1080 (frame +1) LDPNEINEIANTNSRQSIRKLIKDGLIIKKPVAVHSRARVRKNTEARRKGRHCGFGKRKGTANARMPQKVLWVNRMRVL RRLLKKYRQDKKIDRHLYHHLYMKAKGNVFKNKRVLMEFIH KKKAEKARMKMLNDQAEARRQKVKEAKKRRE
NL006	1081	SEQ ID NO: 1082 (frame +3) VLVSSGVVEYIDTLEEETTMIAMSPDDLRQDKEYAYCTTYTHCEIHPAMILGVCASIIPPDHNQSPRNTYQSAMGKQAM GVYITNFHVRMDTLAHVLFYPHKPLVTTRSMEYLRFRELPAGINSVVAIACYTGYNQEDSVILNASAVERGFFRSVFFRS YKDAESKRIGDQEEQFEKPTRQTCQGMRNAIYDKLDDDGIIAPGLRVSGDDVVIGKTITLPDNDDELEGTTKRFTKRDAS TFLRNSETGIVDQVMLTLNSEGYKFCKIRVRSVRIPQIGDKFASRHGQKGTCGIQYRQEDMPFTSEGIAPDIIINPHAIPSR MTIGHLIECLQGKVSSNKGEIGDATPFN
NL007	1083	SEQ ID NO: 1084 (frame +2) FRDFLLKPEILRAILDCGFEHPSEVQHECIPQAVLGMDILCQAKSGMGKTAVFVLATLQQIEPTDNQVSVLVMCHTRELA FQISKEYERFSKCMPNIKVGVFFGGLPIQRDEETLKLNCPHIVVGTPGRILALVRNKKLDLKHLKHFVLDECDKMLELLDM RRDVQEIFRNTPHSKQVMMFSATLSKEIRPVCKKFMQDPMEVYVDDEAKLTLHGLQQHYVKLKENEKNKLFELLDILE FNQVVIFVKSVQRCMALSQLLTEQNFPAVAIHRGMTQEERLKKYQEFKEFLKRILVATNLFGRGMDIERVNIVFNYDMP
NL008	1085	SEQ ID NO: 1086 (frame +1) GRIENQKRVVGVLLGCWRPGGVLDVSNSFAVPFDEDDKEKNVWFLDHDYLENMFGMFKKVNAREKVVGWYHTGPKL

NL009	1087	HQNDVAINELIRRYCPNCVLVIIDAKPKDLGLPTEAYRVVEEIHDDGSPTSKTFEHVMSEIGAEEAEEIGVEHLLRDIKDTT VGSLSQRVTNQLMGLKGLHLQLQDMRDYLNQVVEGKLPMNHQIVYQLQDIFNLLPDIGHGNFVDSLY
NL009	1087	SEQ ID NO: 1088 (frame +1) CDYDRPPGRGQVCDVDVKNWFPCTSENNFNYHQSSPCVFLKLNKIIGWQPEYYNETEGFPDNMPGDLKRHIAQQKSI NKLFMQTIWITCEGEGPLDKENAGEIQYIPRQGFPGYFYPYTN A
NL010	1089	SEQ ID NO: 1090 (amino terminus end) (frame +2) SSRLEATRLVVPVGCLYQPLKERPDLPPVQYDPVLCTRNTCRAILNPLCQVDYRAKLWVCNFCFQRNPFPPQYAAISEQ HQPAELIPSFSTIEYIITRAQTMPPMFVLVVDTCLDDEELGALKDSLQMSLSLLPPNALIGLITFGKMVQVHELGCDGCSK SYVFRGVKDLTAKQIQDMLGIGKMAAAPQPMQQRIPGAAPSAPVNRFLQPVGKCDMSLTDLLGELQRDPWNVAQGKR PLR STGVALSIAVGLLECT
	1115	SEQ ID NO: 1116 (carboxy terminus end) (frame +3) LNVKGSCVSDTDIGLGGTSQWKMCAFTPHTTCAFFFEVVNQHAAPIPQGGRGCIQFITQYQHSSGQRRIRVTTIARNWA DASTNLAHISAGFDQEAGAVLMARMVVHRAETDDGPDVMRWADRMLIRLCQRFGEYSKDDPNSFRLPENFTLYPQFM YHLRRSQFLQVFNNSPDETSYYRHILMREDLTQSLIMIQPILYSYSFNGPPEPVLLDTSSIQPDRILLMDTFFQILIFHGETI A
NL011	1091	SEQ ID NO: 1092 (frame +2) DGGTGKTTFVKRHLTGEFEKKYVATLGVEVHPLVFHTNRGVIRFNVWDTAGQEKFGGLRDGYYIQGQCAIIMFDVTSRV TYKNVPNWHRDLVRVCENIPIVLCGNKVDIKDRKVKAKSIVFHRKKNLQYYDISAKSNYNFEKPFLWLAKKLIGDPNLEFV AMPALLPPEVTMDPQX
NL012	1093	SEQ ID NO: 1094 (frame +2) QQTQAQVDEVVDIMKTNVEKVLERDQKLSELDDRADALQQGASQFEQQAGKLRKF
NL013	1095	SEQ ID NO: 1096 (frame +2) AEQVYISSLALLKMLKHGRAGVPMEVMGLMLGEFVDDYTVRVIDVFAMPQSGTGVSVEAVDPVFQAKMLDMLKQTGR PEMVVGWYHSHPGFGCWLSGVDINTQESFEQLSKRAVAVVV
NL014	1097	SEQ ID NO: 1098 (frame +2) FIEQEANEKAEEIDAKAEEEFNIEKGRLVQHQRLKIMEYYDRKEKQVELQKKIQSSNMLNQARLKALKVREDHVRSVLEE SRKRLGEVTRNPAKYKEVLQYLIVQGLLQLLESNVVLRVR EADVSLIEGIVGSSCAEQYAKMTGKEVVVKLDADNFLAAETCGGVELFARNGRIKIPNTLESRLDLISQQLVPEIRVALF
NL015	1099	SEQ ID NO: 1100 (frame +1) IVLSDETCPFEKIRMNRVVRKNLRVRLSDIVSIQPCPDVKYGKRIHVLPIDDTVEGLTGNLFEVYLKPYFLEAYRPIHKDDA FIVRGGMRAVEFKVVETDPSPYCIVAPDTVIHCEGDPIKREDEEDAANAVGYDDIGGCRKQLAQIKEMVELPLRHPSLFK AIGVKPPRGILLYGPPGTGKTLIARAVANETGAFFLINGPEIMSKLAGESESNLRKAFEEADKNAPAIIFIDELDAIAPKRE KTHGEVERRIVSQLLTLMDGLKQSSHVIVMAATNRPNSIDAALRRFGRFDREIDIGIPDATGRLEVLRIHTKNMKLADDVD

		LEX
NL016	1101	**SEQ ID NO: 1102 (frame +2)** TPVSEDMLGRVFNGSGKPIDKGPPILAEDYLDIQGQPINPWSRIYPEEMIQTGISAIDVMNSIARGQKIPIFSAAGLPHNEIA AQICRQAGLVKLPGKSVLDDSEDNFAIVFAAMGVNMETARFFKQDFEENGSMENVCLFLNLANDPTIERIITPRLALTAAE FLAYQCEKHVLVILTDMSSYAEALREVSAAREEVPGRRGFPGYMYTDLATIYERAGRVEGRNGSIT
NL018	1103	**SEQ ID NO: 1104 (frame +2)** MQMPVPRPQIESTQQFIRSEKTTYSNGFTTIEEDFKVDTFEYRLLREVSFRESLIRNYLHEADMQMSTVVDRALGPPSAP HIQQKPRNSKIQEGGDAVFSIKLSANPKPRLVWFKNGQRIGQTQKHQASYSNQTATLKVNKVSAQDSGHYTLLAENPQ GCTVSSAYLAVESAGTQDTGYSEQYSRQEVETTEAVDSSKMLAPNFVRVPADRDASEGKMTRFDCRVTGRPYPDVA WFINGQQVADDATHKILVNESGNHSLMITGVTRLDHGVVGCIARNKAGETSFQCNLNVIEKELVVAPKFVERFAQVNVK EGEPVVLSARAVGTPVPRITWQKDGAPIQSGPSVSLFVDGGATSLDIPYAKAS
NL019	1105	**SEQ ID NO: 1106 (frame +2)** DDTYTESYISTIGVDFKIRTIDLDGKTIKLQIWOTAGQERFRTITSSYYRGAHGIIVVYDCTDQESFNNLKQWLEEIDRYAC DNVNKLLVGNKCDQTNKKVVDYTQAKEYADQLGIPFLETSAKNATNVEQAF
NL021	1107	**SEQ ID NO: 1108 (frame +2)** VSLNSVTDISTTFILKPQENVKITLEGAQACFISHERLVISLKGGELYVLTLYSDSMRSVRSFHLEKAAASVLTTCICVCEE NYLFLGSRLGNSLLLLRFTEKELNLIEPRAIESSQSQNPAKKKKLDTLGDWMASDVTEIRDLDELEVYGSETQTSMQIASYI F
NL022	1109	**SEQ ID NO: 1110 (frame +2)** TLHREFLSEPDLQSYSVMIIDEAHERTLHTDILFGLVKDVARFRPDLKLLISSATLDAQKFSEFFDDAPIFRIPGRRFPVDIY YTKAPEADYVDACVVSILQIHATQPLGDILVFLTGQEEIETCQELLQDRVRRLGPRIKELLILPVYSNLPSDMQAKIFLPTPP NARKVVLATNIAETSLTIDNIIYVIDPGFCKQNNFNSRTGMESLVVPVSKASANQRAGRAGRVAAGKCFRLYT
NL023	1111	**SEQ ID NO: 1112 (frame +2)** RSFSQERQHEEMKESSGRMHHSDPLIVETHSGHVRGISKTVLGREVHVFTGIPFAKPPIGPLRFRKPVPVDPWHGVLDA TALPNSCYQERYEYFPGFEGEEMWNPNTNLSEDCLYLNIWVPHRLRIRHRANSEENKPRAKVPVLIWIYGGGYMSGTA TLDVYDADMVAATSDVIVASMQYRVGAFGFLYAQDLPRGSEEAPGNMGLWDQALAIRWLKDNIAAFGGDPELMTLFG ESAGGGSVSIHLVSPITRGLARRGIMQSGTMNAPWSFMTAERATEIAKTLIDDCGCNSSLLTDAPSRVMSCMRSVEAKII SVGQWNSYSGILGLPSAPTIDGIFLPKHPLDLLKEGDFQDTEILIGSNQDEGTYFILYDFIDFFQKDGPSFLQRDKFLDIINT IFKNMTKIEREAIIFQYTDWEHVMDGYLNQKMIGDVVGDYFFICPTNHFAQQAFAEHGKKVYYFFTQRTSTSLWGEWMG VMHGDEIEYVFGHPLNMSLQFNARERDLSLRIMQAYSRFALTGKPVPDDVNWPIYSKDQPQYYIFNAETSGTGRGPRA TACAF
NL027	1113	**SEQ ID NO: 1114 (frame +2)** PIVLTGSEDGTVRIWHSGTYRLESSLNYGLERVWTICCMRGSNNVALGYDEGSIMVKVGREEPAISMDVNGEKIVWARH SEIQQVNLKAMPEGVEIKDGERLPVAVKDMGSCEIYPQTIAHNPNGRFLVVCGDGEYIIHTSMVLRNKAFGSAQEFIWG

| | | QDSSEYAIREGTSTVKVFKNFKEKKSFKPEFGAESIFGGYLLGVCSLSGLALYDWETLELVRRIEIQPKHVYWSESGELV ALATDDSYFVLRYDAQAVLAARDAGDDAVTPDGVEDAFEVLGEVHETVKTGLWVGDCFIYT |

Table 3-CS

Target ID	cDNA SEQ ID NO	Corresponding amino acid sequence of cDNA clone
CS001	1682	SEQ ID NO: 1683 (frame +1) KAWMLDKLGGVYAPRPSTGPHKLRECLPLVIFLRNRLKYALTGNEVLKIVKQRLKVDGKVRTDPTYPAGFMDVV SIEKTNELFRLIYDVKGRFTIHRITPEEAKYKLCKVRRVATGPKNVPYLVTHDGRTVRYPDPLIKVNDSIQLDIATSK IMDFIKFESGNLCMITGGRNLGRVGTIVSRERHPGSFDIVHIRDSTGHTFATRLNNVFIIGKGTKAYISLPRGKGVR LT
CS002	1684	SEQ ID NO: 1685 (frame +1) SFFSKVFGGKKEEKGPSTHEAIQKLRETEELLQKKQEFLERKIDTELQTARKHGTKNKRAAIAALKRKRYEKQLT QIDGTLTQIEAQREALEGANTNTQVLNTMRDAATAMRLAHKDIDVDKVHDLMDDI
CS003	1686	SEQ ID NO: 1687 (frame +1) GLRNKREVWRVKYTLARIRKAARELLTLEEKDPKRLFEGNALLRRLVRIGVLDEKQMKLDYVLGLKIEDFLERRLQ TQVFKAGLAKSIHHARILRQRHIRVRKQVVNIPSFIVRLDSGKHIDFSLKSPFGGGRP
CS006	1688	SEQ ID NO: 1689 (frame +1) TCQGMRNALYDKLDDDGIIAPGIRVSGDDVVIGKTITLPENDDELEGTSRRYSKRDASTFLRNSETGIVDQVMLTL NSEGYKFCKIRVRSVRIPQIGDKFASRHGQKGTCGIQYRQEDMPFTCEGLTPDIIINPHAIPSRMTIGHLIECIQGK VSSNKGEIGDATPFNDAVNVQKI
CS007	1690	SEQ ID NO: 1691 (frame +3) SEISCWNQRFWGLSSIAVSSTLQKFNMNVFPKLFWEWIFFVKAKSGMGKTAVFVLATLQQLEPSENHVYVLVMC HTRELAFQISKEYERFSKYMAGVRVSVFFGGMPIQKDEEVLKTACPHIVVGTPGRILALVNNKLNLKHLKHFILD ECDKMLESLDMRRDVQEIFRNTPHGKQVMMFSATLSKEIRPVCKFMQDPMEVVYDDEAKLTLHGLQQHYVKL KENEKNKKLFELLDVLEFNQVIFVKSVQRCIALAQLLTDQNFPAIGIHRNMTQDERLSRYQQFKDFQKRILVATN LFGRGMDIERVNIVFNYDMP
CS009	1692	SEQ ID NO: 1693 (frame +1) LVAICIWTFLQRLDSREPMWQLDESIIGTNPGLGFRPTPPEVASSVIWYKGNDPNSQQFWVQETSNFLTAYKRD GKKAGAGQNIHNCDFKLPPPAGKVCDVDISAWSPCVEDKHFGYHKSTPCIFLKLNKIFGWRPHFYNSSDSLPTD MPDDLKEHIRNMTAYDKNYLNMVWVSCEGENP

CS011	1694	SEQ ID NO: 1695 (frame +1) GSGKTTFVKRHLTGEFEKRYVATLGVEVHPLVFHTNRGPIRFNVWDTAGQEKFGGLRDGYYIQGQCAIIMFDVTSRVTYKNVPNWHRDLVRVCEGIPIVLCGNKVDIKDRKVKAKTIVFHRKKNLQYYDISAKSNYNFEKPFLWLARKLIGDGNLEFVAMQPCFH
CS013	1696	SEQ ID NO: 1697 (frame +2) DAPVVDTAEQVYISSLALLKMLKHGRAGVPMEVMGLMLGEFVDDYTVRVIDVFAMPQTGTGVSVEAVDPVFQAKMLDMLKQTGRPEMVVGWYHSHPGFGCWLSGVDINTQQSFEALSERAVAVVVDPIQSVKG
CS014	1698	SEQ ID NO: 1699 (frame +2) QKQIKHMMAFIEQEANEKAEEIDAKAEEEFNIEKGRLVQQORLKIMEYYEKKEKQVELQKKIQSSNMLNQARLKVLKVREDHVRNVLDEARKRLAEVPKDVKLYTDLLVTLVVQALFQLMEPTVTVRRQADVSLVQSILGKAQQDYKAKIKKDVQLKIDTENSLPADTCGGVELIAARGRIKISNTLESRLELIAQOLLPEIRTALF
CS015	1700	SEQ ID NO: 1701 (frame +1) IVLSDDNCPDEKIRMNRVVRNNLRVRLSDIVSIAPCPSVKYGKRVHILPIDDSVEGLTGNLFEVYLKPYFMEAYRPIHRDDTFMVRGGMRAVEFKVVETDPSPYCIVAPDTVIHCEGDPIKREEEEALNAVGYDDIGGCRKQLAQIKEMVELPLRHPSLFKAIGVKPPRGILMYGPPGTGKTLIARAVANETGAFFLINGPEIMSKLAGESESNLRKAFEEADKNSPAIIFIDELDAIAPKREKTHGEVERRIVSQLLTLMDGMKKSSHVIVMAATNRPNSIDPAL
CS016	1702	SEQ ID NO: 1703(frame -3) TPVSEDMLGRVFNGSGKPIDKGPPILAEDFLDIQGQPINPWSRIYPEEMIQTGISAIDVMNSIARGQKIPIFSAAGLPHNEIAAQICRQAGLVKIPGKSVLDDHEDNFAIVFAAMGVNMETARFFKQDFEENGSMENVCLFLNLANDPTIERIITPRLALTAAEFLAYQCEKHVLVILTDMSSYAEALREVSAAREEVPGRRGFPGYMYTDLATIYERAGRVEGRNGSITQIPILTMPNDDITHPIPDLTGYITEGQIYVDRQLHNRQIYPPVNVLPSLSRLMKSAIGEGMTRKDHSDVSNQLYACYAIGKDVQAMKAVVGEEALTPDDLLYLEFLTKFEKNFITQGNYENRTVFESLDIGWQLLRIFPKEMLKRIPASI
CS018	1704	SEQ ID NO: 1705 (frame +2) SVYIQPEGVPVPAQQSQQQSYRHVSESVEHKSYGTQGYTTSEQTKQTQKVAYTNGSDYSSTDDFKVDTFEYRLLREVSFRESITKRYIGETDIQISTEVDKSLGVVTPPKIAQKPRNSKLQEGADAQFQVQLSGNPRPRVSWFKNGQRIVNSNKHEIVTTHNQTILRVRNTQKSDTGNYTLAENPNGCVVTSAYLAVESPQETYGQDHKSQYIMDNQQTAVEERVEVNEKALAPQFVRVCQDRDVTEGKMTRFDCRVTGRPYPEVTWFINDRQIRDDYXHKILVNESCNHALMITNVDLSDSGVVSCIARNKTGETSFQCRLNVIEKEQVVAPKFVERFSTLNVREGEPVQLHARAVGTPTPRITWQKDGVQVIPNPELRINTEGGASTLDIPRAKASDAGWYRC

Table 3-PX

Target ID	cDNA SEQ ID NO	Corresponding amino acid sequence of cDNA clone
PX001	2100	SEQ ID NO: 2101 (frame +1) GPKKHLKRLNAPRAWMLDKLGGVYAPRPSTGPHKLRECLPLVIFLQPPQVRAQRQRGAEDREAAPHQGGRQGPH RPHLPGWIHGCCVD*KDQ*AVPSDLRCEGTLHHPPHHSRGGQVQAVQGEARGDGPQERAVHRDAQRPHAALPRP AHQGQRLHPARHRHLQDHGHHQVRLR*PVHDHGRA*LGASGHHRVPREAPRELRHRPHQGHHRTHLRHQVEQRV HHRQGHE
PX009	2102	SEQ ID NO: 2103 (frame +3) TLIWYKGTGYDSYKYWENQLIDFLSVYKKKGQTAGAGQNIFNCDFRNPPPHGKVCDVDIRGWEPCIDENHFSFHKS SPCIFLKLNKIYGWRPEFYNDTANLPEAMPVDLQTHIRNITAFNRDYANMVWVSCHGETPADKENIGPVRYLPYPGFP GYFYPYENAEGYLSPLVAVHLERPRTGIVINIECKAWA
PX010	2104	SEQ ID NO: 2105 (frame +3) GCIQFITQYQHSSGQRRVRVTTVARNWGDAAANLHHISAGFDQEAAAVVMARLVVYRAEQEDGPDVLRWLDRMLIR LCQKFGEYAKDDPNSFRLSENFSLYPQFMYHLRRSQFLQVFNNSPDETTFYRHMLMREDLTQSLIMIQPILYSYSFG GAPEPVLLDTSSIQPDRILLMDTFFQILIYHGETMAQWRALRYQDMAEYENFKQLLRAPVDDAQEILQTRFPVPRYIDT EHGGSQARFLLSKVNPSQTHNNMYAYGGAMPIPSADGGAPVLTDDVSLQVFMEQP
PX015	2106	SEQ ID NO: 2107 (frame +3) RKETVCIVLSDDNCPDEKIRMNRVVRNNLRVRLSDIVSIAPCPSVKYGKRVHILPIDDSVEGLTGNLFEVYLKPYFMEA YRPIHRDDTFMVRGGMRAVEFKVVETDPSPYCIVAPDTVIHCEGEPIKREEEEALNAVGYDIGGCRKQLAQIKEMV ELPLRHPSLFKAIGVKPPRGILMYGPPGTGKTLIARAVANETGAFFLINGPEIMSKLAGESESNLRKAFEEADKNSPAI ILIDELDAI
PX016	2108	SEQ ID NO: 2109 (frame +2) FTGDILRTPVSEDMLGRIFNGSGKPIDKGPPILAEEYLDIQGQPINPWSRIYPEEMIQTGISAIDVMNSIARGQKIPIFSA AGLPHNEIAAQICRQAGLVKVPGKSVLDDHEDNFAIVFAAMGVNMETARFFKQDFEENGSMENVCLFLNLANDPTIE RIITPRLALTAAEFLAYQCEKHVLVILTDMSSYAEALREVSAAREEVPGRRGFPGYMYTDLATIYERAGRVEGRNGSIT QIPILTMPNDDITHPIPDLTGYITEGQIYVDRQLHNRQIYPPVNVLPSLSRLMKSAIGEGMTRKDHSDVSNQLYACYAIG KDVQAMKAVVGEEALTPDDLLYLEFLTKFEKNFITQGSYENRTVFESLDIGWQPLRIFPKEM

Table 3-AD

Target ID	cDNA SEQ ID NO	Corresponding amino acid sequence of cDNA clone
AD001	2364	SEQ ID NO: 2365 (frame +1) GPKKHLKRLNAPKAWMLDKLGGVFAPRPSTGPHKLRECLPLVIFLRNRLKYALTNCEVTKIVMQRLIKVDGKVRTDPN YPAGFMDVVTIEKTGEFFRLVYDVKGRFTIHRISAEEAKYKLCKVRRVQTGPKGIPFLVTHDGRTIRYPDPVIKVNDSI QLDIATCKIMDHIRFESGNLCMITGGRNLGRVGTVVSRERHPGSFDIVHIKDTQGHTFATRLNNVFIIGKATKPYISLPK GKGVKLSIAEERDK
AD002	2366	SEQ ID NO: 2367 (frame +2) SFFSKVFGGKKDGKAPTTGEAIQKLRETEEMLIKKQEFLEKKIEQEINVAKKNGTKNKRAAIQALKRKKRYEKQLQQID GTLSTIEMQREALEGANTNTAVLQTMKSAADALKAAHQHMDVDKVHDLMDDI
AD009	2368	SEQ ID NO: 2369 (frame +3) VLAALVAVCLWVFFQTLDPRIPTWQLDSSIIGTSPGLGFRPMPEDSNVESTLIWYRGTDRDDFRQWTDTLDEFLAVY KTPGLTPGRGQNIHNCDYDKPPKKGQVCNVDIKNWHPCIQENHYNYHKSSPCIFIKLNKIYNWIPEYYNESTNLPEQM PEDLKQYIHNLESNNSREMNTVWVSCEGENP
AD015	2370	SEQ ID NO: 2371 (frame +2) DELQLFRGDTVLLKGKRRKETVCIVLSDDTCPDGKIRMNRVVRNNLRVRLSDVVSVQPCPDVKYGKRIHVLPIDDTVE GLTGNLFEVYLKPYFLEAYRPIHKDDAFIVRGGMRAVEFKVVETDPSPYCIVAPDTVIHCEGDPIKREEEEALNAVGY DDIGGCRKQLAQIKEMVELPLRHPSLFKAIGVKPPRGILLYGPPGTGKTLIARAVANETGAFFLINGPEIMSKLAGESE SNLRKAFEEADKNAPAIIFIDELDAIAPKREKTHGEVERRIVSQLLTLMDGLKQSSHVIVMAATNRPNSIDGALRRFGRF DREIDIGIPDATGRLEILRIHTKNMKLADDVDLEQIAAESHG
AD016	2372	SEQ ID NO: 2373 (frame +2) FTGDILRVPVSEDMLGRTFNGSSGIPIDGGPPIVAETYLDVQGMPINPQTRIYPEEMIQTGISTIDVMTSIARGQKIPIFSG AGLPHNEIAAQICRQAGLVQHKENKDDFAIVFAAMGVNMETARFFKREFAQTGACNVVLFLNLANDPTIERIITPRLAL TVAEFLAYQCNKHVLVIMTDMTSYAEALREVSAAREEVPGRRGFPGYMYTDLSTIYERAGRVQGRPGSITQIPILTMP NDDITHPI

Table 4-LD

Target ID	SEQ ID NO	Sequences*	Example Gi-number and species
LD001	49	GGCCCCAAGAAGCATTTGAAGCGTTT	3101175 (Drosophila melanogaster), 92477283 (Drosophila erecta)
LD001	50	AATGCCCCAAAAGCATGGATGTTGGATAAATTGGGAGGTGT	70909480 (Carabus granulatus), 77325294 (Chironomus tentans), 900945 (Ctenocephalides felis), 60297219 (Diaprepes abbreviatus), 37951951 (Ips pini), 75735533 (Tribolium castaneum), 22039624 (Ctenocephalides felis)
LD001	51	GAAGTTACTAAGATTGTTATGCA	33368080 (Glossina morsitans)
LD001	52	ATTGAAAAAACTGGTGAATTTTTCCG	60297219 (Diaprepes abbreviatus)
LD001	53	ACACACGACGCGCCGCACCATCCGCT	27555937 (Anopheles gambiae), 33355008 (Drosophila yakuba), 22474232 (Helicoverpa armigera), 3738704 (Manduca sexta)
LD001	54	ACACACGACGCGCCGCACCATCCGCTA	92477283 (Drosophila erecta)
LD001	55	CCCAAGAAGCATTTGAAGCGTTTG	92954810 (Drosophila ananassae), 92231605 (Drosophila willistoni)
LD002	56	GCAATGTCATCCATCATGTCGTG	17861597 (Drosophila melanogaster), 92223378 (Drosophila willistoni), 92471309 (Drosophila erecta)
LD003	57	CAGGTTCTTCCTCTTGACGCGGTCCAGG	24975810 (Anopheles gambiae), 3478578 (Antheraea yamamai), 42764756 (Armigeres subalbatus), 24661714 (Drosophila melanogaster), 68267151 (Drosophila simulans), 33355000 (Drosophila yakuba), 49532931 (Plutella xylostella), 76552910 (Spodoptera frugiperda), 92959651 (Drosophila ananassae), 92467993 (Drosophila erecta)
LD003	58	TTGAGCGGAGAAGTCAATATGCTTCT	49558930 (Boophilus microplus)
LD003	59	TTCCAAGAAATCTTCAATCTTCAAACCCAA	62238687 (Diabrotica virgifera), 76169907 (Diploptera punctata), 67872253 (Drosophila pseudoobscura), 55877642 (Locusta migratoria), 66548956 (Apis mellifera)

LD003	60	TTCATCCAACACTCCAATACG	22040140 (Ctenocephalides felis)
LD003	61	AAGAGCATTGCCTTCAAACAACCT	2459311 (Antheraea yamamai)
LD003	62	AGTTCTCTGGCAGCTTTACGGATTT	76169907 (Diploptera punctata)
LD003	63	CCACACTTCACGTTTGTTCCT	57963694 (Heliconius melpomene)
LD003	64	CCGTATGAAGCTTGATTACGT	108742527 (Gryllus rubens), 108742525 (Gryllus pennsylvanicus), 108742523 (Gryllus veletis), 108742521 (Gryllus bimaculatus), 108742519 (Gryllus firmus), 109194897 (Myzus persicae)
LD003	65	AGGAACAAACGTGAAGTGTGGCG	109194897 (Myzus persicae)
LD006	66	AGCGCTATGGGTAAGCAAGCTATGGG	27819970 (Drosophila melanogaster)
LD006	67	TGTTATACTGGTTATAATCAAGAAGAT	55801622 (Acyrthosiphon pisum), 66535130 (Apis mellifera)
LD007	68	GAAGTTCAGCACGAATGTATTCC	50563603 (Homalodisca coagulata)
LD007	69	CAAGCAAGTGATGATGTTCAGTGCCAC	50563603 (Homalodisca coagulata)
LD007	70	TGCAAGAAATTCATGCAAGATCC	21068658 (Chironomus tentans)
LD007	71	AAATGAAAAGAATAAAAAATT	49201437 (Drosophila melanogaster)
LD007	72	CAGAATTTCCCAGCCATAGGAAT	67895225 (Drosophila pseudoobscura)
LD007	73	AGCAGTTCAAAGATTTCCAGAAG	77848709 (Aedes aegypti)
LD007	74	TTCCAAATCAGCAAAGAGTACGAG	91083250 (Tribolium castaneum)
LD010	75	TACCCGCAGTTCATGTACCAT	29558345 (Bombyx mori)
LD010	76	CAGTCGCTGATCATGATCCAGCC	49559866 (Boophilus microplus)
LD010	77	CTCATGGACACGTTCTTCCAGAT	60293559 (Homalodisca coagulata)
LD010	78	GGGGCTGCATACAGTTCATCAC	92971011 (Drosophila mojavensis)
LD010	79	CCCGCAGTTCATGTACCATTTG	92952825 (Drosophila ananassae)
LD010	80	GACAATGCCAAATACATGAAGAA	92921253 (Drosophila virilis)

LD010	81	TTCGATCAGGAGGCAGCCGCCAGTG	92921253 (Drosophila virilis)
LD011	82	AGCAGGGCTGGCATGGCGACAAA	28317118 (Drosophila melanogaster)
LD011	83	TTCTCAAAGTTGTAGTTAGATTTGGC	37951963 (Ips pini)
LD011	84	TACTGCAAATTCTTCTTCCTATG	55883846 (Locusta migratoria)
LD011	85	GGTACATTCTTGTATGTAACTC	67885713 (Drosophila pseudoobscura)
LD011	86	TCAAACATGATAATAGCACACTG	68771114 (Acanthoscurria gomesiana)
LD011	87	TCTCCTGACCGGCAGTGTCCCATA	17944197 (Drosophila melanogaster), 77843537 (Aedes aegypti), 94469127 (Aedes aegypti), 24664595 (Drosophila melanogaster)
LD011	88	GCTACTTTGGGAGTTGAAGTCCATCC	101410627 (Plodia interpuntella)
LD011	89	TAACTACAACTTTGAGAAGCCTTTCCT	90813103 (Nasonia vitripennis)
LD011	90	AAGTTTGGTGGTCTCCGTGATGG	84267747 (Aedes aegypti)
LD014	91	GCAGATCAAGCATATGATGGC	9732 (Manduca sexta), 90814338 (Nasonia vitripennis), 87266590 (Choristoneura fumiferana)
LD014	92	ATCAAGCATATGATGGCTTTCATTGA	75470953 (Tribolium castaneum), 76169390 (Diploptera punctata)
LD014	93	AATATTGAAAAGGGGCGCCCTTGT	78055682 (Heliconius erato)
LD014	94	CAACGTCTCAAGATTATGGAATA	37659584 (Bombyx mori)
LD014	95	ATTATGGAATATTATGAGAAGAAAGA	66556286 (Apis mellifera)
LD014	96	AACAAAATCAAGATCAGCAATACT	25958976 (Curculio glandium)
LD016	97	ATGTCGTCGTTGGGCATAGTCA	27372076 (Spodoptera littoralis)
LD016	98	GTAGCTAAATCGGTGTACATGTAACCTGGGAAACCACGACG	27372076 (Spodoptera littoralis), 55797015 (Acyrthosiphon pisum), 73615307 (Aphis gossypii), 4680479 (Aedes aegypti), 9713 (Manduca sexta), 76555122 (Spodoptera frugiperda), 237458 (Heliothis virescens), 53883819 (Plutella xylostella), 22038926 (Ctenocephalides felis), 101403557 (Plodia interpuntella), 92969578 (Drosophila grimshawi), 91829127

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			(Bombyx mori)
LD016	99	GCAGATACCTCACGCAAAGCTTC	62239897 (Diabrotica virgifera)
LD016	100	GGATCGTTGGCCAAATTCAAGAACACAGGCA	67882712 (Drosophila pseudoobscura), 92985459 (Drosophila grimshawi)
LD016	101	TTCTCCATAGAACCGTTCTCTTCGAAATCCTG	4680479 (Aedes aegypti), 27372076 (Spodoptera littoralis)
LD016	102	GCTGTTTCCATGTTAACACCCAT	49558344 (Boophilus microplus)
LD016	103	TCCATGTTAACACCCATAGCAGCGA	62238871 (Diabrotica virgifera)
LD016	104	CTACAGATCTGGGCAGCAATTTCATTGTG	22038926 (Ctenocephalides felis), 16898595 (Ctenocephalides felis)
LD016	105	GGCAGACCAGCTCGCAGAGAAAT	22038926 (Ctenocephalides felis), 16898595 (Ctenocephalides felis)
LD016	106	GAGAAAATGGGGATCTTCTGACCACGAGCAATGGAGTTCATCACGTC	4680479 (Aedes aegypti), 9713 (Manduca sexta), 22038926 (Ctenocephalides felis), 16898595 (Ctenocephalides felis), 67877903 (Drosophila pseudoobscura), 10763875 (Manduca sexta), 76554661 (Spodoptera frugiperda), 77905105 (Aedes aegypti), 50562965 (Homalodisca coagulata), 27372076 (Spodoptera littoralis)
LD016	107	ATGGAGTTCATCACGTCAATAGC	9713 (Manduca sexta), 237458 (Heliothis virescens), 76554661 (Spodoptera frugiperda), 22474331 (Helicoverpa armigera)
LD016	108	GTCTGGATCATTCCTCAGGATAGATACGGGACCACGGATTGATTGGTTGACCCTGGATGTCCAAGAAGTCTTCAGCCAAAATTGGGGGACCTTTGTC	16898595 (Ctenocephalides felis), 22038926 (Ctenocephalides felis), 50562965 (Homalodisca coagulata), 49395165 (Drosophila melanogaster), 6901845 (Bombyx mori), 9293100 (Drosophila virilis)
LD016	109	ATTGGGGGACCTTTGTCGATGGG	10763875 (Manduca sexta)

Target ID	SEQ ID NO	Sequence	Example Gi-number and species
LD016	110	ATGGGTTTTCCTGATCCATTGAAAACACGTCCCAACATATCTTCAGAAACAGGAGTCCTCAAAATATCTCCTGTGAATTCACAAGCGGTGTTTTTGGGCGTCGATTCCTGATGTGCCCTCGAACACTTGAACCACCAGCTTT	49395165 (Drosophila melanogaster), 55905051 (Locusta migratoria)
LD016	111	ACAGCTTTTGACCCACTGACTTCCAG	21642266 (Amblyomma variegatum)
LD016	112	GACCCACTGACTTCCAGAACTTGTCCCGAACGTATAGTGCCATCAGCCAGTTTGAGT	49395165 (Drosophila melanogaster)
LD016	113	GGACCGTTCACCACCAGACACAGT	24646342 (Drosophila melanogaster)
LD016	114	GACTGTGTCTGGTGTGAACGGTCCTCT	103769163 (Drosophila melanogaster), 92048971 (Drosophila willistoni)
LD016	115	TTCTCTTCGAAATCCTGTTTGAA	84116133 (Dermatophagoides farinae)
LD016	116	GACTGTGTVTGGTGTGAACGGTCC	24646342 (Drosophila melanogaster)
LD016	117	GGTCGTCGTGTGGTTTCCCAGGTTACATGTACACCGATTT	92231646 (Drosophila willistoni), 91755555 (Bombyx mori), 84228226 (Aedes aegypti)
LD016	118	TGACAGCTGCCGAATTCTTGGC	92231646 (Drosophila willistoni)
LD018	119	CAAGTCACCGACGACCACCAACCACAA	91080016 (Tribolium castaneum)
LD018	120	ATCGCGATTGACGGTGGAGCC	91080016 (Tribolium castaneum)
LD027	121	AGACGATCGGTTGGTTAAAATC	66501387 (Apis mellifera)
LD027	122	GATATGGGAGCATGTGAAATATA	77326476 (Chironomus tentans)
LD027	123	TTAGAGAATTGTTTGAATTAT	90129719 (Bicyclus anynana)

Table 4-PC

Target ID	SEQ ID NO	Sequence*	Example Gi-number and species
PC001	275	AAAATTGTCATGCAAAGGTTGAT	37952206 (Ips pini)

PC001	276	AAAGCATGGATGTTGGACAAA	98994282 (Antheraea mylitta) 109978109 (Gryllus pennsylvanicus) 55904580 (Locusta migratoria)
PC001	277	AAAGCATGGATGTTGGACAAATT	31366663 (Toxoptera citricida)
PC001	278	AAAGCATGGATGTTGGACAAATTGGG	60311985 (Papilio dardanus)
PC001	279	AAAGCATGGATGTTGGACAAATTGGGGGGGTGT	37951951 (Ips pini)
PC001	280	AAATACAAGTTGTGTAAAGTAA	84647793 (Myzus persicae)
PC001	281	AAGCATGGATGTTGGACAAATTGGGGGGGGTGT	70909486 (Mycetophagus quadripustulatus)
PC001	282	ATGGATGTCATTACTATTGGAGAA	25957367 (Carabus granulatus)
PC001	283	CATCAAATTTGAATCTGGCAACCT	37952206 (Ips pini)
PC001	284	CATGATGGCAGAACCATTCGTTA	60303405 (Julodis onopordi)
PC001	285	CCAAAGCATGGATGTTGGACAA	90138164 (Spodoptera frugiperda)
PC001	286	CCATTTTTGGTAACACATGATGG	111011915 (Apis mellifera)
PC001	287	CCCAAAGCATGGATGTTGGACAA	50565112 (Homalodisca coagulata)
PC001	288	CCCAAAGCATGGATGTTGGACAAA	103790417 (Heliconius erato) 101419954 (Plodia interpunctella)
PC001	289	CCCAAAGCATGGATGTTGGACAAATT	73612809 (Aphis gossypii)
PC001	290	CCCAAAGCATGGATGTTGGACAAATTGGG	77329254 (Chironomus tentans)
PC001	291	CCCAAAGCATGGATGTTGGACAAATTGGGGGGGTGT	60305420 (Mycetophagus quadripustulatus)
PC001	292	CCCAAAGCATGGATGTTGGACAAATTGGGGGGGGTGTCTTCGC	84647995 (Myzus persicae)
PC001	293	CGTTACCCTGACCCCAACATCAA	73613065 (Aphis gossypii)
PC001	294	GCAAAATACAAGTTGTGTAAAGTAA	83662334 (Myzus persicae)
PC001	295	GCATGGATGTTGGACAAATTGGG	92969396 (Drosophila grimshawi)
PC001	296	GCATGGATGTTGGACAAATTGGGGG	67885868 (Drosophila pseudoobscura)
PC001	297	GCATGGATGTTGGACAAATTGGGGGGGTGT	25956479 (Biphyllus lunatus)
PC001	298	GCATGGATGTTGGACAAATTGGGGGGGGTGTCT	90814901 (Nasonia vitripennis)
PC001	299	GCTCCCAAAGCATGGATGTTGGA	110260785 (Spodoptera frugiperda)
PC001	300	GCTCCCAAAGCATGGATGTTGGACAA	76551269 (Spodoptera frugiperda)
PC001	301	GCTCCCAAAGCATGGATGTTGGACAAA	56085210 (Bombyx mori)
PC001	302	GCTCCCAAAGCATGGATGTTGGACAAATTGGG	22474232 (Helicoverpa armigera)
PC001	303	GGTCCCAAAGGAATCCCATTTTTGGT	50565112 (Homalodisca coagulata)
PC001	304	GGTGTCTTCGCCCCTCGTCCA	82575022 (Acyrthosiphon pisum)
PC001	305	GTGAAGTCACTAAAATTGTCATGCAAAG	25956820 (Biphyllus lunatus)

		Sequence	Accession (Organism)
PC001	306	TCCACCGGGCCTCACAAGTTGCG	58371410 (Lonomia obliqua)
PC001	307	TCCCAAAGCATGGATGTTGGA	110263957 (Spodoptera frugiperda)
PC001	308	TGCTCCCAAAGCATGGATGTTGGACAA	48927129 (Hydropsyche sp.)
PC001	309	TGGATGTTGGACAAATTGGGGGGTGTCT	90814560 (Nasonia vitripennis)
PC003	310	AAAATTGAAGATTTCTTGGAA	10742519 (Gryllus firmus) 109978291 (Gryllus pennsylvanicus) 62083482 (Lysiphlebus testaceipes) 56150446 (Rhynchosciara americana)
PC003	311	AACAAACGTGAAGTGTGGAGAGT	57963755 (Heliconius melpomene)
PC003	312	AAGTCGCCCTTCGGGGGTGGCCG	77884026 (Aedes aegypti)
PC003	313	ACTTCTCCCTGAAGTCGCCCTTCGG	92992453 (Drosophila mojavensis)
PC003	314	AGATTGTTTGAAGGTAATGCACTTCT	60298816 (Diaphorina citri)
PC003	315	ATCCGTAAAGCTGCTCGTGAA	33373689 (Glossina morsitans)
PC003	316	ATCGACTTCTCCCTGAAGTCGCC	92987113 (Drosophila grimshawi)
PC003	317	ATCGACTTCTCCCTGAAGTCGCCCT	1899548 (Drosophila melanogaster)
PC003	318	ATGAAGCTTGATTATGTTTGGGTCTGAAAATTGAAGATTTCT TGGAAAGA	71539459 (Diaphorina citri)
PC003	319	ATTGAAGATTTCTTGGAAAGA	62240069 (Diabrotica virgifera)
PC003	320	CACATCGACTTCTCCCTGAAGTC	71550961 (Oncometopia nigricans)
PC003	321	CAGAAGCACATCGACTTCTCCCTGAAGTCGCCCTTCGG	68267151 (Drosophila simulans) 33355000 (Drosophila yakuba)
PC003	322	CAGAAGCACATCGACTTCTCCCTGAAGTCGCCCTTCGGGGG	2152719 (Drosophila melanogaster)
PC003	323	CGACTTCTCCCTGAAGTCGCC	107324644 (Drosophila melanogaster)
PC003	324	CTCCCTGAAGTCGCCCTTCGG	15461311 (Drosophila melanogaster)
PC003	325	CTGGACTCGCGAGAAGCACATCGACTTCTCCCTGAA	38624772 (Drosophila melanogaster)
PC003	326	GACTTCTCCCTGAAGTCGCCCTTCGG	92959651 (Drosophila ananassae) 92981958 (Drosophila mojavensis) 76552467 (Spodoptera frugiperda)
PC003	327	GCTAAAATCCGTAAAGCTGCTCGTGA	60296953 (Diaprepes abbreviatus)
PC003	328	GCTAAAATCCGTAAAGCTGCTCGTGAACT	77329341 (Chironomus tentans)
PC003	329	GTGCGCAAGCAGGTGGTGAACATCCC	60312414 (Papilio dardanus)
PC003	330	TACACTTTGGCTAAAATCCGTAAAGCTGC	22040140 (Ctenocephalides felis)
PC003	331	TCGCGAGAAGCACATCGACTTCTC	18883211 (Anopheles gambiae)

PC003	332	TCGCAGAAGCACATCGACTTCTCCCTGAAGTCGCCCTTCGG	92963738 (Drosophila grimshawi)
PC003	333	TCTCCCTGAAGTCGCCCTTCGG	38047836 (Drosophila yakuba) 27260897 (Spodoptera frugiperda)
PC003	334	TGAAAATTGAAGATTTCTTGGAA	61646980 (Acyrthosiphon pisum) 73615225 (Aphis gossypii) 83661890 (Myzus persicae) 37804775 (Rhopalosiphum padi) 30049209 (Toxoptera citricida)
PC003	335	TGAAAATTGAAGATTTCTTGGAAAGA	90813959 (Nasonia vitripennis)
PC003	336	TGGACTCGCAGAAGCACATCGACTTCTCCCT	25959408 (Meladema coriacea)
PC003	337	TGGCTAAAATCCGTAAAGCTGC	76169907 (Diploptera punctata)
PC003	338	TGGGTCTGAAAATTGAAGATTTCTTGGA	34788046 (Callosobruchus maculatus)
PC003	339	TTCTCCCTGAAGTCGCCCTTCGG	107331362 (Drosophila melanogaster) 110240861 (Spodoptera frugiperda)
PC003	340	TTGGGTCTGAAAATTGAAGATTTCTTGGAAAG	37952462 (Ips pini)
PC003	341	GGGTGCGCAAGCAGGTGGTGAAC	110887729 (Argas monolakensis)
PC005	342	CTCCTCAAAAGTACAGGGAGGCCAAGAA	63512537 (Ixodes scapularis)
PC005	343	AAAAGAAGGTGTGTGTTGGATCC	33491424 (Trichoplusia ni)
PC005	344	AAAAAGAAGGTGTGGTTGGATCCAAATGAAATCAA	91759273 (Bombyx mori) 55908261 (Locusta migratoria)
PC005	345	AAAGAAGGTGTGGTTGGATCCAAATGAAATCA	101414616 (Plodia interpunctella)
PC005	346	AACACCAACTCAAGACAAAACAT	25957531 (Cicindela campestris)
PC005	347	AACACCAACTCAAGACAAAACATCCGTAA	25958948 (Curculio glandium)
PC005	348	AACTCAAGACAAAACATCCGTAA	60314333 (Panorpa cf. vulgaris APV-2005)
PC005	349	AAGAACACTGAGCCAGAAGGAAGGGAAGGCATTGTGG	25958948 (Curculio glandium)
PC005	350	AATGAAATCAACGAAATCGCCAACAC	92979160 (Drosophila grimshawi) 92232072 (Drosophila willistoni)
PC005	351	ATGGAGTACATCCACAAGAAGAAGGC	15454802 (Drosophila melanogaster)
PC005	352	CAAGATGCTGTCTGACCAGGC	67872905 (Drosophila pseudoobscura)
PC005	353	CGCCTCCTCAAAAAGTACAGGGAGGC	75471260 (Tribolium castaneum)
PC005	354	CGTATCGCCACCAAGAAGCAG	68267374 (Drosophila simulans)
PC005	355	CTGTACATGAAAGCGAAGGGTAA	25957246 (Carabus granulatus)
PC005	356	GAACAAGAGGGTCCTTATGGAG	90977107 (Aedes aegypti)

PC005	357	GAACAAGAGGGTCCTTATGGAGTACATCCA	40544432 (Tribolium castaneum)
PC005	358	GAGCGTATCGCCACCAAGAAGCA	92480972 (Drosophila erecta) 33354497 (Drosophila yakuba)
PC005	359	GAGTACATCCACAAGAAGAGGC	15516174 (Drosophila melanogaster)
PC005	360	GATCCAAATGAAATCAACGAAAT	56149737 (Rhynchosciara americana)
PC005	361	GCCAACACCAACTCAAGACAAAACATCCG	103019061 (Tribolium castaneum)
PC005	362	GCCAACAACCAACTCAAGACAACAAAACATCCGTAAGCTCAT	56149737 (Rhynchosciara americana)
PC005	363	GGCAAAAAGAAGGTGTGGTTGGATCCAAATGAAATCA	101417042 (Plodia interpunctella)
PC005	364	GGGTCCTTATGGAGTACATCCACAAGAA	67885759 (Drosophila pseudoobscura)
PC005	365	TGCGATGCGGCAAAAAGAAGGT	56149531 (Rhynchosciara americana)
PC005	366	TGGTTGGATCCAAATGAAATCAACGAAAT	15355452 (Apis mellifera) 83662749 (Myzus persicae)
PC005	367	TTGGATCCAAATGAAATCAACGAAAT	110985444 (Apis mellifera) 11158439 (Myzus persicae)
PC010	368	CCGCAGTTCATGTACCATTTG	92952825 (Drosophila ananassae)
PC010	369	CTGATGGAGATGAAGCAGTGCTGCAATTC	58395529 (Anopheles gambiae str. PEST)
PC010	370	GACGTGCTCAGATGGGTGGACAG	56152422 (Rhynchosciara americana)
PC010	371	GCCCGAGCCTGTGTTGTTGGA	92939820 (Drosophila virilis)
PC010	372	GGCACATGCTGCTGATGCGTGAGGAT	83937570 (Lutzomyia longipalpis)
PC010	373	GGGCCACATGGTCATGGGCGATTC	3337934 (Drosophila melanogaster)
PC014	374	AAGATCATGGAGTACTACGAGAA	85577611 (Aedes aegypti)
PC014	375	ACGAGAAAAAGGAGAAGCAAG	67838315 (Drosophila pseudoobscura)
PC014	376	ATGGAGTACTACGAGAAAAAGGAGAAGCAAGT	92928915 (Drosophila virilis)
PC014	377	CAAAAACAAATCAAACACACATGATGGC	82574001 (Acyrthosiphon pisum) 111160670 (Myzus persicae)
PC014	378	CTCAAGATCATGGAGTACTACGA	55692554 (Drosophila yakuba)
PC014	379	CTCAAGATCATGGAGTACTACGAGAA	92942301 (Drosophila ananassae) 92476196 (Drosophila erecta) 53884266 (Plutella xylostella)
PC014	380	GAACAAGAAGCCAATGAGAAAGC	111160670 (Myzus persicae)
PC014	381	GACTCAAGATCATGGAGTACT	112432414 (Myzus persicae)
PC014	382	GATGTTCAAAAACAAATCAAACACACATGATGGC	73618688 (Aphis gossypii)
PC014	383	TACTACGAGAAAAAGGAGAAGC	62239529 (Diabrotica virgifera)

PC014	384	TTCATTGAACAAGAAGCCAATGA	15357365 (Apis mellifera)
PC016	385	ACACGACCGGCGGCGCTCGTAAAT	75710699 (Tribolium castaneum)
PC016	386	ACCAGCACGTGCTTCTCGCACTGGTAGGCCAAGAATTCGGC	92048971 (Drosophila willistoni)
PC016	387	AGCACGTGCTTCTCGCACTGGTAGGC	92985459 (Drosophila grimshawi)
PC016	388	ATACGCGACCACGGGGTTGATCGG	18868609 (Anopheles gambiae) 31206154 (Anopheles gambiae str. PEST)
PC016	389	ATCGGTGTACATGTAACCGGGGAAACC	2921501 (Culex pipiens) 62239897 (Diabrotica virgifera) 92957249 (Drosophila ananassae) 92477818 (Drosophila erecta) 92965644 (Drosophila grimshawi) 24646342 (Drosophila melanogaster) 67896654 (Drosophila pseudoobscura) 75710699 (Tribolium castaneum)
PC016	390	ATCGTTGGCCAAGTTCAAGAACAG	92950254 (Drosophila ananassae)
PC016	391	CACGTGCTTCTCGCACTGGTAGGCCAAGAA	4680479 (Aedes aegypti)
PC016	392	CCAGTCTGGATCATTTCCTCGGG	67884189 (Drosophila pseudoobscura)
PC016	393	CCAGTCTGGATCATTTCCTCGGGGATA	92940287 (Drosophila virilis)
PC016	394	CGCTCGATGGTCGGATCGTTGGCCAAGTTCAAGAACA	2921501 (Culex pipiens)
PC016	395	CGCTCGATGGTCGGATCGTTGGCCAAGTTCAAGAACAGACA CACGTTCTCCAT	92477818 (Drosophila erecta) 15061308 (Drosophila melanogaster)
PC016	396	CGTGCTTCTCGCACTGGTAGGCCAAGAA	13752998 (Drosophila melanogaster)
PC016	397	CTGGCAGTTTCCATGTTGACACCCATAGC	16898595 (Ctenocephalides felis)
PC016	398	CTTAGCATCAATACCTGATGT	61646107 (Acyrthosiphon pisum)
PC016	399	GACATGTCGGTCAAGATGACCAGCACGTG	9713 (Manduca sexta)
PC016	400	GACATGTCGGTCAAGATGACCAGCACGTGCTTCTCGCACTG	92933153 (Drosophila virilis)
PC016	401	GACATGTCGGTCAAGATGACCAGCACGTGCTTCTCGCACTG GTA	2921501 (Culex pipiens)
PC016	402	GAGCCGTTCTCTTCGAAGTCCTG	237458 (Heliothis virescens)
PC016	403	GATGACCAGCACGTGCTTCTC	18883474 (Anopheles gambiae)
PC016	404	GATGACCAGCACGTGCTTCTCGCACTG	92477818 (Drosophila erecta)
PC016	405	GATGACCAGCACGTGCTTCTCGCACTGGTAGGCCAAGAA	15061308 (Drosophila melanogaster) 67883622 (Drosophila pseudoobscura)

PC016	406	GATGACCAGCACGTGCTTCTCGCACTGTGGTAGGCCAAGAATTCGGC	31206154 (Anopheles gambiae str. PEST)
PC016	407	GATGGGGATCTGCGTGATGGA	101403557 (Plodia interpunctella)
PC016	408	GATGGGGATCTGCGTGATGGAGCCGTTGCGGCCCTCCAC	53883819 (Plutella xylostella)
PC016	409	GGAATAGGATGGGTGATGTCGTCGTTGGGCATAGT	110240379 (Spodoptera frugiperda)
PC016	410	GGAATAGGATGGGTGATGTCGTCGTTGGGCATAGTCA	27372076 (Spodoptera littoralis)
PC016	411	GGATCGTTGGCCAAGTTCAAGAA	91757299 (Bombyx mori)
PC016	412	GGATCGTTGGCCAAGTTCAAGAACA	103020368 (Tribolium castaneum)
PC016	413	GGATCGTTGGCCAAGTTCAAGAACAG	237458 (Heliothis virescens)
PC016	414	GGATGGGTGATGTCGTCGTTGGGCAT	101403557 (Plodia interpunctella)
PC016	415	GGCAGTTTCCATGTTGACACCCATAGC	4680479 (Aedes aegypti)
PC016	416	GGCATAGTCAAGATGGGGATCTG	92924977 (Drosophila virilis)
PC016	417	GTCTGGATCATTTCCTCGGGATA	92966144 (Drosophila grimshawi)
PC016	418	GTGATGATGCGCTCGATGGTCGGATCGTTGGCCAAGTTCAAGAACAGACACGTTCTCCAT	15514750 (Drosophila melanogaster)
PC016	419	GTGTACATGTAACCGGGGAAACC	92924977 (Drosophila virilis)
PC016	420	GTTTCCATGTTGACACCCATAGC	91826756 (Bombyx mori)
PC016	421	TCAATGGGTTTTCCTGATCCATTGAA	49395165 (Drosophila melanogaster) 99009492 (Leptinotarsa decemlineata)
PC016	422	TCATCCAGCACAGACTTGCCAG	10763875 (Manduca sexta)
PC016	423	TCATCCAGCACAGACTTGCCAGG	9713 (Manduca sexta)
PC016	424	TCCATGTTGACACCCATAGCAGC	92962756 (Drosophila ananassae)
PC016	425	TCCATGTTGACACCCATAGCAGCAAACAC	60295607 (Homalodisca coagulata)
PC016	426	TCGAAGTCCTGCTTGAAGAACCTGGC	101403557 (Plodia interpunctella)
PC016	427	TCGATGGTCGGATCGTTGGCCAAGTTCAAGAACAGACACACGTTCTCCAT	4680479 (Aedes aegypti)
PC016	428	TCGGATCGTTGGCCAAGTTCAAGAACAGACACACGTTCTCCAT	2793275 (Drosophila melanogaster)
PC016	429	TCGTTGGCCAAGTTCAAGAACAG	90137502 (Spodoptera frugiperda)
PC016	430	TGGGTGATGTCGTCGTTGGGCAT	53883819 (Plutella xylostella)
PC016	431	TTCTCGCACTGGTAGGCCAAGAA	110240379 (Spodoptera frugiperda) 27372076 (Spodoptera littoralis)
PC016	432	TTCTCTTCGAAGTCCTGCTTGAAGAACCTGGC	9713 (Manduca sexta)
PC016	433	TTGGCCAAGTTCAAGAACAGACACACGTT	55905051 (Locusta migratoria)

PC016	434	GTTTCCATGTTGACACCCATAGCAGCAAA	84116133 (Dermatophagoides farinae)

Table 4-EV

Target ID	SEQ ID NO	Sequence *	Example GI-number and species
EV005	533	AAGCGACGTGAAGAGCGTATCGC	76553206 (Spodoptera frugiperda)
EV005	534	ATTAAAGATGGTCTTATTATTAA	15355452 (Apis mellifera)
EV005	535	CGTAAGCGACGTGAAGAGCGTATCGC	33491424 (Trichoplusia ni)
EV005	536	GGTCGTCATTGTGGATTTGGTAAAAG	60314333 (Panorpa cf. vulgaris APV-2005)
EV005	537	TGCGATGCGGCAAGAAGAAGGT	15048930 (Drosophila melanogaster)
EV005	538	TGCGGCAAGAAGAAGGTTTGG	93002524 (Drosophila mojavensis) 92930455 (Drosophila virilis) 92044532 (Drosophila willistoni)
EV005	539	TTGTGGATTTGGTAAAAGGAA	60306723 (Sphaerius sp.)
EV010	540	CAAGTGTTCAATAATTCACCA	83937567 (Lutzomyia longipalpis)
EV010	541	CATTCTATAGGCACATGTTGATG	29558345 (Bombyx mori)
EV010	542	CTGGGCGGCCACATGGTCATGGG	92476940 (Drosophila erecta) 92977931 (Drosophila grimshawi) 2871327 (Drosophila melanogaster)
EV015	543	AACAGGCCCAATTCCATCGACCC	92947821 (Drosophila ananassae)
EV015	544	AGAGAAAAAATGGACCTCATCGAC	62239128 (Diabrotica virgifera)
EV015	545	CGCCATCCGTCGCTGTTCAAGGCGATCGG	18866954 (Anopheles gambiae)
EV015	546	CTGGCAGTTACCATGGAGAACTTCCGTTACGCCATG	62239128 (Diabrotica virgifera)
EV015	547	GTGATCGTGATGGCGGCCACGAA	18887285 (Anopheles gambiae)
EV015	548	GTGATCGTGATGGCGGCCACGAAC	83423460 (Bombyx mori)
EV015	549	TGATGGACGGCCATGAAGAAAG	91086234 (Tribolium castaneum)
EV016	550	AATATGGAAACAGCCAGATTCTT	109193659 (Myzus persicae)
EV016	551	ATGATCCAGACTGGTATTTCTGC	92938857 (Drosophila virilis)
EV016	552	ATTGATGTGATGAATTCCATTGCC	55905051 (Locusta migratoria)
EV016	553	GAAATGATCCAGACTGGTATTTCTGC	50562965 (Homalodisca coagulata)
EV016	554	GAAGAAATGATCCAGACTGGTAT	92969748 (Drosophila mojavensis)
EV016	555	GACTGTGTCTGGTGTGAACGG	2286639 (Drosophila melanogaster) 92042621 (Drosophila willistoni)

EV016	556	GATATGTGTGGGTCGTGTGTTTAA	92969748 (Drosophila mojavensis)
EV016	557	GATCCTACCATTGAAAGAATTAT	99011193 (Leptinotarsa decemlineata)
EV016	558	GTGTCTGAAGATATGTTGGGTCGTGT	76554661 (Spodoptera frugiperda)
EV016	559	GTGTCTGGTGTGAACGGACCG	22474331 (Helicoverpa armigera)
EV016	560	TCTGAAGATATGTTGGGTCGTGT	27372076 (Spodoptera littoralis)
EV016	561	TGGCATATCAATGTGAGAAGCA	60336595 (Homalodisca coagulata)
EV016	562	TTGAACTTGGCCAATGATCCTACCAT	91827863 (Bombyx mori)

Table 4-AG

Target ID	SEQ ID NO	Sequence *	Example GI-number and species
AG001	621	AAAACTGGTGAATTCTTCCGTTTGAT	37953169 (Ips pini)
AG001	622	AAAGCATGGATGTTGGACAAA	98994282 (Antheraea mylitta) 109978109 (Gryllus pennsylvanicus) 55904580 (Locusta migratoria)
AG001	623	AAAGCATGGATGTTGGACAAATT	31366663 (Toxoptera citricida)
AG001	624	AAAGCATGGATGTTGGACAAATTGGG	60311985 (Papilio dardanus)
AG001	625	AAAGCATGGATGTTGGACAAATTGGGGGGGTGT	37951951 (Ips pini) 109195107 (Myzus persicae)
AG001	626	AAATACAAATTGTGCAAAGTCCG	25958703 (Curculio glandium)
AG001	627	AACTTGTGCATGATCACCGGAG	22039624 (Ctenocephalides felis)
AG001	628	AAGCATGGATGTTGGACAAATTGGGGG	112433559 (Myzus persicae)
AG001	629	AAGCATGGATGTTGGACAAATTGGGGGGTGTT	70909486 (Mycetophagus quadripustulatus)
AG001	630	ACTGGTGAATTCTTCCGTTTGAT	77327303 (Chironomus tentans)
AG001	631	ATTGAAAAAACTGGTGAATTCTTCCGTTTGATCTCATGATGTTA A	22039624 (Ctenocephalides felis)
AG001	632	CCAAAGCATGGATGTTGGACAA	90138164 (Spodoptera frugiperda)
AG001	633	CCCAAAGCATGGATGTTGGACAA	48927129 (Hydropsyche sp.) 76551269 (Spodoptera frugiperda)
AG001	634	CCCAAAGCATGGATGTTGGACAAA	91835558 (Bombyx mori) 103783745 (Heliconius erato) 101419954 (Plodia interpunctella)
AG001	635	CCCAAAGCATGGATGTTGGACAAATT	73619372 (Aphis gossypii)

		Sequence	Accession (Species)
AG001	636	CCCAAAGCATGGATGTTGGACAAATTGGGG	77329254 (Chironomus tentans) 22474232 (Helicoverpa armigera)
AG001	637	CCCAAAGCATGGATGTTGGACAAATTGGGGG	84647382 (Myzus persicae)
AG001	638	CCCAAAGCATGGATGTTGGACAAATTGGGGGGTGT	84647995 (Myzus persicae)
AG001	639	CCCAAAGCATGGATGTTGGACAAATTGGGGGGTGTGTT	60305420 (Mycetophagus quadripustulatus)
AG001	640	CTGGATTCATGGATGTGATCA	27617172 (Anopheles gambiae)
AG001	641	GAATTCTTCCGTTTGATCTATGATGT	50565112 (Homalodisca coagulata) 71049326 (Oncometopia nigricans)
AG001	642	GCATGGGATGTTGGACAAATTGGG	92969396 (Drosophila grimshawi) 93001617 (Drosophila mojavensis) 92929731 (Drosophila virilis)
AG001	643	GCATGGGATGTTGGACAAATTGGGGG	67885868 (Drosophila pseudoobscura)
AG001	644	GCATGGGATGTTGGACAAATTGGGGGGTGT	90814901 (Nasonia vitripennis)
AG001	645	GCATGGGATGTTGGACAAATTGGGGGGTGTGTTCGCCCC	25956479 (Biphyllus lunatus)
AG001	646	GCCCCCAAAGCATGGATGGATGTTGGACAA	50565112 (Homalodisca coagulata)
AG001	647	GCTGGATTCATGGATGTGATC	103775903 (Heliconius erato)
AG001	648	GGATCATTCGATATTGTCCACAT	113017118 (Bemisia tabaci)
AG001	649	GGCAACTTGTGCATGATCACCGGAGG	25958703 (Curculio glandium)
AG001	650	TACAAATTGTGCAAAGTCCGCAA	56161193 (Rhynchosciara americana)
AG001	651	TATCCTGCTGGATTCATGGATGT	40934103 (Bombyx mori)
AG001	652	TCACCATTGAAAAAACTGGTGAATTCTTC	62083410 (Lysiphlebus testaceipes)
AG001	653	TGCATGATCACCGGAGGCAGGAA	3478550 (Antheraea yamamai)
AG001	654	TGCATGATCACCGGAGGCAGGAATTTGGG	14627585 (Drosophila melanogaster) 33355008 (Drosophila yakuba)
AG001	655	TGGATGTTGGACAAATTGGGGGGTGT	90814560 (Nasonia vitripennis)
AG001	656	TGTGCATGATCACCGGAGGCAG	92949859 (Drosophila ananassae) 92999306 (Drosophila grimshawi)
AG001	657	TGTGCATGATCACCGGAGGCAGGAATTGGG	67842487 (Drosophila pseudoobscura)
AG005	658	AAGATCGACAGGCATCTGTACCACG	83935651 (Lutzomyia longipalpis)
AG005	659	AAGATCGACAGGCATCTGTACCACGCCCCTGTACATGAAGGC	76552995 (Spodoptera frugiperda)
AG005	660	AAGGGTAACGTGTTCAAGAACAA	18932248 (Anopheles gambiae) 60306606 (Sphaerius sp.)

AG005	661	AAGGGTAACGTGTTCAAGAACAAG	18953735 (Anopheles gambiae) 25957811 (Cicindela campestris) 60311920 (Euclidia glyphica)
AG005	662	AAGGGTAACGTGTTCAAGAACAAGAGAGT	25958948 (Curculio glandium) 90812513 (Nasonia giraulti)
AG005	663	ACAAGAGAAGAGGCTGAGAAGGC	60311700 (Euclidia glyphica)
AG005	664	ATCAAGGATGGTTTGATCATTAA	25957811 (Cicindela campestris)
AG005	665	ATGGAATACATCCACAAGAAGAAG	56149737 (Rhynchosciara americana)
AG005	666	CAAAACATCCGTAAATTGATCAAGGATGGT	60314333 (Panorpa cf. vulgaris APV-2005)
AG005	667	CAAAACATCCGTAAATTGATCAAGGATGGTTTGATCAT	25958948 (Curculio glandium)
AG005	668	CAAGGGTAACGTGTTCAAGAA	476608 (Drosophila melanogaster) 38048300 (Drosophila yakuba)
AG005	669	CAAGGGTAACGTGTTCAAGAACAAG	92946023 (Drosophila ananassae) 2871633 (Drosophila melanogaster) 68267374 (Drosophila simulans) 33354497 (Drosophila yakuba) 83937096 (Lutzomyia longipalpis)
AG005	670	CATCTGTACCACGCCCCTGTACATGAAGGC	101417042 (Plodia interpunctella)
AG005	671	GAAGAAGGCTGAGAAGGCCCCG	40874303 (Bombyx mori)
AG005	672	GACAGGCATCTGTACCACGCCCCTGTACATGAAGGC	90135865 (Bicyclus anynana)
AG005	673	GAGAAGGCCCCGTGCCAAGATGTTG	82572137 (Acyrthosiphon pisum)
AG005	674	GATCCAAATGAAATCAATGAGATTGC	60312128 (Papilio dardanus)
AG005	675	GCTCGTATGCCTCAAAAGGAACTATGG	25957246 (Carabus granulatus)
AG005	676	GGGTAACGTGTTCAAGAACAAG	4447348 (Drosophila melanogaster)
AG005	677	GGTAACGTGTTCAAGAACAAG	18948649 (Anopheles gambiae)
AG005	678	TACATCCACAAGAAGAAGGCTGAGAAG	2871633 (Drosophila melanogaster)
AG005	679	TACCACGCCCCTGTACATGAAGGC	10764114 (Manduca sexta)
AG005	680	TCAATGAGATTGCCAACACCAACTC	83935651 (Lutzomyia longipalpis)
AG005	681	TGATCAAGGATGGTTTGATCAT	77642775 (Aedes aegypti) 27615052 (Anopheles gambiae) 92982271 (Drosophila grimshawi) 67896961 (Drosophila pseudoobscura)
AG005	682	TGATCAAGGATGGTTTGATCATTAAGAA	92042883 (Drosophila willistoni)

AG005	683	TGGTTGGATCCAAATGAAATCA	40867709 (Bombyx mori) 101417042 (Plodia interpunctella)
AG005	684	TGGTTGGATCCAAATGAAATCAA	15355452 (Apis mellifera) 83662749 (Myzus persicae)
AG005	685	TGGTTGGATCCAAATGAAATCAATGAGAT	63013469 (Bombyx mori) 55908261 (Locusta migratoria)
AG005	686	TGTACCACGCCCTGTACATGAAGGC	23573622 (Spodoptera frugiperda)
AG005	687	TTGATCAAGGATGGTTTGATCA	113019292 (Bemisia tabaci)
AG005	688	TTGATCAAGGATGGTTTGATCAT	61674956 (Aedes aegypti)
AG005	689	TTGATGGAATACATCCACAAGAAGAAGGC	41576849 (Culicoides sonorensis)
AG005	690	AGGATGCGTGTCTTGAGGCGTCT	92225847 (Drosophila willistoni)
AG005	691	AAGGCCAAGGGTAACGTGTTCAAGAACAAG	110887217 (Argas monolakensis)
AG010	692	CGTTTGTCTCAAAAGTTTGGAGAATA	110887217 (Argas monolakensis)
AG010	693	GATGTTTAAGATGGGTCGATCG	78539702 (Glossina morsitans)
AG010	694	TTTTACAGGCATATGCTTATGAGGGAAGATTT	110759793 (Apis mellifera)
AG010	695	TTTTTCGAGGTGGTCAATCAGCATTCGGC	55902158 (Locusta migratoria)
AG014	696	AACATGCTGAACCAAGCCCGT	92925934 (Drosophila virilis) 75466802 (Tribolium castaneum)
AG014	697	AACATGCTGAACCAAGCCCGTCT	87266590 (Choristoneura fumiferana) 103779114 (Heliconius erato)
AG014	698	AAGATCATGGAATACTATGAGAAGAA	101403826 (Plodia interpunctella)
AG014	699	AAGATCATGGAATACTATGAGAAGAAGGAGAA	81520950 (Lutzomyia longipalpis)
AG014	700	AATGAAAAGGCCGAGGAAATTGATGC	62239529 (Diabrotica virgifera)
AG014	701	ATGGAATACTATGAGAAGAAGGA	16901350 (Ctenocephalides felis)
AG014	702	CAATCCTCCAACATGCTGAACCA	53148472 (Plutella xylostella)
AG014	703	CAGATCAAGCACATATGATGGCCTTCAT	53148472 (Plutella xylostella)
AG014	704	GCAGATCAAGCACATATGATGGCCTTCAT	87266590 (Choristoneura fumiferana) 9732 (Manduca sexta) 90814338 (Nasonia vitripennis)
AG014	705	GCGGAAGAAGAATTTAACATTGAAAAGGG	50558386 (Homalodisca coagulata) 715552170 (Oncometopia nigricans)
AG016	706	AACGACGACATCACCCATCCTATTC	110248186 (Spodoptera frugiperda) 27372076 (Spodoptera littoralis)

AG016	707	AACGGTTCCATGGAGAACGTGTG	2921501 (Culex pipiens) 92950254 (Drosophila ananassae) 110240379 (Spodoptera frugiperda)
AG016	708	AACGGTTCCATGGAGAACGTGTGTCT	24646342 (Drosophila melanogaster)
AG016	709	AACGGTTCCATGGAGAACGTGTGTCTCTTCTTGAA	91829127 (Bombyx mori)
AG016	710	ATGATCCAGACGACCGGTATCTCCGC	22474040 (Helicoverpa armigera)
AG016	711	ATGCCGAACGACGACATCACCCATCC	31206154 (Anopheles gambiae str. PEST)
AG016	712	CAATGCGAGAAACACGTGCTGGT	9713 (Manduca sexta)
AG016	713	CCGCACAACGAGAAATCGCCGCGCCAAAT	75469507 (Tribolium castaneum)
AG016	714	CGTTTCTTCAAGCAGGACTTCGA	83937868 (Lutzomyia longipalpis)
AG016	715	CTTGGACATCCAAGGTCAACCCATCAACCCATGGTC	104530890 (Belgica antarctica)
AG016	716	GAAATGATCCAGACCGGTATCTC	2921501 (Culex pipiens) 92966144 (Drosophila grimshawi)
AG016	717	GAAATGATCCAGACCGGTATCTCCGGCCATCGACGTGATGAACTC	31206154 (Anopheles gambiae str. PEST)
AG016	718	GAAGAAATGATCCAGACCGGTAT	75469507 (Tribolium castaneum)
AG016	719	GAAGAAGTACCCGGACGTCGTGG	22038926 (Ctenocephalides felis)
AG016	720	GACATCCAAGGTCAACCCATCAA	16898595 (Ctenocephalides felis)
AG016	721	GCCCGTTTCTTCAAGCAGGACTTCGA	31206154 (Anopheles gambiae str. PEST)
AG016	722	GCCGCCCAAATCTGTAGACAGGC	60295607 (Homalodisca coagulata)
AG016	723	GGATCAGGAAAACCCATTGACAAAGGTCC	49395165 (Drosophila melanogaster) 99009492 (Leptinotarsa decemlineata)
AG016	724	GGTTACATGTACACCGATTTGGC	91829127 (Bombyx mori)
AG016	725	GGTTACATGTACACCGATTTGGCCACCAT	77750765 (Aedes aegypti) 9713 (Manduca sexta) 110248186 (Spodoptera frugiperda) 27372076 (Spodoptera littoralis)
AG016	726	GGTTACATGTACACCGATTTGGCCACCATTTACGAA	92231646 (Drosophila willistoni)
AG016	727	GTGTCGGAGGATATGTTGGGGCCG	92460250 (Drosophila erecta) 24646342 (Drosophila melanogaster) 55694673 (Drosophila yakuba)
AG016	728	TACATGTACACCGATTTGGCCACCAT	31206154 (Anopheles gambiae str. PEST)
AG016	729	TTCAACGGATCAGGAAAACCCATTGACAAAGGTCC	99010653 (Leptinotarsa decemlineata)

AG016	730	TTCCCCGGTTACATGTACACCGATTTGGCCAC	2921501 (Culex pipiens) 75710699 (Tribolium castaneum)
AG016	731	TTCCCCGGTTACATGTACACCGATTTGGCCACCAT	62239897 (Diabrotica virgifera) 92957249 (Drosophila ananassae) 92477149 (Drosophila erecta) 67896654 (Drosophila pseudoobscura)
AG016	732	TTCCCCGGTTACATGTACACCGATTTGGCCACCATTTA	92969578 (Drosophila grimshawi)
AG016	733	TTCCCCGGTTACATGTACACCGATTTGGCCACCATTTACGA	103744758 (Drosophila melanogaster)
AG016	734	TTCGCCATCGTGTTCGCGCCATGGGGTGT	31206154 (Anopheles gambiae str. PEST)
AG016	735	TTCTTCAAGCAGGACTTCGAAGA	9713 (Manduca sexta)
AG016	736	TTCTTGAATTTGGCCAACGATCC	92972277 (Drosophila grimshawi) 99011193 (Leptinotarsa decemlineata)
AG016	737	TTCTTGAATTTGGCCAACGATCCCACCATCGAG	67839381 (Drosophila pseudoobscura)
AG016	738	GCCGAATTTTTGGCTTATCAATG	84116133 (Dermatophagoides farinae)

Table 4-TC

Target ID	SEQ ID NO	Sequence *	Example GI-number and species
TC001	813	AAAGCATGGATGTTGGATAAA	70909480 (Carabus granulatus) 16898765 (Ctenocephalides felis) 60298000 (Diaprepes abbreviatus)
TC001	814	AATTTGTGTATGATTACTGGAGG	55904576 (Locusta migratoria)
TC001	815	ACTGGAGGTCGTAACTTGGGGCGTGT	60298000 (Diaprepes abbreviatus)
TC001	816	ATGATTACTGGAGGTCGTAACTTGGGGCGTGT	73619372 (Aphis gossypii) 37804548 (Rhopalosiphum padi)
TC001	817	ATGCAAAGATTGATTAAAGTTGACGG	70909478 (Biphyllus lunatus)
TC001	818	ATTAAAGTTGACGGAAAAGTT	110763874 (Apis mellifera)
TC001	819	ATTGAGAAAACTGGGGAATTCTTCCG	37952206 (Ips pini)
TC001	820	ATTGTTATGCAAAGATTGATTAAAGTTGACGGAAAAGT	70909486 (Mycetophagus quadripustulatus)
TC001	821	CCAAGAAGCATTTGAAGCGTCT	55904580 (Locusta migratoria)
TC001	822	CCAAGAAGCATTTGAAGCGTCTC	83935971 (Lutzomyia longipalpis)
TC001	823	GCGCCCAAAGCATGGATGTTGGA	103790417 (Heliconius erato) 101419954 (Plodia interpunctella)

TC001	824	GGCCCCAAGAAGCATTTGAAGCGT	14700642 (Drosophila melanogaster)
TC001	825	TGATTACTGGAGGTCGTAACTTGGGGCGTGT	73612212 (Aphis gossypii)
TC001	826	TGTATGATTACTGGAGGTCGTAACTTGGGGCGTGT	70909478 (Biphyllus lunatus)
TC001	827	TTGATTTATGATGTTAAGGGA	77325485 (Chironomus tentans)
TC001	828	TTGTGTATGATTACTGGAGGTCGTAA	60305816 (Mycetophagus quadripustulatus)
TC002	829	AAAAACAAACGAGCGGCCATCCAGGC	18920284 (Anopheles gambiae)
TC002	830	ATCGACCAAGAGATCCTCACAGCGAAGAAAACGCGTCGAAA AACAAACGAGCGGCCATCCAGGCC	75717966 (Tribolium castaneum)
TC002	831	CTCCAGCAGATCGATGGCCACCCT	92475657 (Drosophila erecta) 13763220 (Drosophila melanogaster)
TC002	832	TCAAGAGGAAGAAAGCGTACGAAAAGCAGCTCCAGCAGATC GATGGCCACCCTCAGCACCATCGAGATGCAGCGGGGAGGCCCT CGAGGGGGCCCAACACCAACACAGCCGTACTCAAAACGATGA AAAACGCAGCGGACGCGCCCTCAAAAATGCCCACCTCAACATG GATGTTGATGAGGT	75717966 (Tribolium castaneum)
TC010	833	AACCTCAAGTACCAGGACATGCCCGA	90973566 (Aedes aegypti)
TC010	834	AGCCGATTTTGTACAGTTATA	92944620 (Drosophila ananassae)
TC010	835	ATGGACACATTTTCCAAATT	33427937 (Glossina morsitans)
TC010	836	ATGGACACATTTTCCAAATTTTGATTTTCCACGG	56151768 (Rhynchosciara americana)
TC010	837	CAAGTACCAGGACATGCCCGA	18911059 (Anopheles gambiae)
TC010	838	CACATGCTGATGCGGGGAGGACCTC	67893321 (Drosophila pseudoobscura)
TC010	839	CCTCAAGTACCAGGACATGCCCGA	67893324 (Drosophila pseudoobscura)
TC010	840	TCAAGTACCAGGACATGCCCGA	67893321 (Drosophila pseudoobscura)
TC010	841	TTCATGTACCATTTGCGCCGCTC	92952825 (Drosophila ananassae)
TC014	842	AAAATTCAGTCGTCAAACATGCTGAA	76169390 (Diploptera punctata)
TC014	843	AACATGCTGAACCAAGCCCGT	87266590 (Choristoneura fumiferana) 103779114 (Heliconius erato)
TC014	844	CACAGCAACTTGTGCCAGAAAT	92923718 (Drosophila virilis)
TC014	845	GAGAAAGCCGAAGAAATCGATGC	77325830 (Chironomus tentans)
TC014	846	GCCCGCAAACGTCTGGGCGAA	92232132 (Drosophila willistoni)
TC014	847	TAAAAGTGCGTGAAGACCACGT	58371699 (Lonomia obliqua)
TC015	848	ACACTGATGGACGGCGATGAAGAA	78531609 (Glossina morsitans)
TC015	849	ATCGGCGCGGTTGTCGCCAAACAACT	6904417 (Bombyx mori)

TC015	850	CCCGATGAGAAGATCCGGATGAA	83922984 (Lutzomyia longipalpis)
TC015	851	CTGCCCCGATGAGAAGATCCG	92948836 (Drosophila ananassae)
TC015	852	AACGAAACCGGTGCTTTCTTCTT	84116975 (Dermatophagoides farinae)

Table 4-MP

Target ID	SEQ ID NO	Sequence *	Example GI-number and species
MP001	908	AAAGCATGGATGTTGGACAAA	98994282 (Antheraea mylitta) / 108789768 (Bombyx mori) / 109978109 (Gryllus pennsylvanicus) / 55904580 (Locusta migratoria)
MP001	909	AAAGCATGGATGTTGGACAAAT	77325485 (Chironomus tentans) / 37951951 (Ips pini) / 60311985 (Papilio dardanus) / 30031258 (Toxoptera citricida)
MP001	910	AAGAAGCATTTGAAGCGTTTAAAACGCACC	3658572 (Manduca sexta)
MP001	911	AAGCATTTGAAGCGTTTAAACGC	103790417 (Heliconius erato) / 22474232 (Helicoverpa armigera)
MP001	912	AAGCATTTGAAGCGTTTAAAACGCACC	25957217 (Carabus granulatus)
MP001	913	AAGTCCGTACCGACCCTAATTATCCAGC	46994131 (Acyrthosiphon pisum)
MP001	914	ACGCACCCAAAGCATGGATGTT	46999037 (Acyrthosiphon pisum)
MP001	915	ACTATTAGATACGATATTGCA	46998791 (Acyrthosiphon pisum)
MP001	916	ACTGGACCCAAAGGTGTGCCATTTTTAACTACTCATGATGGCCGTACTAT	46997137 (Acyrthosiphon pisum)
MP001	917	AGAAGCATTTGAAGCGTTTAAA	27620566 (Anopheles gambiae)
MP001	918	AGAAGCATTTGAAGCGTTTAAAACGCACC	98994282 (Antheraea mylitta)
MP001	919	AGAAGCATTTGAAGCGTTTAAACGCACCCAAAGCATGGATGTTGGACAAAT	73619191 (Aphis gossypii)
MP001	920	AGTAAGGGAGTTAAATTGACTA	46998791 (Acyrthosiphon pisum)
MP001	921	ATACAAGTTGTGTAAAGTAAAG	29553519 (Bombyx mori)
MP001	922	ATGGATGTTATATCTATCCAAAAGACCAGTGAGCACTTTAGATTGATCTATGATGTGAAAGGTCGTTTCAC	46998791 (Acyrthosiphon pisum)
MP001	923	ATTGATCTATGATGTGAAAGGTCGTTTCAC	46999037 (Acyrthosiphon pisum)
MP001	924	CAAAAGACCAGTGAGCACTTTAGATTGAT	30031258 (Toxoptera citricida)

MP001	925	CACAGAATTACTCCTGAAGAAGC	73619191 (Aphis gossypii)
MP001	926	CACAGAATTACTCCTGAAGAAGCAAAATACAAG	46998791 (Acyrthosiphon pisum) 30031258 (Toxoptera citricida)
MP001	927	CATCCAGGATCTTTTGATATTGTTCACATTAA	31364848 (Toxoptera citricida)
MP001	928	CATCCAGGATCTTTTGATATTGTTCACATTAAGGATGCAAATG AACATATTTTTGCTAC	37804548 (Rhopalosiphum padi)
MP001	929	CATCTAAAATTTTGGATCATATCCGTTTTGAAACTGGAAACTT GTGCATGAT	46998791 (Acyrthosiphon pisum)
MP001	930	CATTTGAAGCGTTTAAACGCACC	30031258 (Toxoptera citricida)
MP001	931	CATTTGAAGCGTTTAAACGCACCCAAAGCATGGATGTT	46998791 (Acyrthosiphon pisum)
MP001	932	CCAAAGCATGGATGTTGGACAA	90138164 (Spodoptera frugiperda)
MP001	933	CCAAGGAGTAAGGGAGTTAAATTGACTA	73615238 (Aphis gossypii) 31364848 (Toxoptera citricida)
MP001	934	CCCAAAGCATGGATGTTGGAC	108789768 (Bombyx mori)
MP001	935	CCCAAAGCATGGATGTTGGACAA	50565112 (Homalodisca coagulata) 48927129 (Hydropsyche sp.) 76551269 (Spodoptera frugiperda)
MP001	936	CCCAAAGCATGGATGTTGGACAAA	56085210 (Bombyx mori) 103792451 (Heliconius erato) 101419954 (Plodia interpunctella)
MP001	937	CCCAAAGCATGGATGTTGGACAAAT	22474095 (Helicoverpa armigera)
MP001	938	CGTCCAAGCACCGGTCCACACAAACT	47537863 (Acyrthosiphon pisum)
MP001	939	CTGGAAACTTGTGCATGATAACTGGAGG	78524585 (Glossina morsitans)
MP001	940	GAAAGACATCCAGGATCTTTTGATATTGTTCACATTAAGGATG CAAATGAACATATTTTTGCTACCCGGATGAACAAATGTTTTTAT TATTGGAAAAGGTCAAAAGAACTACATTTCTCTACCCAAG	46997137 (Acyrthosiphon pisum)
MP001	941	GATCATATCCGTTTTGAAACTGGAAACTTGTGCATGAT	73614725 (Aphis gossypii)
MP001	942	GATGCAAATGAACATATTTTTGCTAC	31364848 (Toxoptera citricida)
MP001	943	GCACCCAAAGCATGGATGTTGGA	70909486 (Mycetophagus quadripustulatus)
MP001	944	GCACCCAAAGCATGGATGTTGGACAAAT	77329254 (Chironomus tentans) 60305420 (Mycetophagus quadripustulatus)
MP001	945	GGATCTTTTGATATTGTTCACAT	60303405 (Julodis onopordi)
MP001	946	GGATCTTTTGATATTGTTCACATTAAGGATGCAAATGAACATA TTTTTGCTAC	73619191 (Aphis gossypii)

MP001	947	GGCCCCAAGAAGCATTTGAAGCGTTTAA	14693528 (Drosophila melanogaster)
MP001	948	GGGCGTGTTGGTATTGTTACCAACAG	31365398 (Toxoptera citricida)
MP001	949	GGGCGTGTTGGTATTGTTACCAACAGGGAAAG	73612212 (Aphis gossypii) / 37804548 (Rhopalosiphum padi)
MP001	950	GGTACAAACTGGACCCAAAGG	60297572 (Diaprepes abbreviatus)
MP001	951	GTTTTTATTATTGGAAAAGGTCAAAAGAACTACATTTCTCT	73619191 (Aphis gossypii) / 31364848 (Toxoptera citricida)
MP001	952	TGAAGTATGCACTTACTGGTGC	73619191 (Aphis gossypii)
MP001	953	TGTAAAGTAAAGAGGGTACAAACTGGACCCAAAGGTGT	73619191 (Aphis gossypii)
MP001	954	TGTGTAAAGTAAAGAGGGTACAAACTGGACCCAAAGGTGT	30031258 (Toxoptera citricida)
MP001	955	TTCTTGCGTAATCGTTTGAAGTATGCACTTACTGGTGCCGAA GTCACCAAGAGTGTCATGCAAAGATTAATCAAGGTTGATGGC AAAGTCCGTACCGACCCTAATTATCCAGC	46998791 (Acyrthosiphon pisum)
MP001	956	TTGGAAAAGGTCAAAAGAACTACATTTCTCT	73615060 (Aphis gossypii)
MP001	957	TTGGATCATATCCGTTTTGAAACTGGAAACTTGTGCATGAT	37804548 (Rhopalosiphum padi)
MP002	958	AAAAAAAATGGTACAACTAATAAACGAGCTGCATTGCAAGC	47537017 (Acyrthosiphon pisum)
MP002	959	AAGAAACGGTACGAACAACAA	15363283 (Apis mellifera)
MP002	960	ACAAGAATTTTTAGAAAAAAATTGAACAAGAAGTAGCGATA GC	47537017 (Acyrthosiphon pisum)
MP002	961	CAAATTGATGGTACCATGTTAACTATTGAACAACAGCG	47537017 (Acyrthosiphon pisum)
MP002	962	GAAGATGCGATACAAAAGCTTCGATCCAC	47537017 (Acyrthosiphon pisum)
MP002	963	GAGTTTCTTTAGTTAAAGTATTCGGTGG	110762684 (Apis mellifera)
MP010	964	AAAAGATGATCCAAATAGTTT	110759793 (Apis mellifera)
MP010	965	AAAATATTATTGATGGACACATTTTTCCATATTTTGATATTCCA	47520567 (Acyrthosiphon pisum)
MP010	966	AATAGTCCTGATGAAACATCATATTATAG	47520567 (Acyrthosiphon pisum)
MP010	967	CAAAAAGATGATCCAAATAGTTTCCGATTGCCAGAAAACTTCA GTTTATATCCACACAGTTCATGTATCATTTAAGAAGGTCTCAATTT CTACAAGTTTTAA	47520567 (Acyrthosiphon pisum)
MP010	968	CAACATTCCAGTGGCTATAAACGAAT	47520567 (Acyrthosiphon pisum)
MP010	969	CACATGTTGATGCGTGAAGATGTTAC	47520567 (Acyrthosiphon pisum)
MP010	970	CCAATTCTGTATAGCTATAGTTTTAATGGTAGGCCAGAACCTG TACTTTGGATACCAG	47520567 (Acyrthosiphon pisum)
MP010	971	CCATCTCAAACACATAATAATATGTATGCTTATGGAGG	55814942 (Acyrthosiphon pisum)
MP010	972	CTCAAAACTCGATTCCCAATGCCTCGGTATATTGACACAGAA	55814942 (Acyrthosiphon pisum)

MP010	973	CAAGGTGGTAGTCAGGCAAGATTTTACTATGCAAAGT	55814942 (Acyrthosiphon pisum)
MP010	974	GGTGATGGTGGGAGCACCAGTTTTGACAGATGATGTAAGCTTGCA	28571527 (Drosophila melanogaster)
MP010	975	GTGGCTGCATACAGTTCATTACGCAGTA	47520567 (Acyrthosiphon pisum)
MP010	976	TAATGGCTCGTATGGTAGTGAAACCGTGCTGAAACTGA	40924332 (Bombyx mori)
MP010	977	TATAGGCACATGTTGATGCGTGAAGAT	47520567 (Acyrthosiphon pisum)
MP010	978	TGGGCTGATCGTACGCTTATACGCTTGTGTCA	47520567 (Acyrthosiphon pisum)
MP016	979	TTAGCTAGGAATTGGGCAGACCCTGT	35508791 (Acyrthosiphon pisum)
MP016	980	AAACAAGATTTTGAGGAAAATGG	35508791 (Acyrthosiphon pisum)
MP016	981	AACCTGGTAAATCAGTTCTTGA	110240379 (Spodoptera frugiperda) 27372076 (Spodoptera littoralis)
MP016	982	AACGACGACATCACCCATCCTATTC	15366446 (Apis mellifera)
MP016	983	AATTTAGCTAATGATCCTACTATTGA	237458 (Heliothis virescens)
MP016	984	ACTATGCCTAACGACGACATCACCCATCC	30124460 (Toxoptera citricida)
MP016	985	ATAGTATTTGCTGCTATGGGTGTTAATATGGAAAC	103020368 (Tribolium castaneum)
MP016	986	CAAATTTGTAGACAAGCTGGTCT	35508791 (Acyrthosiphon pisum)
MP016	987	CATGAAGACAATTTGCTATAGTATTTGCTGCTATGGGTGTTAATATGGAAAC	35508791 (Acyrthosiphon pisum)
MP016	988	CCGATAGATAAAGGACCTCCTATTTGGCTGAAGATTATTGGATATTGAAGGCCAACCTATTAATCCATA	55905051 (Locusta migratoria)
MP016	989	CCTATTTTGGCTGAAGATTAT	30124460 (Toxoptera citricida)
MP016	990	CGTATCATTACCACCACGTCTTGCTTAACTGCTGCTGAATTTTAGCTTA	35508791 (Acyrthosiphon pisum)
MP016	991	CGTCTTGCTTTAACTGCTGCTGAATTTTTAGCTTA	30124460 (Toxoptera citricida)
MP016	992	GAAGAAGTAGCTGGGCGTCGTGGTTTCCCTGGTTACATGTACAC	30124460 (Toxoptera citricida)
MP016	993	GAAGGAAGAAATGGTTCTATCACACAAATACCTATTTTAACTATGCCTAA	73615307 (Aphis gossypii)
MP016	994	GAAGGAAGAAATGGTTCTATCACACAAATACCTATTTTAACTATGCCTAACGA	30124460 (Toxoptera citricida)
MP016	995	GATTTAGCTACAATTTATGAACG	30124460 (Toxoptera citricida)
MP016	996	GCCAGATTCTTTAAACAAGATTTTGAGGAAAATGG	75469507 (Tribolium castaneum)
MP016	997	GCTGCAGGTTTACCACATAATGAGATTGCTGCTCAAATTTG	35508791 (Acyrthosiphon pisum)

Target ID	SEQ ID NO	Sequence	Example Gi-number and species
MP016	998	GCTGGGCGGTGTAGAAGGAAGAAATGGTTCTATCACACAAATACCTATTTTAACTATGCCTAACGA	55813096 (Acyrthosiphon pisum)
MP016	999	GGTTACACATGTACACCGATTTAGCTACAATTTATGAACG	55813096 (Acyrthosiphon pisum) 73615307 (Aphis gossypii)
MP016	1000	GTGGACAAAAATTCCAATATTTTC	55813096 (Acyrthosiphon pisum)
MP016	1001	GTGTCGGAGGATATGTTGGGCCG	92460250 (Drosophila erecta) 2286639 (Drosophila melanogaster) 55694673 (Drosophila yakuba)
MP016	1002	GTTCTTGAATTTAGCTAATGATCCTACTATTGA	82563007 (Acyrthosiphon pisum)
MP016	1003	TCAATGGAGAATGTTTGTTTGTTCTTGAATTTAGCTAATGATCCTACTATTGA	35508791 (Acyrthosiphon pisum) 30124460 (Toxoptera citricida)
MP016	1004	TCAGCTATTGATATCATGAACTCTATTGCTCGTCGTGGACAAAAAATTCCAATATTTTC	35508791 (Acyrthosiphon pisum)
MP016	1005	TCATATGCTGAAGCTTTAAGAGAAGTTTCTGCTCTCG	30124460 (Toxoptera citricida)
MP016	1006	TCCAGAACATATCCTCAAGAAAATGATTCAAACTGGTAT	35508791 (Acyrthosiphon pisum)
MP016	1007	TCTATTGCTCGTGGACAAAAAATTCC	110764393 (Apis mellifera)
MP016	1008	TGTGAAAAGCATGTCTTAGTTATTTAAACTGACATGAGTTCATATGCTGAAGCTTTAAGAGAAGTTTCTGCTCGTCGTGAAGAAGTACCTGGGCGGTCGTGGTTTCCC	55813096 (Acyrthosiphon pisum)
MP016	1009	TTAACTGACATGAGTTCATATGCTGAAGCTTTAAGAGAAGTTTCTGCTGCTCGTGAAGAAGTACCTGG	73615307 (Aphis gossypii)
MP027	1010	TTTTTAAAAATTTTAAAGAAAAAAA	47522167 (Acyrthosiphon pisum)

Table 4-NL

Target ID	SEQ ID NO	Sequence *	Example Gi-number and species
NL001	1161	CTGAAGAAGCTAAGTACAAGCT	16566724 (Spodoptera frugiperda)
NL001	1162	TTCTTCCGTTTGATCTATGATGTTAA	16900870 (Ctenocephalides felis)
NL001	1163	CAGCTGAAGAAGCTAAGTACAA	16900870 (Ctenocephalides felis), 56199521 (Culicoides sonorensis)
NL001	1164	GAGTTCTTCCGTTTGATCTATGATGTTAA	16900945 (Ctenocephalides felis)
NL001	1165	AAGTACAAGCTGTGCAAAGTGAAG	22474232 (Helicoverpa armigera)

NL001	1166	TTCGACATCGTGCACATCAAGGAC	22474232 (Helicoverpa armigera)
NL001	1167	ATCACAGCTGAAGAAGCTAAGTACAAG	25956820 (Biphyllus lunatus)
NL001	1168	TGTGTATGATCACTGGAGGTCGTAA	25957367 (Carabus granulatus)
NL001	1169	AACGTTTCATCATCGGCAAG	27613698 (Anopheles gambiae)
NL001	1170	CCAAAATCATGGACTTCATCA	3738704 (Manduca sexta)
NL001	1171	TGATCTATGATGTTAAGGGACG	3738704 (Manduca sexta)
NL001	1172	CATGGATGTTGGACAAATTGGG	37951951 (Ips pini), 56772312 (Drosophila virilis), 60305420 (Mycetophagus quadripustulatus), 67885868 (Drosophila pseudoobscura), 77321575 (Chironomus tentans), 25956479 (Biphyllus lunatus), 22474232 (Helicoverpa armigera);
NL001	1173	TTTTGCCACTAGGTTGAACAACGT	37953169 (Ips pini)
NL001	1174	GCAGCGTCTCATCAAGGTTGACGGGCAA	48927129 (Hydropsyche sp.)
NL001	1175	AAGGGACGTTTCACCATCCAC	50818668 (Heliconius melpomene)
NL001	1176	AACCTGTGTATGATCACTGGAGG	60293875 (Homalodisca coagulata)
NL001	1177	ACTAACTGTGAAGTGAAGAAATTGT	60293875 (Homalodisca coagulata)
NL001	1178	TTCTTCCGTTTGATCTATGATGT	60293875 (Homalodisca coagulata), 71047771 (Oncometopia nigricans)
NL001	1179	TGTATGATCACTGGAGGTCGTAACTTGGG	60297219 (Diaprepes abbreviatus)
NL001	1180	CATGGATGTTGGACAAATTGGGTGG	60311985 (Papilio dardanus)
NL001	1181	GCTGAAGAAGCTAAGTACAAG	68758383 (Acanthoscurria gomesiana)
NL001	1182	GGAGGTCGTAACTTGGGTCGTGT	77327303 (Chironomus tentans)
NL001	1183	TATGATGTTAAGGGACGTTTCACCAT	77327303 (Chironomus tentans)
NL001	1184	CATGGATGTTGGACAAATTGGG	93002561 (Drosophila grimshawi) 93001617 (Drosophila mojavensis) 92939328 (Drosophila virilis) 112433559 (Myzus persicae)

NL001	1185	CTGAAGAAGCTAAGTACAAGCT	90814922 (Nasonia vitripennis)
NL001	1186	GAAGAAGCTAAGTACAAGCTGTG	110264122 (Spodoptera frugiperda)
NL001	1187	TTGCACAGCTTGTACTTAGCTTCTTC	90820001 (Graphocephala atropunctata)
NL001	1188	AAGTACAAGCTGTGCAAAGTGAAG	90013075 (Bicyclus anynana)
NL001	1189	ATGATCACTGGAGGTCGTAACTTGGGTCG	112350104 (Helicoverpa armigera)
NL001	1190	GGTCGTAACTTGGGTCGTGTGGGG	113017118 (Bemisia tabaci)
NL001	1191	TTCGACATCGTGCACATCAAGGAC	109978109 (Gryllus pennsylvanicus)
NL001	1192	ACATCGTGCACATCAAGGACG	112350104 (Helicoverpa armigera)
NL003	1193	CAGGAGTTGAAGATCATCGGAGAGTATGG	90981811 (Aedes aegypti); 15457393 (Drosophila melanogaster), 76551770 (Spodoptera frugiperda)
NL003	1194	CGTAAGGCCGCTCGTGAGCTG	1797555 (Drosophila melanogaster)
NL003	1195	AAGGTAACGCCCTGCTGCGTCG	18863433 (Anopheles gambiae)
NL003	1196	CAGGAGTTGAAGATCATCGGAGAGTA	2459311 (Antheraea yamamai), 49532931 (Plutella xylostella)
NL003	1197	GCCAAGTCCATCCATCACGCCCG	33354488 (Drosophila yakuba), 60312414 (Papilio dardanus)
NL003	1198	AAGTCCATCCATCACGCCCGT	33528372 (Trichoplusia ni)
NL003	1199	TGTTTGAAGGTAACGCCCTGCT	34788046 (Callosobruchus maculatus)
NL003	1200	CAGGAGTTGAAGATCATCGGAGA	35505798 (Acyrthosiphon pisum), 56772256 (Drosophila virilis)
NL003	1201	GTGCGCCTGGACTCGCAGAAGCACAT	38624772 (Drosophila melanogaster)
NL003	1202	GAGTTGAAGATCATCGGAGAGTA	4158332 (Bombyx mori)
NL003	1203	TTGGGTTTAAAAATTGAAGATTTC	56150446 (Rhynchosciara americana)
NL003	1204	TCGCAGAAGCACATTGACTTCTC	56772256 (Drosophila virilis)
NL003	1205	AGAATGAAGCTCGATTACGTC	60306665 (Sphaerius sp.)
NL003	1206	TTTGTGGTGCGCCTGGACTCG	60312414 (Papilio dardanus)
NL003	1207	AGAAGCACATTGACTTCTCGCTGAAGTC	63514675 (Ixodes scapularis)

NL003	1208	TCGCAGAAGCACATTGACTTCTCGCT	70979521 (Anopheles albimanus)
NL003	1209	CTCATCAGACAAAGACATATCAGAGT	71536734 (Diaphorina citri)
NL003	1210	TTGAAGATCATCGGAGAGTATGG	73612958 (Aphis gossypii)
NL003	1211	AAAATTGAAGATTTCCTTGAA	75467497 (Tribolium castaneum)
NL003	1212	CAGAAGCACATTGACTTCTCGCT	77730066 (Aedes aegypti)
NL003	1213	CGTAAGGCCGCTCGTGAGCTG	24661714 (Drosophila melanogaster)
NL003	1214	GCGTGATGGATGGACTTGGCCAA	90813959 (Nasonia vitripennis)
NL003	1215	GCCAAGTCCATCCATCACGCCCG	92467993 (Drosophila erecta)
NL003	1216	GCCAAGTCCATCCATCACGCCCGT	112349903 (Helicoverpa armigera)
NL003	1217	CTCATCAGACAAAGACATATCAGAGT	110671455 (Diaphorina citri)
NL003	1218	CAGGAGTTGAAGATCATCGGAGA	86464397 (Acyrthosiphon pisum); 92938865 (Drosophila virilis)
NL003	1219	CAGGAGTTGAAGATCATCGGAGAGTATGG	101417830 (Plodia interpunctella); 110254389 (Spodoptera frugiperda)
NL003	1220	GAGTTGAAGATCATCGGAGAGTA	112984021 (Bombyx mori)
NL003	1221	TCGCAGAAGCACATTGACTTCTC	93002641 (Drosophila mojavensis); 92938865 (Drosophila virilis)
NL003	1222	TTGAAGATCATCGGAGAGTATGG	111158779 (Myzus persicae)
NL003	1223	CAGAAGCACATTGACTTCTCGCTGAA	92232387 (Drosophila willistoni)
NL003	1224	CTCCGTAACAAGCGTGAGGTGTGG	92232387 (Drosophila willistoni)
NL003	1225	CGTAACAAGCGTGAGGTGTGG	110558371 (Drosophila ananassae)
NL003	1226	GTCAAATACGCCCTGGCCAAGAT	93001117 (Drosophila grimshawi)
NL004	1227	TACGCCCATTTCCCCATCAACTGTGT	14994663 (Spodoptera frugiperda), 53883415 (Plutella xylostella)
NL004	1228	TGCTCTCACATCGAAAACATG	22039837 (Ctenocephalides felis)
NL004	1229	AACTTCCTGGGCGGAGAAGTACATC	25959088 (Meladema coriacea)
NL004	1230	GCCGTGTACGCCCATTTCCCCATCAACTG	25959088 (Meladema coriacea)
NL004	1231	GTGTACGCCCATTTCCCCATCAACTGTGAC	2761563 (Drosophila melanogaster)
NL004	1232	GTGTACGCCCATTTCCCCATCAACTGTGT	33354902 (Drosophila yakuba)
NL004	1233	ATGCGGTGCCGTGTACGCCCATTT	33433477 (Glossina morsitans)

NL004	1234	TCAGCTGCCCTCATCCAACAGTC	33491496 (Trichoplusia ni)
NL004	1235	AAGGATATTCGTAAATTCTTGGA	37952094 (Ips pini), 56199511 (Culicoides sonorensis)
NL004	1236	GCCCATTTCCCCATCAACTGTGT	42766318 (Armigeres subalbatus)
NL004	1237	AACTTCCTGGGCGAGAAGTACAT	49547659 (Rhipicephalus appendiculatus)
NL004	1238	AAGAACAAGGATATTCGTAAATTCTTGGA	56152793 (Rhynchosciara americana)
NL004	1239	AACTTCCTGGGCGAGAAGTACATCCG	58079798 (Amblyomma americanum), 49554219 (Boophilus microplus)
NL004	1240	CATTTCCCCATCAACTGTGTGAC	60312171 (Papilio dardanus)
NL004	1241	CGTAACTTCCTGGGCGAGAAGTACATCCG	63516417 (Ixodes scapularis)
NL004	1242	AGATCAGCTGCCCTCATCCAACA	71539722 (Diaphorina citri)
NL004	1243	GTGTACGCGCCCATTTCCCCATCAACTGTGT	24583601 (Drosophila melanogaster)
NL004	1244	TACGCCCATTTCCCCATCAACTGT	113017826 (Bemisia tabaci)
NL004	1245	TACGCCCATTTCCCCATCAACTGTGT	110263092 (Spodoptera frugiperda)
NL004	1246	GCCCATTTCCCCATCAACTGTGT	94468811 (Aedes aegypti)
NL004	1247	ACACAGTTGATGGGGAAATGGGC	90136736 (Bicyclus anynana)
NL004	1248	GCCCATTTCCCCATCAACTGTGT	110671493 (Diaphorina citri), 110249018 (Spodoptera frugiperda)
NL004	1249	GTCACACAGTTGATGGGGAAATGGGC	87266195 (Choristoneura fumiferana)
NL004	1250	CCATTTCCCCATCAACTGTGT	90981351 (Aedes aegypti)
NL005	1251	AAGGGTAACGTATTCAAGAACAAGCG	1900283 (Drosophila melanogaster)
NL005	1252	AAGGGTAACGTATTCAAGAACAAG	25956594 (Biphyllus lunatus)
NL005	1253	CGTGTATTGATGGAGTTCATTCA	30124405 (Toxoptera citricida), 60294294 (Homalodisca coagulata), 71046487 (Oncometopia nigricans), 73612243 (Aphis gossypii)
NL005	1254	AAAGGTCAAGGAGGCCAAGAAG	67875089 (Drosophila pseudoobscura)
NL005	1255	AAGATGTTGAACGACCAGGCTGAAGC	77324118 (Chironomus tentans)
NL005	1256	ACGTTACCCTTAGCCTTCATGTA	90812513 (Nasonia giraulti)
NL005	1257	AAGGGTAACGTATTCAAGAACAAGCG	45552830 (Drosophila melanogaster)
NL005	1258	CGTGTATTGATGGAGTTCATTCA	112433619 (Myzus persicae)

NL005	1259	AGGTCAAGGAGGCCAAGAAGC	92941126 (Drosophila virilis)
NL005	1260	ACGTTACCCTTAGCCTTCATGTA	90812513 (Nasonia giraulti)
NL005	1261	AAGGGTAACGTATTCAAGAACAAGCG	45552830 (Drosophila melanogaster)
NL006	1262	AGTCCCAGGAACACCTATCAG	21464337 (Drosophila melanogaster)
NL006	1263	ATTATTCCCTTCCCGATCACAA	24646762 (Drosophila melanogaster)
NL006	1264	CACGCTATCCCATCTCGTATGACAATTGG	24646762 (Drosophila melanogaster)
NL006	1265	TACAAGTTCTGCAAAATTCGAGT	49573116 (Boophilus microplus)
NL006	1266	ATGACAATTGGCCATTTAATTGAATG	50564037 (Homalodisca coagulata)
NL006	1267	ACCTACACGCACTGCGAGATCCA	58384759 (Anopheles gambiae str. PEST)
NL006	1268	GGTGTGTGGAGTACATTGACAC	58384759 (Anopheles gambiae str. PEST)
NL006	1269	ATTATTCCCTTCCCGATCACAA	24646762 (Drosophila melanogaster)
NL006	1270	AGTCCCAGGAACACCTATCAG	22026793 (Drosophila melanogaster)
NL006	1271	CACGCTATCCCATCTCGTATGACAATTGG	24646762 (Drosophila melanogaster)
NL006	1272	TCTCGTATGACAATTGGCCATTT	93000469 (Drosophila mojavensis)
NL007	1273	GCAAACAAGTCATGATGTTCAG	15354019 (Apis mellifera)
NL007	1274	GGTATGGGAAAAACTGCTGTATTTGTGTT	15354019 (Apis mellifera)
NL007	1275	GAATGCATTCCTCAAGCTGTA	21068658 (Chironomus tentans)
NL007	1276	TGCAAGAAATTCATGCAAGATCC	21068658 (Chironomus tentans)
NL007	1277	TTCCAAATCAGCAAAGAGTATGA	2890413 (Drosophila melanogaster)
NL007	1278	GATGACGAGGCCAAGCTGACGCT	49536419 (Rhipicephalus appendiculatus)
NL007	1279	TGTGGTTTTGAACATCCATCTGAAGTACAACA	60308907 (Hister sp.)
NL007	1280	GAAAACGAAAAGAACAAAAAG	77642464 (Aedes aegypti)
NL007	1281	GGTATGGGAAAAACTGCTGTATTTGTGTT	110759359 (Apis mellifera)
NL007	1282	GCAAACAAGTCATGATGTTCAG	110759359 (Apis mellifera)
NL007	1283	CTGCAGCAGCACTATGTCAAACTCAA	90137538 (Spodoptera frugiperda)
NL007	1284	GAAAACGAAAAGAACAAAAAG	94468805 (Aedes aegypti)
NL008	1285	TGCCAAGCCTAAAGATTTGGG	60315277 (Dysdera erythrina)
NL008	1286	ATGTTCAAGAAAGTTAATGCTAGAGA	60336214 (Homalodisca coagulata)

NL008	1287	GAGTTGTTGGTGTTCTTTTGGGGATG	66522334 (Apis mellifera)
NL008	1288	TTTCAAACAGTTTTGCAGTTCC	75735289 (Tribolium castaneum)
NL008	1289	GAGTTGTTGGTGTTCTTTTGGGGATG	110762109 (Apis mellifera)
NL010_1	1290	AAGGACCTGACTGCCAAGCAG	2761430 (Drosophila melanogaster)
NL010_1	1291	GCCAAGCAGATCCAGGACATG	49559867 (Boophilus microplus)
NL010_1	1292	TGCTCGAAGAGCTACGTGTTCCG	49559867 (Boophilus microplus)
NL010_1	1293	AAGAGCTACGTGTTCCGTGGC	92043082 (Drosophila willistoni)
NL010_1	1294	AAGGACCTGACTGCCAAGCAG	92481328 (Drosophila erecta) 28571527 (Drosophila melanogaster)
NL010_2	1295	ATGGACACATTTTTCCAAATTCTCAT	33427937 (Glossina morsitans)
NL010_2	1296	ACCAGCAGTATTCAACCCGACA	47520567 (Acyrthosiphon pisum)
NL010_2	1297	TATTGATGGACACATTTTTCCA	47520567 (Acyrthosiphon pisum)
NL010_2	1298	TTCAACAACAGTCCTGATGAAAC	55891325 (Locusta migratoria)
NL010_2	1299	ATGGACACATTTTTCCAAATT	56151768 (Rhynchosciara americana), 75736992 (Tribolium castaneum)
NL010_2	1300	CCGCAGTTCATGTACCATCTGCG	6932015 (Anopheles gambiae), 29558345 (Bombyx mori)
NL010_2	1301	ATGGACACATTTTTCCAAATT	91086194 (Tribolium castaneum)
NL011	1302	AAGAAGTATGTTGCCACCCTTGG	21640529 (Amblyomma variegatum)
NL011	1303	GACATCAAGGACAGGAAAGTCAAGGCCAAGAGCATAGT	25959135 (Meladema coriacea)
NL011	1304	CAACTACAACTTCGAGAAGCCGTTCCTGTGG	25959135 (Meladema coriacea), 77646995 (Aedes aegypti)
NL011	1305	TACAAGAACGTTCCCAACTGGCA	3114090 (Drosophila melanogaster)
NL011	1306	TGCGAAAACATTCCCATTGTACT	37951963 (Ips pini)
NL011	1307	AGGAAGAAGAAACCTTCAGTACTACGA	40544671 (Tribolium castaneum)
NL011	1308	AGCAACTACAACTTCGAGAAGCC	49565237 (Boophilus microplus), 49538692 (Rhipicephalus appendiculatus)
NL011	1309	AACAAAGTAGACATCAAGGACAGGAAAGTCAA	76552920 (Spodoptera frugiperda)

NL011	1310	CCCAACTGGCACAGAGATTTAGTG	78230577 (Heliconius erato/himera mixed EST library)
NL011	1311	GATGGTGGTACCGGCAAAACTAC	78538667 (Glossina morsitans)
NL011	1312	TACAAGAAACGTTCCCAACTGGCAC	84267747 (Aedes aegypti)
NL011	1313	AACAAAGTAGACATCAAGGACACAGGAAAGTCAA	110263840 (Spodoptera frugiperda)
NL011	1314	TTGACTTTCCTGTCCTTGATGTC	90136305 (Bicyclus anynana)
NL011	1315	GACATCAAGGACACAGGAAAGTCAAGGC	90813103 (Nasonia vitripennis)
NL011	1316	AGGAAGAAGAAACCTTCAGTACTACGA	91091115 (Tribolium castaneum)
NL011	1317	GATGTCGTAGTACTGAAGGTTCTT	90136305 (Bicyclus anynana)
NL011	1318	CAACTACAACTTCGAGAAGCCGTTCCTGTGG	90977910 (Aedes aegypti)
NL011	1319	CCAACCTGGAGTTCGTCGCCATGCC	92465523 (Drosophila erecta)
NL011	1320	GAATTTGAAAGAAGTATGTTGC	113015058 (Bemisia tabaci)
NL011	1321	CTTCAGTACTACGACATCAGTGCGAA	110086408 (Amblyomma cajennense)
NL011	1322	AGCAACTACAACTTCGAGAAGCC	110086408 (Amblyomma cajennense)
NL011	1323	AAGCTGATCGGTGACCCCAACCTGGAGTT	110086408 (Amblyomma cajennense)
NL012	1324	CACAGTTTGAACAGCAAGCTGG	29552409 (Bombyx mori)
NL012	1325	GCAGCAGACGCAGGCACAGGTAGA	77823921 (Aedes aegypti)
NL012	1326	CACAGTTTGAACAGCAAGCTGG	94435913 (Bombyx mori)
NL013	1327	CAAGCGAAGATGTTGGACATGCT	15536506 (Drosophila melanogaster)
NL013	1328	ATGGTGGTGGGCTGGTACCACTCGCACCC	49547019 (Rhipicephalus appendiculatus)
NL013	1329	GTGGTGGGCTGGTACCACTCGCACCC	58079586 (Amblyomma americanum)
NL013	1330	GTGGGCTGGTACCACTCGCACCC	82848521 (Boophilus microplus)
NL013	1331	AAGATGTTGGACATGCTAAAGCAGACAGG	92229701 (Drosophila willistoni)
NL013	1332	TGTCGGGTGTCGACATCAACAC	92962655 (Drosophila ananassae)
NL013	1333	GTTCCCATGGAAGTTATGGGC	112433067 (Myzus persicae)
NL013	1334	GTGGGCTGGTACCACTCGCACCC	110085175 (Amblyomma cajennense)
NL014	1335	GAGATCGATGCCAAGGCCGAGGA	1033187 (Drosophila melanogaster)
NL014	1336	GAATTCAACATTGAAAAGGGA	16900951 (Ctenocephalides felis)
NL014	1337	GAAGAATTCAACATTGAAAAGGGG	47518467 (Acyrthosiphon pisum)
NL014	1338	GAAGCCAATGAGAAAGCCGAAGA	47518467 (Acyrthosiphon pisum)
NL014	1339	TCGTCAAACATGCTGAACCAAGC	61954844 (Tribolium castaneum)

NL014	1340	TTTCATTGAGCAAGAAGCCAATGA	62239529 (Diabrotica virgifera), 76169390 (Diploptera punctata), 61954844 (Tribolium castaneum), 16900951 (Ctenocephalides felis)
NL014	1341	CAAGAAGCCAATGAGAGAAGCCGA	111160670 (Myzus persicae)
NL014	1342	TTTCATTGAGCAAGAAGCCAATGA	91092061 (Tribolium castaneum)
NL014	1343	AGAAGCCAATGAGAGAAGCCGA	112432414 (Myzus persicae)
NL014	1344	TCGTCAAACATGCTGAACCAAGC	91092061 (Tribolium castaneum)
NL014	1345	GCCAATGAGAAAGCCGAAGAGATCGATGCCAA	93001435 (Drosophila grimshawi)
NL014	1346	AAAGCCGAAGAGATCGATGCCAA	92936169 (Drosophila virilis)
NL014	1347	GAGATCGATGCCAAGGCCGAGGA	24644299 (Drosophila melanogaster)
NL014	1348	GAAGAATTCAACATTGAAAAGGG	86463006 (Acyrthosiphon pisum) 111160670 (Myzus persicae)
NL014	1349	GAAGAATTCAACATTGAAAAGGGAAGGCT	90819999 (Graphocephala atropunctata)
NL014	1350	AAGAATTCAACATTGAAAAGGG	111158385 (Myzus persicae)
NL015	1351	GAGGTGCTGCGCATCCACACCAA	18887285 (Anopheles gambiae)
NL015	1352	ATCCATGTGCTGCCCATTGATGA	21641659 (Amblyomma variegatum)
NL015	1353	CATGTGCTGCCCATTGATGAT	22039735 (Ctenocephalides felis)
NL015	1354	CTGCGCATCCACACCAAGAACATGAAGTTGG	22474136 (Helicoverpa armigera)
NL015	1355	TTCTTCTTCCTCATCAACGGACC	49552586 (Rhipicephalus appendiculatus)
NL015	1356	GAGATGGTGGAGTTGCCGCTG	58371722 (Lonomia obliqua)
NL015	1357	CAGATCAAAGAGATGGTGGAG	92947821 (Drosophila ananassae)
NL015	1358	ATCAACGGACCCGAGATTATG	92947821 (Drosophila ananassae)
NL015	1359	ATGAAGATGATGGCCGGTGCGTT	92470977 (Drosophila erecta)
NL015	1360	CCGGCCATCATCTTCATCGATGAG	92480997 (Drosophila erecta)
NL015	1361	ATCATCTTCATCGATGAGCTGGACGC	99007898 (Leptinotarsa decemlineata)
NL015	1362	CAGCTGCTGACGCGCTGATGGACGG	92941440 (Drosophila virilis)
NL015	1363	ATCGACATTGGCATTCCCGATGCCACCGG	92947821 (Drosophila ananassae)
NL016	1364	TCTATGGAGAACGTGTGCCTGTTCTTGAAC	27372076 (Spodoptera littoralis)
NL016	1365	TACCAGTGCGAGAAGCACGTGCT	2921501 (Culex pipiens)
NL016	1366	ATGGAGAACGTGTGCCTGTTCTTGAACCTGGC	31206154 (Anopheles gambiae str. PEST)
NL016	1367	CGTGGCCAGAAAATCCCCATCTT	3945243 (Drosophila melanogaster)

NL016	1368	TGGCCTACCAGTGCGAGAAGCACGTG	4680479 (Aedes aegypti)
NL016	1369	TGGCCACCATCTACGAGCGCGCCGG	53883819 (Plutella xylostella)
NL016	1370	ATGGAGAACGTGTGCCTGTTCTTGAA	67883622 (Drosophila pseudoobscura)
NL016	1371	CCCGAGGAAATGATCCAGACTGG	67883622 (Drosophila pseudoobscura)
NL016	1372	TGGCCTACCAGTGCGAGAAGCACGTGCT	67883622 (Drosophila pseudoobscura), 31206154 (Anopheles gambiae str. PEST)
NL016	1373	GAGGAGGTGCCCGGCCGTCGTGGTTTCCCCGG TTACATGTACACCGAT	67896654 (Drosophila pseudoobscura)
NL016	1374	GAGGGTCGCAACGGCTCCATCAC	67896654 (Drosophila pseudoobscura)
NL016	1375	GAGGTGCCCGGCCGTCGTGGTTTCCCCGGTTAC ATGTACACCGAT	75710699 (Tribolium castaneum)
NL016	1376	ATGGAGAACGTGTGCCTGTTCTTGAAC	76554661 (Spodoptera frugiperda)
NL016	1377	TGGCCTACCAGTGCGAGAAGCACGTGCTCGTCA TCCT	9992660 (Drosophila melanogaster)
NL016	1378	CGTCGTGGTTTCCCCGGTTACATGTACACCGAT	9992660 (Drosophila melanogaster), 2921501 (Culex pipiens), 6239897 (Diabrotica virgifera)
NL016	1379	TGGTCGCGTATCTATCCCGAGGAAATGATCCAG AC	92999374 (Drosophila grimshawi)
NL016	1380	TGGTCGCGTATCTATCCCGAGGAAATGATCCAG ACTGG	92940538 (Drosophila virilis)
NL016	1381	TCTATGGAGAACGTGTGCCTGTTCTTGAAC	92938622 (Drosophila virilis)
NL016	1382	ATGGAGAACGTGTGCCTGTTCTTGAAC	92950254 (Drosophila ananassae), 90137502 (Spodoptera frugiperda)
NL016	1383	AACGTGTGCCTGTTCTTGAAC	92946927 (Drosophila ananassae)
NL016	1384	TGGCCTACCAGTGCGAGAAGCACGTGCT	24646342 (Drosophila melanogaster), 92231646 (Drosophila willistoni)
NL016	1385	TGGCCTACCAGTGCGAGAAGCACGTGCTCGTCA TCCT	107256717 (Drosophila melanogaster)
NL016	1386	GCCTACCAGTGCGAGAAGCACGTGCT	92985459 (Drosophila grimshawi)
NL016	1387	GAGGAGGTGCCCGGCCGTCGTGGTTTCCCCGG TTACATGTACAC	92938622 (Drosophila virilis)

NL016	1388	GAGGAGGTGCCCGGCGCCGTCGTGGTTTCCCCGG TTACATGTACACCGAT	92477818 (Drosophila erecta)
NL016	1389	GAGGTGCCCCGGCGCCGTCGTGGTTTCCCCGGTTAC ATGTACACCGAT	91090030 (Tribolium castaneum)
NL016	1390	CGTCGTGGTTTCCCCGGTTACAT	104530890 (Belgica antarctica)
NL016	1391	CGTCGTGGTTTCCCCGGTTACATGTACACCGAT	92981037 (Drosophila grimshawi) 24646342 (Drosophila melanogaster)
NL016	1392	CGTGGTTTCCCCGGTTACATGTACACCGAT	92957249 (Drosophila ananassae)
NL016	1393	ATCGGTGTACATGTAACCGGGGAAACCA	103744758 (Drosophila melanogaster)
NL016	1394	CGTCCGGCGGCGCTCGTAGATGGT	91829127 (Bombyx mori)
NL016	1395	GAGGGTGCGAACGGCTCCATCAC	92957249 (Drosophila ananassae)
NL018	1396	CGGACGTGGCCTGGTTCATCA	92479742 (Drosophila erecta)
NL019	1397	GTGGTGTACGACTGCACCGACCAGGAGTCGTTC AACAAC	84343006 (Aedes aegypti)
NL019	1398	GAAAGTTACATCAGTACCATTGGTGT	113018639 (Bemisia tabaci)
NL019	1399	CACCGACCAGGAGTCGTTCAACAAC	85857059 (Aedes aegypti)
NL019	1400	AGTACCATTGGTGTAGATTTTAAAAT	91087112 (Tribolium castaneum)
NL019	1401	ATTGGTGTAGATTTTAAAATTAG	78542465 (Glossina morsitans)
NL019	1402	GGTGTAGATTTTAAAATTAGAAC	92232411 (Drosophila willistoni)
NL019	1403	GGTGTAGATTTTAAAATTAGAAACAAT	90986845 (Aedes aegypti)
NL019	1404	GTTCTAATTTTAAAATCTACAC	92043152 (Drosophila willistoni)
NL019	1405	TGGGACACGGCCGGCCAGGAG	91091115 (Tribolium castaneum)
NL019	1406	TGGGACACGGCCGGCCAGGAGCG	90982219 (Aedes aegypti)
NL019	1407	TGGGACACGGCCGGCCAGGAGCGGT	94433465 (Bombyx mori)
NL019	1408	GACCAGCTGGGCATTCCGTTCCT	10708384 (Amblyomma americanum)
NL019	1409	ATTGGTGTAGATTTTAAAATT	18864897 (Anopheles gambiae)
NL019	1410	TGGGACACGGCCGGCCAGGAGCGGTT	18888926 (Anopheles gambiae)
NL019	1411	CAGGAGCGGTTCCGCACGATCAC	21640713 (Amblyomma variegatum)
NL019	1412	ATTGGTGTAGATTTTAAAAATTAGAAC	22039832 (Ctenocephalides felis)
NL019	1413	ATTGGTGTAGATTTTAAAATTAG	33378174 (Glossina morsitans)
NL019	1414	TGGGACACGGCCGGCCAGGAG	3738872 (Manduca sexta), 25959135 (Meladema coriacea), 40542849 (Tribolium castaneum), 67840088 (Drosophila pseudoobscura)

NL019	1415	TGGGACACGGCGGCGGCCAGGAGGCGGT	4161805 (Bombyx mori)
NL019	1416	GATGACACATACACAGAAAGTTACATCAGTAC	50562545 (Homalodisca coagulata), 71047909 (Oncometopia nigricans)
NL019	1417	ACGGCCGGCCAGGAGCGGTTCCG	58378591 (Anopheles gambiae str. PEST)
NL019	1418	AGTACCATTGGTGTAGATTTTAAAAT	61954135 (Tribolium castaneum)
NL019	1419	TAAAGCTTCAGATTTGGGACAC	68758530 (Acanthoscurria gomesiana)
NL019	1420	ATTTGGGACACGGCCGGCCAGGA	77667315 (Aedes aegypti)
NL019	1421	GTGGTGTACGACTGCACCGACCAGGAGTCGTTCAACAAC	77705629 (Aedes aegypti)
NL019	1422	GGTGTAGATTTTAAAATTAGAACAAT	77890715 (Aedes aegypti)
NL019	1423	TGGGACACGGCCGGCCAGGAGCG	82851662 (Boophilus microplus), 49536894 (Rhipicephalus appendiculatus)
NL022	1424	TCTTCCTCACCGGTCAGGAGGAGAT	6928515 (Anopheles gambiae)
NL022	1425	AAATTCTCCGAGTTTTCGACGATGC	91082872 (Tribolium castaneum)
NL022	1426	TTCCTCACCGGTCAGGAGGAGAT	90976120 (Aedes aegypti)
NL022	1427	TAGTATTGGCCACAAATATTGCAGA	92042565 (Drosophila willistoni)
NL023	1428	TATTTGAACATATGGGTGCCGCA	20384699 (Plutella xylostella)
NL023	1429	GAGGGAGAGGAAATGTGGAATCC	22085301 (Helicoverpa armigera)
NL023	1430	CCGAAGATTGTCTGTATTTGAA	27531022 (Apis mellifera)
NL023	1431	GATTCCGTTTGCGAAACCTCC	57929927 (Anopheles gambiae str. PEST)
NL023	1432	GGTGCGTTCGGCTTCCTCTACCT	58380563 (Anopheles gambiae str. PEST)
NL023	1433	CAATTCAATGCTAGGGAAAGG	110759012 (Apis mellifera)
NL023	1434	GAGGGAGAGGAAATGTGGAATCC	55793188 (Helicoverpa assulta)
NL023	1435	CCGAAGATTGTCTGTATTTGAA	58585075 (Apis mellifera)
NL023	1436	GACGTCATCGTCGCCTCCATGCA	91077117 (Tribolium castaneum)
NL027	1437	GGAGACCCTGGAGCTGGTGCG	49543279 (Rhipicephalus appendiculatus)

Table 4-CS

Target ID	SEQ ID NO	Sequence *	Example Gi-number and species
CS001	1730	AAAGCATGGATGTTGGACAAA	73619372 (Aphis gossypii); 77325485 (Chironomus tentans); 22474232 (Helicoverpa armigera); 37951951 (Ips pini); 60305420 (Mycetophagus quadripustulatus); 84647995 (Myzus persicae)
CS001	1731	AAAGCATGGATGTTGGACAAACT	40877657 (Bombyx mori); 103783745 (Heliconius erato); 55904580 (Locusta migratoria); 101413238 (Plodia interpunctella)
CS001	1732	AACCGGCTCAAGTACGCGCTCAC	22474232 (Helicoverpa armigera)
CS001	1733	AACCGGCTCAAGTACGCGCTCACCGG	90134075 (Bicyclus anynana)
CS001	1734	AAGATCATGGACTTCATCAAGTT	90134075 (Bicyclus anynana)
CS001	1735	ACCAGATTGAACAACGTGTTCAT	71536878 (Diaphorina citri) 3658573 (Manduca sexta)
CS001	1736	ATCATGGACTTCATCAAGTTTGAATC	103783745 (Heliconius erato)
CS001	1737	CAAGATCATGGACTTCATCAAGTT	3478550 (Antheraea yamamai)
CS001	1738	CCCCACAAGTTGCGCGAGTGC	63011732 (Bombyx mori)
CS001	1739	CCCGCTGGATTATGGATGTTGT	101403940 (Plodia interpunctella)
CS001	1740	CCTCCAAGATCATGGACTTCATCAAGTT	22474232 (Helicoverpa armigera)
CS001	1741	CCTGCCGCTGGTGATCTTCCT	27597800 (Anopheles gambiae)
CS001	1742	CGACGGGCCCCAAGAACGTGCC	22474232 (Helicoverpa armigera)
CS001	1743	CTCATCAAGGTCAACGACTCC	103783745 (Heliconius erato) 112350001 (Helicoverpa armigera) 101418268 (Plodia interpunctella)
CS001	1744	CTCATCAAGGTCAACGACTCCATCCAGCTCGAC AT	3738704 (Manduca sexta)
CS001	1745	CTCATCAAGGTCAACGACTCCATCCAGCTCGAC ATCGCCACCT	53884106 (Plutella xylostella)
CS001	1746	CTGCCGCTGGTGATCTTCCTC	27603050 (Anopheles gambiae)
CS001	1747	GACCCCACATATCCCGCTGGATT	103783745 (Heliconius erato)
CS001	1748	GCAGCGACTTATCAAAGTTGA	109978109 (Gryllus pennsylvanicus)

CS001	1749	GCATGGATGTTGGACAAACTGGG	67899746 (Drosophila pseudoobscura)
CS001	1750	GCCACCTCCAAGATCATGGACTTCAT	110259010 (Spodoptera frugiperda)
CS001	1751	GCGCGTGGCGGACGGGCGCCAAGAACGTGCC	53884106 (Plutella xylostella)
CS001	1752	GCTGGATTTATGGATGTTGTTT	29553519 (Bombyx mori)
CS001	1753	GGCTCAAGTACGCGCTCACCGG	5498893 (Antheraea yamamai)
CS001	1754	GTGGGCACCATCGTGTCCCGCGAG	3953837 (Bombyx mandarina) 53884106 (Plutella xylostella)
CS001	1755	GTGGGCACCATCGTGTCCCGCGAGCG	3478550 (Antheraea yamamai)
CS001	1756	GTGGGCACCATCGTGTCCCGCGAGCGAGCGACATCC CGG	22474232 (Helicoverpa armigera)
CS001	1757	TAAAGCATGGATGTTGGACAA	58371410 (Lonomia obliqua)
CS001	1758	TAAAGCATGGATGTTGGACAAA	60311985 (Papilio dardanus) 31366663 (Toxoptera citricida)
CS001	1759	TAAAGCATGGATGTTGGACAAACT	10978109 (Gryllus pennsylvanicus)
CS001	1760	TAAAGCATGGATGTTGGACAAACTGGG	98994282 (Antheraea mylitta)
CS001	1761	TACAAGCTGTGTGCAAGGTGCGGGCGCGCGTGGCGGAC GGGCCC	98993531 (Antheraea mylitta)
CS001	1762	TACAAGCTGTGTGCAAGGTGCGGGCGCGCGTGGCGGAC GGGCCCCAA	5498893 (Antheraea yamamai)
CS001	1763	TACCCCGACCCCACTCACTCATCAAGGT	90134075 (Bicyclus anynana)
CS001	1764	TGAACAACGTGTTCATAATCGG	98993531 (Antheraea mylitta)
CS001	1765	TGCGCGAGTGCGCCTGCCGCTGGT	22474232 (Helicoverpa armigera)
CS001	1766	TGTATGATCACGGGAGGCCGTAACTTGGG	60311445 (Euclidia glyphica)
CS001	1767	TGTATGATCACGGGAGGCCGTAACTTGGGGGCG	3953837 (Bombyx mandarina)
CS001	1768	TGTATGATCACGGGAGGCCGTAACTTGGGGCG CGTGGGCACCATCGTGTCCCGCGAG	91826697 (Bombyx mori)
CS001	1769	TGTGCAAGGTGCGGGCGCGCGTGGCGGACGGGCCC CAAG	3478550 (Antheraea yamamai)
CS001	1770	TTGAACAACGTGTTCATAATCGGCAAGGGCACG AA	3953837 (Bombyx mandarina) 40915191 (Bombyx mori)
CS002	1771	ATTGAGGCCCAAAGGGGAAGCGCTAGAAGG	91849872 (Bombyx mori)
CS002	1772	CACGATCTGATGGATGACATTG	33498783 (Anopheles gambiae)
CS002	1773	GAGTTTCTTTAGTAAAGTATTCGGTGG	110762684 (Apis mellifera)
CS002	1774	TATGAAAGCAGCTTACCCAGAT	49552807 (Rhipicephalus appendiculatus)

CS003	1775	AGGCACATCCGTGTCCGCAAGCA	10707186 (Amblyomma americanum)
CS003	1776	AAGATTGAGGAGACTTCTTGGAA	60295192 (Homalodisca coagulata)
CS003	1777	AAGCACATTGACTTCTCGCTGAA	92219983 (Drosophila willistoni)
CS003	1778	ATCAGAGAGAGGCACATCCGTGT	27260897 (Spodoptera frugiperda)
CS003	1779	ATCCGTAAGGCTGCCCGTGAG	101413529 (Plodia interpunctella)
CS003	1780	ATCCGTAAGGCTGCCCGTGAGCTG	92042852 (Drosophila willistoni)
CS003	1781	ATCCGTAAGGCTGCCCGTGAGCTGCT	92959651 (Drosophila ananassae) 112349903 (Helicoverpa armigera)
CS003	1782	ATCCGTAAGGCTGCCCGTGAGCTGCTCAC	90138123 (Spodoptera frugiperda)
CS003	1783	CACATCCGTGTCCGCAAGCAAG	60306665 (Sphaerius sp.)
CS003	1784	CACATCCGTGTCCGCAAGCAAGT	77329341 (Chironomus tentans)
CS003	1785	CACATCCGTGTCCGCAAGCAAGTTG	60306676 (Sphaerius sp.)
CS003	1786	CGCAACAAGCGTGAGGTGTGG	92473214 (Drosophila erecta) 67888665 (Drosophila pseudoobscura)
CS003	1787	CGTGTCCGCAAGCAAGTTGTGAACATCCC	90134575 (Bicyclus anynana) 29553137 (Bombyx mori)
CS003	1788	CTCGCTGAAGTCTCCGTTCGGCGGGCGGCCG	3986375 (Antheraea yamamai)
CS003	1789	CTCGGTCTGAAGATTGAGGAGACTT	112349903 (Helicoverpa armigera) 49532931 (Plutella xylostella)
CS003	1790	CTGGACTCTGGCAAGCACATTGACTTCTC	29553137 (Bombyx mori) 58371398 (Lonomia obliqua)
CS003	1791	GACTTCTCGCTGAAGTCTCCGTTCGGCGGCGG	60312414 (Papilio dardanus)
CS003	1792	GACTTCTCGCTGAAGTCTCCGTTCGGCGGCGGCCG	49532931 (Plutella xylostella)
CS003	1793	GAGGAGAAAGACCCTAAGAGGTTATTCGAAGGTAA	37952462 (Ips pini)
CS003	1794	GATCCGTAAGGCTGCCCGTGA	67568544 (Anoplophora glabripennis)
CS003	1795	GATCCGTAAGGCTGCCCGTGAGCTGCT	67843629 (Drosophila pseudoobscura) 56772258 (Drosophila virilis)
CS003	1796	GATTATGTACTCGGTCTGAAGATTGAGGACTT	101413529 (Plodia interpunctella)
CS003	1797	GGTCTGAAGATTGAGGAGACTTCTTGGA	2699490 (Drosophila melanogaster)
CS003	1798	GTGTGGAGGGTGAAGTACACGCT	60312414 (Papilio dardanus)
CS003	1799	GTGTTCAAGGCTGGTCTGCTAGCTAAGTC	78230982 (Heliconius erato/himera mixed EST library)

CS003	1800	GTGTTGGATGAGAAGCAGAGATGAAGCTCGATTAT GT	112349903 (Helicoverpa armigera)
CS003	1801	TGAAGATTGAGGACTTCTTGGA	3986375 (Antheraea yamamai)
CS003	1802	TGGACTCTGGCAAGCACATTGACTTCTC	78230982 (Heliconius erato/himera mixed EST library)
CS003	1803	TGGATGAGAAGCAGATGAAGCT	60312414 (Papilio dardanus)
CS003	1804	TGGTCTCCGCAACAAGCGTGAGGT	76552467 (Spodoptera frugiperda)
CS003	1805	TGGTCTCCGCAACAAGCGTGAGGTGTGG	33528372 (Trichoplusia ni)
CS006	1806	CGTATGACAATTGGTCACTTGATTGA	91831926 (Bombyx mori)
CS006	1807	GAAGATATGCCTTTCACTTGTGAAGG	55801622 (Acyrthosiphon pisum)
CS006	1808	GGAAAAACTATAACTTTGCCAGAAAA	40926289 (Bombyx mori)
CS006	1809	GGTGATGCTACACCATTTAACGATGCTGT	31366154 (Toxoptera citricida)
CS006	1810	TCTCGTATGACAATTGGTCACTTGAT	49201759 (Drosophila melanogaster)
CS006	1811	CTGTCAACGTGCGAGAGATCTC	49573116 (Boophilus microplus)
CS007	1812	TGGATGAATGTGACAAAATGCTTGAA	84114516 (Blomia tropicalis)
CS007	1813	TTTATGCAAGATCCTATGGAAGT	84114516 (Blomia tropicalis)
CS007	1814	AAATTTATGCAAGATCCTATGGAAGTTTATGT	78525380 (Glossina morsitans)
CS007	1815	AATATGACTCAAGATGAGCGTCT	90137538 (Spodoptera frugiperda)
CS007	1816	ATGACTCAAGATGAGCGTCTCTCCCG	103792212 (Heliconius erato)
CS007	1817	ATGCAAGATCCTATGGAAGTTTA	77336752 (Chironomus tentans)
CS007	1818	ATGCAAGATCCTATGGAAGTTTATGT	77873166 (Aedes aegypti)
CS007	1819	CGCTATCAGCAGTTCAAAGATTTCCAGAAG	77873166 (Aedes aegypti)
CS007	1820	GAAAATGAAAAGAATAAGAAG	110759359 (Apis mellifera) 78525380 (Glossina morsitans)
CS007	1821	GAAGTTCAACATGAATGTATTCC	110759359 (Apis mellifera)
CS007	1822	GATGAGCGTCTCTCCCGCTATCA	40932719 (Bombyx mori)
CS007	1823	TGCCAATTCAGAAAGATGAAGAAGT	110759359 (Apis mellifera)
CS007	1824	TGTAAGAAATTTATGCAAGATC	45244844 (Bombyx mori)
CS009	1825	AGGTGTGCGACGTGGACATCA	92460383 (Drosophila erecta)
CS009	1826	GACTTGAAGGAGCACATCAGGAA	29534871 (Bombyx mori)
CS009	1827	GGCCAGAACATCCACAACTGTGA	29534871 (Bombyx mori)
CS009	1828	TCTTGCGAGGGAGAATCCA	111005781 (Apis mellifera)
CS011	1829	AAAACTATTGTTTTCCACAGAAAAAAGAA	86465126 (Bombyx mori)
CS011	1830	ATCAAGGACAGAAAAGTCAAAGC	78230577 (Heliconius erato/himera mixed EST library)

CS011	1831	ATCTCTGCCAAGTCAAACTACAA	101406907 (Plodia interpunctella)
CS011	1832	CAATGTGCCATCATCATGTTCGA	110242457 (Spodoptera frugiperda)
CS011	1833	CCCAACTGGCACAGAGATTTAGTGCG	78230577 (Heliconius erato/himera mixed EST library)
CS011	1834	GACACTTGACTGGAGAGTTCGAGAAAAGATA	101410627 (Plodia interpunctella)
CS011	1835	GATATCAAGGACAGAAAAGTCAA	60312108 (Papilio dardanus)
CS011	1836	GCCAAGTCAAACTACAATTTCGA	67873076 (Drosophila pseudoobscura)
CS011	1837	GCTGGCCAAGAAAAGTTTGGTGGT	111031693 (Apis mellifera)
CS011	1838	GGCCAAGAAAAGTTTGGTGGTCTCCG	84267747 (Aedes aegypti)
CS011	1839	TACAAAAATGTACCCAACTGGCA	92963426 (Drosophila grimshawi) 37951963 (Ips pini)
CS011	1840	TACAAAAATGTACCCAACTGGCACACAGAGA	60312108 (Papilio dardanus)
CS011	1841	TATGGGATACTGCTGGCCAAGAA	40929360 (Bombyx mori)
CS011	1842	TATGGGATACTGCTGGCCAAGAAA	110749704 (Apis mellifera)
CS011	1843	TGGGATACTGCTGGCCAAGAA	73618835 (Aphis gossypii) 112432160 (Myzus persicae)
CS011	1844	TGTGCCATCATCATGTTCGATGT	84346664 (Aedes aegypti)
CS011	1845	TTTGACTGGAGAGTTCGAGAAA	90136305 (Bicyclus anynana) 78230577 (Heliconius erato/himera mixed EST library) 60312108 (Papilio dardanus)
CS011	1846	TTTGACTGGAGAGTTCGAGAAAA	86465126 (Bombyx mori) 110262261 (Spodoptera frugiperda)
CS011	1847	TGGGATACTGCTGGCCAAGAA	21639295 (Sarcoptes scabiei)
CS013	1848	GATCCCATTCAGTCTGTCAAGGG	3626535 (Drosophila melanogaster)
CS013	1849	TTCCAAGCAAAGATGTTGGATATGTTGAA	112433067 (Myzus persicae)
CS014	1850	AAAAAGATCCAATCTTCGAACATGCTGAA	103775905 (Heliconius erato)
CS014	1851	AAACAAGTGGAACTCCAGAAAAA	101403826 (Plodia interpunctella)
CS014	1852	AAAGTGCGTGAGGACCACGTACG	87266590 (Choristoneura fumiferana) 3738660 (Manduca sexta)
CS014	1853	AAGATCAGCAACACTCTGGAGTC	58371699 (Lonomia obliqua)
CS014	1854	AAGATCAGCAACACTCTGGAGTCTCG	91848497 (Bombyx mori)
CS014	1855	AAGATCCAATCTTCGAACATG	77790417 (Aedes aegypti)
CS014	1856	AAGATCCAATCTTCGAACATGCTGAA	91756466 (Bombyx mori)
CS014	1857	AAGCAGATCAAGCATATGATGGCCTTCATCGAA	90814338 (Nasonia vitripennis)

		CA	
CS014	1858	AAGCAGATCAAGCATATGATGGCCTTCATCGAA CAAGAGGC	87266590 (Choristoneura fumiferana)
CS014	1859	ATGATGGCCTTCATCGAACAAGA	111158385 (Myzus persicae)
CS014	1860	ATGATGGCCTTCATCGAACAAGAGAGGC	98993392 (Antheraea mylitta) 91756466 (Bombyx mori) 103775905 (Heliconius erato)
CS014	1861	CAGATCAAGCATATGATGGCCTTCATCGA	53884266 (Plutella xylostella)
CS014	1862	CAGCAGCGGGCTCAAGATCATGGAATACTA	101403826 (Plodia interpunctella)
CS014	1863	CATATGATGGCCTTCATCGAACAAGAGAGGC	101403826 (Plodia interpunctella)
CS014	1864	CTCAAAGTGCGTGAGGACCACGT	103775905 (Heliconius erato)
CS014	1865	CTCAAGATCATGGAATACTACGA	15068660 (Drosophila melanogaster)
CS014	1866	GAAATCGATGCAAAGGCCGAAGAGGAGTTCAA	103775905 (Heliconius erato)
CS014	1867	GAACTCCAGAAAAAGATCCAATC	76551032 (Spodoptera frugiperda)
CS014	1868	GAACTCCAGAAAAAGATCCAATCTTCGAACATG CTGAA	87266590 (Choristoneura fumiferana)
CS014	1869	GAGGAAATCGATGCAAAGGCCGA	76551032 (Spodoptera frugiperda)
CS014	1870	GCCGAAGAGGAGTTCAACATTGAAAAAGG	33374540 (Glossina morsitans)
CS014	1871	GCGCCTGGCTGAGGTGCCCAA	101403826 (Plodia interpunctella)
CS014	1872	GGCCGCCTGGTGCAGCAGCAGCG	24975647 (Anopheles gambiae)
CS014	1873	GGCTCAAGATCATGGAATACTA	37593557 (Pediculus humanus)
CS014	1874	GGCTCAAGATCATGGAATACTACGA	58371699 (Lonomia obliqua)
CS014	1875	TACGAAAAGAAAGAGAAACAAGT	33374540 (Glossina morsitans)
CS014	1876	TGAAGGTGCTCAAAGTGCGTGAGGA	92976185 (Drosophila grimshawi) 92994742 (Drosophila mojavensis)
CS014	1877	TTCAAAGCAGATCAAGCATATGATGGCCTTCA TCGAACAAGAGGC	3738660 (Manduca sexta)
CS015	1878	AACGGGCCGGAGATCATGTCCAA	92480997 (Drosophila erecta)
CS015	1879	AACTGCCCCGATGAGAAGATCCG	91086234 (Tribolium castaneum)
CS015	1880	ATCTTCATCGATGAACTGGATGC	56152379 (Rhynchosciara americana)
CS015	1881	CATATATTGCCCATTGATGATTC	58371642 (Lonomia obliqua)
CS015	1882	CTCATGTATGGGCGCCGCCTGGTACCGG	83423460 (Bombyx mori)
CS015	1883	CTGCCCCGATGAGAAGATCCGCATGAACCG	92948836 (Drosophila ananassae)

CS015	1884	GAGAAGATCCGCATGAACCGCGT	4691131 (Aedes aegypti) 92466521 (Drosophila erecta) 15070638 (Drosophila melanogaster)
CS015	1885	GTACATATATTGCCCATTGAT	90133859 (Bicyclus anynana)
CS015	1886	TCATCGCACGTGATCGTAATGGC	22474136 (Helicoverpa armigera)
CS015	1887	TTCATGGTTCGCGGGGGGCATG	29551125 (Bombyx mori)
CS016	1888	AAATCGGTGTACATGTAACCTGGGAAACCACG	55797015 (Acyrthosiphon pisum) 73615307 (Aphis gossypii)
CS016	1889	AAGTTGTCCTCGTGGTCGTCCA	91826756 (Bombyx mori)
CS016	1890	ACAGATCTGGGCGGCAATTTC	18950388 (Anopheles gambiae) 31206154 (Anopheles gambiae str. PEST)
CS016	1891	ACAGCCTTCATGGCCTGCACGTCCTT	76169888 (Diploptera punctata) 92953069 (Drosophila ananassae) 92477149 (Drosophila erecta) 8809 (Drosophila melanogaster) 55694467 (Drosophila yakuba)
CS016	1892	ACATCAGAGTGGTCCTTGCGGGTCAT	55694467 (Drosophila yakuba) 110248186 (Spodoptera frugiperda)
CS016	1893	ACCAGCACGTGTTTCTCACACTGGTA	91829127 (Bombyx mori)
CS016	1894	ACCTCCTCACGGGGCGGGACAC	237458 (Heliothis virescens) 27372076 (Spodoptera littoralis)
CS016	1895	ACGACAGCCTTCATGGCCTGCACGTCCTT	67896654 (Drosophila pseudoobscura)
CS016	1896	ACGTAGATCTGTCCCTCAGTGATGTA	53883819 (Plutella xylostella)
CS016	1897	AGAGCCCTCCGCGTACGAAGACATGTC	53883819 (Plutella xylostella)
CS016	1898	AGCAATGGAGTTCATCACGTC	60295607 (Homalodisca coagulata)
CS016	1899	AGCAGCTGCCAGCCGATGTCCAG	92953069 (Drosophila ananassae) 92477149 (Drosophila erecta) 55694467 (Drosophila yakuba) 112349870 (Helicoverpa armigera) 237458 (Heliothis virescens) 9713 (Manduca sexta) 110242332 (Spodoptera frugiperda)

CS016	1900	AGCATCTCCTTGGGGAAGATACG	63005818 (Bombyx mori) 92967975 (Drosophila mojavensis) 92938364 (Drosophila virilis) 92231646 (Drosophila willistoni) 237458 (Heliothis virescens)
CS016	1901	AGGGCTTCCTCACCGACGACAGCCTTCATGGCCTG	4680479 (Aedes aegypti)
CS016	1902	ATACCAGTCTGGATCATTTCCTCAGG	60295607 (Homalodisca coagulata)
CS016	1903	ATACGGGACCAGGGGTTGATGGGCTG	92953552 (Drosophila ananassae)
CS016	1904	ATAGCGGAGATACCAGTCTGGATCAT	237458 (Heliothis virescens) 76554661 (Spodoptera frugiperda)
CS016	1905	ATCTGGGCGGCAATTTCGTTGTG	83937869 (Lutzomyia longipalpis)
CS016	1906	ATGGCAGACTTCATGAGACGA	55894053 (Locusta migratoria)
CS016	1907	ATGGTGGCCAAATCGGTGTACATGTAACC	92965644 (Drosophila grimshawi)
CS016	1908	ATGGTGGCCAAATCGGTGTACATGTAACCT	92969578 (Drosophila grimshawi)
CS016	1909	ATGGTGGCCAAATCGGTGTACATGTAACCTGGGAAACCACG	92231646 (Drosophila willistoni)
CS016	1910	ATTCAAGAACAGGCACACGTTCTCCATGGAGCCGTTCTCCTCGAAGTCCTGCTTGAAGAA	67841091 (Drosophila pseudoobscura)
CS016	1911	ATTGGGGGACCTTTGTCAATGGGGTTTTCC	49395165 (Drosophila melanogaster) 99009492 (Leptinotarsa decemlineata)
CS016	1912	CACACGTTCTCCATGGAGCCGTTCTCCTCGAAGTCCTGCTTGAAGAA	92477818 (Drosophila erecta)
CS016	1913	CACTGGTAGGCCAAGAACTCAGC	4680479 (Aedes aegypti)
CS016	1914	CATCTCCTTGGGGAAGATACG	16899457 (Ctenocephalides felis) 9713 (Manduca sexta)
CS016	1915	CCCTCACCGATGGCAGACTTCAT	4680479 (Aedes aegypti) 92924977 (Drosophila virilis) 110248186 (Spodoptera frugiperda)
CS016	1916	CCGATGGCAGACTTCATGAGACG	71049259 (Oncometopia nigricans)
CS016	1917	CCGTCTCCATGTTCACACCCATGGCGGGCGAACACGATGGC	33547658 (Anopheles gambiae)
CS016	1918	CCGTTCTCCTCGAAGTCCTGCTTGAAGAA	31206154 (Anopheles gambiae str. PEST) 8809 (Drosophila melanogaster)

CS016	1919	CCGTTCTCCTCGAAGTCCTGCTTGAAGAACC	101403557 (Plodia interpunctella)
CS016	1920	CGAGCAATGGAGTTCATCACGTGCGATAGCGGAGATACCAGTCTGGATCAT	27372076 (Spodoptera littoralis)
CS016	1921	CGGGCCGTGTCCATGTTCACACCCATGGCGGCGAACACGATGGC	31206154 (Anopheles gambiae str. PEST)
CS016	1922	CGTCCGGGCCACCTCCTCACGGGCGGC	18883474 (Anopheles gambiae) 31206154 (Anopheles gambiae str. PEST)
CS016	1923	CGTCCGGGCCACCTCCTCACGGGCGGCGGACAC	9713 (Manduca sexta) 110248186 (Spodoptera frugiperda)
CS016	1924	CTACAGATCTGGGCGGGCAATTTC	91826756 (Bombyx mori) 9713 (Manduca sexta) 27372076 (Spodoptera littoralis)
CS016	1925	CTACAGATCTGGGCGGGCAATTTCGTTGTG	237458 (Heliothis virescens) 76554661 (Spodoptera frugiperda)
CS016	1926	CTCGTAGATGGTGGCCAAATC	53883819 (Plutella xylostella)
CS016	1927	CTCGTAGATGGTGGCCAAATCGGTGTACATGTA	18883474 (Anopheles gambiae) 31206154 (Anopheles gambiae str. PEST)
CS016	1928	CTCGTAGATGGTGGCCAAATCGGTGTACATGTAACC	92953069 (Drosophila ananassae) 92477818 (Drosophila erecta) 8809 (Drosophila melanogaster) 67896654 (Drosophila pseudoobscura)
CS016	1929	CTCGTAGATGGTGGCCAAATCGGTGTACATGTAACCTGGGAAACCACG	9713 (Manduca sexta) 110248186 (Spodoptera frugiperda) 27372076 (Spodoptera littoralis)
CS016	1930	GAACAGGCACACGTTCTCCATGGA	92962756 (Drosophila ananassae)
CS016	1931	GACTCGAATACTGTGCGGTTCTCGTAGTT	87266757 (Choristoneura fumiferana) 9713 (Manduca sexta)
CS016	1932	GACTTCATGAGACGAGACAGGGAAGGCAGCACGTT	9713 (Manduca sexta)
CS016	1933	GAGATACCAGTCTGGATCATTTC	92969748 (Drosophila mojavensis)
CS016	1934	GAGATACCAGTCTGGATCATTTCCTC	92935139 (Drosophila virilis)
CS016	1935	GATGAAGTTCTTCTCGAACTTGG	2921501 (Culex pipiens)

CS016	1936	GATGAAGTTCTTCTCGAACTTGGT	4680479 (Aedes aegypti) 31206154 (Anopheles gambiae str. PEST) 92953069 (Drosophila ananassae) 92477149 (Drosophila erecta) 8809 (Drosophila melanogaster) 67896654 (Drosophila pseudoobscura) 55694467 (Drosophila yakuba) 112349870 (Helicoverpa armigera) 237458 (Heliothis virescens)
CS016	1937	GATGAAGTTCTTCTCGAACTTGGTGAGGTAGAGCA	76555122 (Spodoptera frugiperda)
CS016	1938	GATGGGGATCTGCGTGATGGA	101403557 (Plodia interpunctella) 53883819 (Plutella xylostella)
CS016	1939	GCACACGTTCTTCCATGGAGCCGTTCTC	104530890 (Belgica antarctica)
CS016	1940	GCCAAATCGGTGTACATGTAACCTGGGAAACCACGTCGTCCGGG	91829127 (Bombyx mori)
CS016	1941	GCCAAGAACTCAGCAGCAGTCA	237458 (Heliothis virescens)
CS016	1942	GCCGTCTCCATGTTCACACCCA	83937868 (Lutzomyia longipalpis)
CS016	1943	GCCGTCTCCATGTTCACACCCAT	92965644 (Drosophila grimshawi)
CS016	1944	GCCTGCACGTCCTTACCGATGGCGTAGCA	112349870 (Helicoverpa armigera) 237458 (Heliothis virescens) 110248186 (Spodoptera frugiperda)
CS016	1945	GCCTTCATGGCCTGCACGTCCTT	39675733 (Anopheles gambiae) 31206154 (Anopheles gambiae str. PEST)
CS016	1946	GCCTTCATGGCCTGCACGTCCTTACCGATGGCGTAGCA	2921501 (Culex pipiens)
CS016	1947	GCGGGCGAACACGATGGCAAAGTT	2921501 (Culex pipiens) 92965644 (Drosophila grimshawi)
CS016	1948	GCGGGCGAACACGATGGCAAAGTTGTCCTCGTG	77905105 (Aedes aegypti)
CS016	1949	GCGTACAGCTGGTTGGAAACATC	67896654 (Drosophila pseudoobscura)
CS016	1950	GGAATAGGATGGGTGATGTCGTCGTTGGGCATAGT	110248186 (Spodoptera frugiperda)
CS016	1951	GGAATAGGATGGGTGATGTCGTCGTTGGGCATAGTCA	27372076 (Spodoptera littoralis)

CS016	1952	GGATGGGGTGATGTCGTCGTTGGGGCAT	101403557 (Plodia interpunctella)
CS016	1953	GGCAGACACCGGCAGCCGAGAAAATGGGGGATCTT	67841091 (Drosophila pseudoobscura)
CS016	1954	GGCATAGTCAAGATGGGGGATCTG	92924977 (Drosophila virilis)
CS016	1955	GGCCGTCTCCATGTTCACACCCATGGC	101403557 (Plodia interpunctella)
CS016	1956	GGCGGGTAGATCTGTCTGTTGTG	2921501 (Culex pipiens) 92965644 (Drosophila grimshawi) 92924977 (Drosophila virilis)
CS016	1957	GGCGGGTAGATCTGTCTGTTGTGGAGCTGACG GTCTACGTAGATCTGTCCCTCAGT	237458 (Heliothis virescens) 110248186 (Spodoptera frugiperda)
CS016	1958	GGGAAGATACGGGAGCAGCTGCCA	60336551 (Homalodisca coagulata)
CS016	1959	GGGTTGATGGGCGTGTCCCTGGATGTCCAA	76554661 (Spodoptera frugiperda) 27372076 (Spodoptera littoralis)
CS016	1960	GGTTTTCCAGAGCCGTTGAATAC	62238871 (Diabrotica virgifera)
CS016	1961	GTGATGAAGTTCTTCTCGAACTTGGT	87266757 (Choristoneura fumiferana)
CS016	1962	GTGCGGTTCTCGTAGTTGCCCTG	31206154 (Anopheles gambiae str. PEST) 92477149 (Drosophila erecta) 8809 (Drosophila melanogaster) 67896654 (Drosophila pseudoobscura) 92938364 (Drosophila virilis) 92231646 (Drosophila willistoni) 55694467 (Drosophila yakuba)
CS016	1963	GTGGCCAAATCGGTGTACATGTAACC	2921501 (Culex pipiens) 75469507 (Tribolium castaneum)
CS016	1964	GTGTACATGTAACCTGGGAAACCACG	101403557 (Plodia interpunctella)
CS016	1965	GTGTACATGTAACCTGGGAAACCACGTCG	237458 (Heliothis virescens)
CS016	1966	GTGTACATGTAACCTGGGAAACCACGTCGTCC GGGCACCTCCCTCACGGGCGGC	53883819 (Plutella xylostella)
CS016	1967	TCAGAGTGGTCCTTGCGGGTCAT	237458 (Heliothis virescens) 9713 (Manduca sexta)
CS016	1968	TCAGCAAGGATTGGGGGACCTTTGTC	10763875 (Manduca sexta)
CS016	1969	TCCTCACCGACGACAGCCTTCATGGCCTG	92969578 (Drosophila grimshawi)
CS016	1970	TCCTCAGGGTAGATACGGGGACCA	76554661 (Spodoptera frugiperda)

CS016	1971	TCCTCAGGGTAGATACGGGACCAGGGGTTGATGGGCTG	22474040 (Helicoverpa armigera) 237458 (Heliothis virescens) 9713 (Manduca sexta)
CS016	1972	TCGAAGTCCTGCTTGAAGAACC	9713 (Manduca sexta)
CS016	1973	TCGTAGATGGTGGCCAAATCGGTGTACATGTAACC	62239897 (Diabrotica virgifera)
CS016	1974	TCGTAGATGGTGGCCAAATCGGTGTACATGTAACCTGGGAAACCACG	4680479 (Aedes aegypti)
CS016	1975	TCTACGTAGATCTGTCCCTCAGTGATGTA	101403557 (Plodia interpunctella)
CS016	1976	TGCACGTCCTTACCGATGGCGTAGCA	9713 (Manduca sexta) 75710699 (Tribolium castaneum)
CS016	1977	TGGGTGATGTCGTCGTTGGGCAT	53883819 (Plutella xylostella)
CS016	1978	TGGTAGGCCAAGAACTCAGCAGC	9713 (Manduca sexta)
CS016	1979	TTCAAGAACAGGCACACGTTCTCCAT	18883474 (Anopheles gambiae) 31206154 (Anopheles gambiae str. PEST) 92933153 (Drosophila virilis) 27372076 (Spodoptera littoralis)
CS016	1980	TTCAAGAACAGGCACACGTTCTCCATGGA	92950254 (Drosophila ananassae) 76554661 (Spodoptera frugiperda)
CS016	1981	TTCTCACACTGGTAGGCCAAGAA	18883474 (Anopheles gambiae)
CS016	1982	TTCTCCTCGAAGTCCTGCTTGAAGAA	83937868 (Lutzomyia longipalpis)
CS016	1983	TTGAGCATCTCCTTGGGGAAGATACG	92477149 (Drosophila erecta) 8809 (Drosophila melanogaster) 67896654 (Drosophila pseudoobscura) 112349870 (Helicoverpa armigera)
CS016	1984	TTGAGCATCTCCTTGGGGAAGATACGGGAGCA	83928466 (Lutzomyia longipalpis)
CS016	1985	TTGAGCATCTCCTTGGGGAAGATACGGAGCAGCTGCCA	50559098 (Homalodisca coagulata) 71049259 (Oncometopia nigricans)
CS016	1986	TTGAGCATCTCCTTGGGGAAGATACGGAGCAGCTGCCAGCCGATGTC	87266757 (Choristoneura fumiferana)
CS018	1987	TCCGACTACTCTTCCACGGAC	31659029 (Anopheles gambiae)

Table 4-PX

Target ID	SEQ ID NO	Sequence *	Example Gi-number and species
PX001	2120	AACAACGTGTTCATCATCGGCAAGGGCACGAA	112350001 (Helicoverpa armigera)
PX001	2121	AACGTGTTCATCATCGGCAAG	27562760 (Anopheles gambiae) 58378595 (Anopheles gambiae str. PEST)
PX001	2122	AACGTGTTCATCATCGGCAAGG	42764924 (Armigeres subalbatus)
PX001	2123	AACGTGTTCATCATCGGCAAGGG	71048604 (Oncometopia nigricans)
PX001	2124	AACGTGTTCATCATCGGCAAGGGCACGAA	112783858 (Anopheles funestus)
PX001	2125	AACTTGGGGGCGAGTGGGCACCATCGTGTC	90132259 (Bicyclus anynana)
PX001	2126	AACTTGGGGGCGAGTGGGCACCATCGTGTCCCGCGAG	112350001 (Helicoverpa armigera)
PX001	2127	AAGATCGTGAAGCAGCGCCTCATCAAGGTGGACGGCAAGGT	112350001 (Helicoverpa armigera)
PX001	2128	AAGGTCCGCACCGACCCCACCTA	14627585 (Drosophila melanogaster)
PX001	2129	AAGTACAAGCTGTGCAAGGTG	5498893 (Antheraea yamamai) 90132259 (Bicyclus anynana) 92969396 (Drosophila grimshawi) 50818668 (Heliconius melpomene) 58371410 (Lonomia obliqua)
PX001	2130	ACAACGTGTTCATCATCGGCAAGGGCACGAA	103783745 (Heliconius erato)
PX001	2131	ACGGCAAGGTCCGCACCGACCC	77890923 (Aedes aegypti)
PX001	2132	ACGGCCGCACGCTGCCGTACCCCGACCCGCTCATCAAGGTCAACGACTCC	101413238 (Plodia interpunctella)
PX001	2133	ACGTGTTCATCATCGGCAAGGGCAC	109509107 (Culex pipiens)
PX001	2134	AGGAGGCCAAGTACAAGCTGT	27566312 (Anopheles gambiae) 67889891 (Drosophila pseudoobscura)
PX001	2135	AGGAGGCCAAGTACAAGCTGTGCAAGGT	92944919 (Drosophila ananassae) 67886177 (Drosophila pseudoobscura) 92045792 (Drosophila willistoni)
PX001	2136	AGGAGGCCAAGTACAAGCTGTGCAAGGTG	92929731 (Drosophila virilis)
PX001	2137	CAACGTGTTCATCATCGGCAA	109509107 (Culex pipiens)
PX001	2138	CAACGTGTTCATCATCGGCAAGGGCA	55816641 (Drosophila yakuba)
PX001	2139	CACACCTTCGCCACCAGGTTGAACAACGTGTT	3986403 (Antheraea yamamai)
PX001	2140	CCCCAAGAAGCATTTGAAGCG	2886669 (Drosophila melanogaster)
PX001	2141	CCGAGGAGGCCAAGTACACAAGCT	92944919 (Drosophila ananassae)

PX001	2142	CCGAGGAGGCCAAGTACAAGCTGTGCAAGGT	15480750 (Drosophila melanogaster)
PX001	2143	CCGCACAAGCTGCGCGAGTGCCTGCCGCT	22474232 (Helicoverpa armigera)
PX001	2144	CGACGGGCCCCAAGAAACGTGCC	112350001 (Helicoverpa armigera)
PX001	2145	CGAGGAGGCCAAGTACACAAGCT	58378595 (Anopheles gambiae str. PEST)
PX001	2146	CGAGGAGGCCAAGTACAAGCTG	18914191 (Anopheles gambiae)
PX001	2147	CGAGTGGGCACCATCGTGTCCCGCGAG	3986403 (Antheraea yamamai)
PX001	2148	CGCTACCCGACCCGCTCATCAAGGTCAACGACTCC	112350001 (Helicoverpa armigera)
PX001	2149	CGCTTCACCATCCACCGCATCAC	103783745 (Heliconius erato)
PX001	2150	CGGCAACGAGGTGCTGAAGATCGT	90132259 (Bicyclus anynana)
PX001	2151	CGTAACTTGGGCGGCGAGTGGGCAC	60311985 (Papilio dardanus)
PX001	2152	CTACCCGGCTGGATTCATGGATGT	42764924 (Armigeres subalbatus)
PX001	2153	CTCATCAAGGTCAACGACTCC	103783745 (Heliconius erato)
PX001	2154	CTCATCAAGGTCAACGACTCCATCCAGCTCGACAT	3738704 (Manduca sexta)
PX001	2155	GACGGGCAAGGTCCGCACCGAC	109509107 (Culex pipiens)
PX001	2156	GACGGGCAAGGTCCGCACCGACCC	77759638 (Aedes aegypti)
PX001	2157	GAGGAGGCCAAGTACAAGCTGTGCAAGGT	67841491 (Drosophila pseudoobscura)
PX001	2158	GAGGAGGCCAAGTACAAGCTGTGCAAGGTG	56772971 (Drosophila virilis)
PX001	2159	GAGGGCCAAGTACAAGCTGTGCAA	112350001 (Helicoverpa armigera)
PX001	2160	GAGGGCCAAGTACAAGCTGTGCAAGGTG	98993531 (Antheraea mylitta)
PX001	2161	GCCAAGTACAAGCTGTGCAAGGT	67838306 (Drosophila pseudoobscura) 109978109 (Gryllus pennsylvanicus)
PX001	2162	GCCCCAAGAAGCATTTGAAGCG	2151718 (Drosophila melanogaster)
PX001	2163	GCGCGTGGCGACGGGCCCCAA	5498893 (Antheraea yamamai)
PX001	2164	GCGCGTGGCGACGGGGCCCCAAG	3986403 (Antheraea yamamai)
PX001	2165	GGAGGCCAAGTACAAGCTGTGCAAGGT	92942537 (Drosophila ananassae)
PX001	2166	GGCCCCAAGAAGCATTTGAAGCG	4459798 (Drosophila melanogaster)
PX001	2167	GGCGGGCGTGTACGCGCCGCGGCCC	98994282 (Antheraea mylitta)
PX001	2168	GTCCGCACCGACCCCACCTACCC	92472430 (Drosophila erecta) 55854272 (Drosophila yakuba)
PX001	2169	GTGGGCACCATCGTGTCCCGCGAGAG	3953837 (Bombyx mandarina) 29554802 (Bombyx mori)
PX001	2170	TCAAGGTGGACGGCAAGGTCCGCACCGACCC	92944919 (Drosophila ananassae)
PX001	2171	TGATCTACGATGTGAAGGGACG	83935965 (Lutzomyia longipalpis)

PX001	2172	TTCATGGATGTTGTGTCGATTGAAAA	90132259 (Bicyclus anynana)
PX001	2173	GCTGGATTCATGGATGTTGTG	10707240 (Amblyomma americanum)
PX001	2174	AAGCAGCGCCTCATCAAGGTGGACGGCAAGGTCCGCACCGAC	49545866 (Rhipicephalus appendiculatus)
PX009	2175	AACATCTTCAACTGTGACTTC	93001544 (Drosophila mojavensis)
PX009	2176	TGATCAACATCGAGTGCAAAGC	110755556 (Apis mellifera)
PX009	2177	TTCTTGAAGCTGAATAAGATCT	103750396 (Drosophila melanogaster)
PX010	2178	CAGTTCCTGCAGGTCTTCAACAA	71553175 (Oncometopia nigricans)
PX010	2179	CCATCAGCGGACGGTGGCGCCCCCGTG	90139187 (Spodoptera frugiperda)
PX010	2180	CCCGCAGTTCATGTACCACCTGCGCCGCTCGCGCAGTTC	67893194 (Drosophila pseudoobscura)
PX010	2181	CCGAACAGCTTCCGTCTGTCGGAGAACTTCAG	29558345 (Bombyx mori)
PX010	2182	CGCCTGTGCCAGAAGTTCGGGCGAGTACG	58395529 (Anopheles gambiae str. PEST)
PX010	2183	CTGGCCGCGCTCGCAGTTCCTGCAGGT	18872210 (Anopheles gambiae)
PX010	2184	CTGTACCCGCAGTTCATGTACCA	29558345 (Bombyx mori)
PX010	2185	GACGTGCTGCGCGCTGGCTCGACCG	29558345 (Bombyx mori)
PX010	2186	GACGTGTCGCTGCAAGTGTTCATGGAGCA	18872210 (Anopheles gambiae)
PX010	2187	GAGTACGAGAACTTCAAGCAGCAGCTGCTGC	77886140 (Aedes aegypti) 18872210 (Anopheles gambiae) 49376735 (Drosophila melanogaster) 67893324 (Drosophila pseudoobscura)
PX010	2188	GGCGGGGGCGGATGCCGATACCATC	91757875 (Bombyx mori)
PX010	2189	GTGGCTGCATACAGTTCATTACGCGCAGTACCAGCAC	28571527 (Drosophila melanogaster)
PX010	2190	TCGCAGTTCCTGCAGGTCTTCAACAA	92932090 (Drosophila virilis)
PX010	2191	TGCGCCGGCTCGCAGTTCCTGCAGGTCTTCAACAA	67893324 (Drosophila pseudoobscura)
PX010	2192	TGCGCCGGCTCGCAGTTCCTGCAGGTCTTCAACAACTCGCCCGACGAGACCAC	92952825 (Drosophila ananassae)
PX010	2193	TTCATGTACCACCTGCGCCGCTCGCGCAGTTCCTGCAGGTCTTCAACAACTCGCCCGACGAGACCAC	28571527 (Drosophila melanogaster)
PX010	2194	ATCCTGCTCATGGACACCTTCTTCCA	82842646 (Boophilus microplus)
PX015	2195	CACCGCGACGACACGTTCATGGTGCGCGGGCGG	58371643 (Lonomia obliqua)
PX015	2196	CAGATCAAGGAGAGATGGTGGAG	92480997 (Drosophila erecta) 58371722 (Lonomia obliqua)
PX015	2197	CCCGACGAGAAGATCCGCATGAA	67873606 (Drosophila pseudoobscura)

PX015	2198	CCCGACGAGAGAAGATCCGCGATGAACCGCGT	15070733 (Drosophila melanogaster)
PX015	2199	CCGGCAAGGAGAGAGATCCGCGATGAACCGCGT	92459970 (Drosophila erecta)
PX015	2200	CGCAAGGAGAGACCGTGTGCATTGTGCT	67873606 (Drosophila pseudoobscura)
PX015	2201	GACGAGAAGATCCGCGATGAACCG	18914444 (Anopheles gambiae)
PX015	2202	GACGAGAAGATCCGCGATGAACCGCGT	4691131 (Aedes aegypti)
PX015	2203	GCGCAGATCAAGGAGAGATGGTGGAGCT	99007898 (Leptinotarsa decemlineata)
PX015	2204	GGCATGCGCGGCGGTCGAGTTC	6901917 (Bombyx mori)
PX015	2205	GTGCGCGGCGGCGCATGCGCGCC	67891252 (Drosophila pseudoobscura)
PX015	2206	TCAAGGAGATGGTGGAGCTGC	27819993 (Drosophila melanogaster)
PX015	2207	TGAAGCCGTACTTCATGGAGGC	29559940 (Bombyx mori)
PX015	2208	TGCCGCAAGCAGCTGGCGCAGATCAAGGAGAGATGGT	18914444 (Anopheles gambiae)
PX015	2209	TGGAGGCCGTACCGGCCCATCCAC	18914444 (Anopheles gambiae)
PX016	2210	AAGGACCACTCCGACGTGTCCAA	101406307 (Plodia interpunctella)
PX016	2211	AAGGACGCGTGCAGGCGATGAAGGC	112349870 (Helicoverpa armigera) 110248186 (Spodoptera frugiperda)
PX016	2212	ACCAAGTTCGAGAAGAACTTCATC	4680479 (Aedes aegypti) 31206154 (Anopheles gambiae str. PEST) 92953069 (Drosophila ananassae) 92477149 (Drosophila erecta) 24646340 (Drosophila melanogaster) 67900295 (Drosophila pseudoobscura) 55694467 (Drosophila yakuba) 112349870 (Helicoverpa armigera) 237458 (Heliothis virescens)
PX016	2213	ACCAAGTTCGAGAAGAGAACTTCATCAC	87266757 (Choristoneura fumiferana)
PX016	2214	ACCGCCAGGTTCTTCAAGCAGCAGGACTTCGA	9713 (Manduca sexta)
PX016	2215	ACCGGCGATATTCTGCGCACGCCCGTCTC	92940287 (Drosophila virilis)
PX016	2216	AGCAGGACTTCGAGGAGAACGG	67880606 (Drosophila pseudoobscura)
PX016	2217	ATCACGCAGATCCCCATCCTGACGATGCC	31206154 (Anopheles gambiae str. PEST)
PX016	2218	ATCTTGACCGACACATGTCTTCATACGC	104530890 (Belgica antarctica) 92231646 (Drosophila willistoni)
PX016	2219	ATGACCAGGAAGGACCACTCCGACGT	75713096 (Tribolium castaneum)

PX016	2220	ATGCCCAACGACGACGACATCACCCA	101406307 (Plodia interpunctella) 76555122 (Spodoptera frugiperda) 27372076 (Spodoptera littoralis)
PX016	2221	CAGAAGATCCCCATCTTCTCCGCGGCCGGTCTGCCCCACAACGA	92460896 (Drosophila erecta) 24846340 (Drosophila melanogaster)
PX016	2222	CAGGACTTCGAGGAGAACGGTTCCATGGAGAACGT	2921501 (Culex pipiens) 76554661 (Spodoptera frugiperda)
PX016	2223	CCAAGTTCGAGAAGAACTTCATC	2921501 (Culex pipiens)
PX016	2224	CCCATCAACCCGTGGTCCCGTATCTACCCGGAGGA	2921501 (Culex pipiens)
PX016	2225	CCCGACTTGACCGGGTACATCACTGAGGGACAGATCTACGT	101406307 (Plodia interpunctella)
PX016	2226	CCCGGACGACGTGGTTTCCCAGGTTACATGTACAC	91829127 (Bombyx mori)
PX016	2227	CCTGGACATCCAGGGGCAGCCCATCAACCC	91090030 (Tribolium castaneum)
PX016	2228	CGACGTGGTTTCCCAGGTTACATGTACACGGATTTGGC	237458 (Heliothis virescens)
PX016	2229	CGTCTCATGAAGTCCGCCATCGG	91829127 (Bombyx mori)
PX016	2230	CGTCTCATGAAGTCCGCCATCGGAGAGGGCATGACC	237458 (Heliothis virescens)
PX016	2231	CGTGGTCAGAAGATCCCCATCTTCTC	27372076 (Spodoptera littoralis)
PX016	2232	CGTGGTCAGAAGATCCCCATCTTCTCCGC	76554661 (Spodoptera frugiperda)
PX016	2233	CGTGGTTTCCCAGGTTACATGTACAC	55797015 (Acyrthosiphon pisum) 4680479 (Aedes aegypti) 73615307 (Aphis gossypii) 92231646 (Drosophila willistoni) 9713 (Manduca sexta) 76555122 (Spodoptera frugiperda) 27372076 (Spodoptera littoralis)
PX016	2234	CGTGGTTTCCCAGGTTACATGTACACGGATTTGGCCCACAATCTACGAGCGGCGCGGGGCG	101406307 (Plodia interpunctella)
PX016	2235	CTACGAGAACCGCACAGTGTTCGAGTC	112350031 (Heliocverpa armigera) 237458 (Heliothis virescens) 76555122 (Spodoptera frugiperda)

PX016	2236	CTGCGTATCTTCCCCAAGGAGAT	63005818 (Bombyx mori) 9247149 (Drosophila erecta) 24646340 (Drosophila melanogaster) 56773982 (Drosophila pseudoobscura) 92935600 (Drosophila virilis) 92220609 (Drosophila willistoni) 112350031 (Helicoverpa armigera) 237458 (Heliothis virescens) 9713 (Manduca sexta)
PX016	2237	CTGTACGCGTGCTACGCCATCGG	9713 (Manduca sexta)
PX016	2238	CTGTTCTTGAACTTGGCCAATGA	16898595 (Ctenocephalides felis)
PX016	2239	CTGTTCTTGAACTTGGCCAATGACCC	27372076 (Spodoptera littoralis)
PX016	2240	GACAACTTCGCCATCGTGTTCGC	92950254 (Drosophila ananassae)
PX016	2241	GACAACTTCGCCATCGTGTTCGCCGC	92477818 (Drosophila erecta) 24646340 (Drosophila melanogaster) 237458 (Heliothis virescens) 9713 (Manduca sexta) 76554661 (Spodoptera frugiperda)
PX016	2242	GACAACTTCGCCATCGTGTTCGCGCCATGGG	31206154 (Anopheles gambiae str. PEST)
PX016	2243	GACCGTCAGCTGCACAACAGGCA	50564193 (Homalodisca coagulata)
PX016	2244	GACCTGCTCTACCTCGAGTTC	112349870 (Helicoverpa armigera)
PX016	2245	GACGTGATGAACTCCATCGCCCG	237458 (Heliothis virescens)
PX016	2246	GACGTGATGAACTCCATCGCCCGTGG	2247404040 (Helicoverpa armigera)
PX016	2247	GAGAACGGTTCCATGGAGAACGT	91829127 (Bombyx mori)
PX016	2248	GAGGAGATGATCCAGACTGGTATCTCCGCTAT	237458 (Heliothis virescens) 76554661 (Spodoptera frugiperda)
PX016	2249	GAGGAGATGATCCAGACTGGTATCTCCGCTATCGACGTGATG AACTCCAT	27372076 (Spodoptera littoralis)
PX016	2250	GAGGAGGCGGCTCACGCCCGACGAC	9713 (Manduca sexta)
PX016	2251	GAGTTCTTGGCCTACCAGTGCGAGAA	4680479 (Aedes aegypti)
PX016	2252	GCCAGGTTCTTCAAGCAGGACTTCGAGGAGAACGG	101403557 (Plodia interpunctella)
PX016	2253	GCCCGTGGTCAGAAGATCCCCAT	67877903 (Drosophila pseudoobscura)
PX016	2254	GCCCGTGGTCAGAAGATCCCCATCTTCTC	6901845 (Bombyx mori)

PX016	2255	GCCCGTGGTCAGAAGATCCCATCTTCTCCGCCGC	92950254 (Drosophila ananassae)
PX016	2256	GCCGAGTTCTTGGCCTACCAGTGCGAGAA	24646340 (Drosophila melanogaster)
PX016	2257	GCCGAGTTCTTGGCCTACCAGTGCGAGAAACACGTGTTGGT	110240379 (Spodoptera frugiperda)
PX016	2258	GCCGCCCGTGAGGAGGTGCCCGGACG	31206154 (Anopheles gambiae str. PEST) 9713 (Manduca sexta) 110240379 (Spodoptera frugiperda)
PX016	2259	GCCTACCAGTGCGAGAAACACGTGTTGGTAATCTTGACCGACATGTC	101406307 (Plodia interpunctella)
PX016	2260	GGCAGATCTACCCGCCGGTGAA	31206154 (Anopheles gambiae str. PEST)
PX016	2261	GGCGAGGAGGGGCTCACGCCCGACGA	31206154 (Anopheles gambiae str. PEST)
PX016	2262	GGTCAGAAGATCCCCATCTTCTC	60295607 (Homalodisca coagulata)
PX016	2263	GGTTACATGTACACGGATTTGGCCAC	92924977 (Drosophila virilis)
PX016	2264	GTGGTGGGCGAGGAGGCGGCTCACGCC	112349870 (Helicoverpa armigera)
PX016	2265	GTTCACCGGGCGATATTCTGCG	92997483 (Drosophila grimshawi)
PX016	2266	GTTCACCGGGCGATATTCTGCGCAC	92950254 (Drosophila ananassae) 92048971 (Drosophila willistoni)
PX016	2267	TACCAGTGCGAGAAACACGTGTTGGT	237458 (Heliothis virescens)
PX016	2268	TACGCCATCGGCCAAGGACGTGCCAGGGCGATGAAGGC	87266757 (Choristoneura fumiferana)
PX016	2269	TCCATCACGCAGATCCCCATCCT	101406307 (Plodia interpunctella)
PX016	2270	TCCGGCCAAGCCCATCGACAAGGGG	92460896 (Drosophila erecta) 24646340 (Drosophila melanogaster) 22474040 (Helicoverpa armigera) 237458 (Heliothis virescens)
PX016	2271	TCTACGAGCGCGCCGGGGCGAGTC	33528180 (Trichoplusia ni)
PX016	2272	TCTCGTCTCATGAAGTCCGCCATCGG	9713 (Manduca sexta)
PX016	2273	TGACTGCTGCCGAGTTCTTGGCCTACCAGTGCGAGAAACACGTGTTGGT	27372076 (Spodoptera littoralis)
PX016	2274	TGCACAACAGGCAGATCTACCC	62239897 (Diabrotica virgifera)
PX016	2275	TGCCGTATCTTCCCCAAGGAGAT	16900620 (Ctenocephalides felis) 92967975 (Drosophila mojavensis)

PX016	2276	TGCTACGCCATCGGCAAGGACGTGCAGGC	31206154 (Anopheles gambiae str. PEST) 92953069 (Drosophila ananassae) 92477149 (Drosophila erecta) 24646340 (Drosophila melanogaster) 67898824 (Drosophila pseudoobscura) 55694467 (Drosophila yakuba)
PX016	2277	TGCTCTACCTCGAGTTCCTCACCAAGTTCGAGAAGAACTTCATC	76555122 (Spodoptera frugiperda)
PX016	2278	TGTCTGTTCTTGAACTTGGCCAA	4680479 (Aedes aegypti) 92477818 (Drosophila erecta) 24646340 (Drosophila melanogaster)
PX016	2279	TGTCTGTTCTTGAACTTGGCCAATGA	55905051 (Locusta migratoria)
PX016	2280	TGTTCTTGAACTTGGCCAATGA	91090030 (Tribolium castaneum)
PX016	2281	TTCAACGGCTCCGGCAAGCCCAT	76554661 (Spodoptera frugiperda)
PX016	2282	TTCAACGGCTCCGGGCAAGCCCATCGACAAGGG	4680479 (Aedes aegypti) 31206154 (Anopheles gambiae str. PEST) 67877903 (Drosophila pseudoobscura)
PX016	2283	TTCGAGGAGAACGGTTCCATGGAGAA	92972277 (Drosophila grimshawi)
PX016	2284	TTCGAGGAGAACGGTTCCATGGAGAACGT	92950254 (Drosophila ananassae)
PX016	2285	TTCTTCAAGCAGGACTTCGAGGAGAA	83937868 (Lutzomyia longipalpis)
PX016	2286	TTCTTCAAGCAGGACTTCGAGGAGAACGG	92477818 (Drosophila erecta)
PX016	2287	TTCTTCAAGCAGGACTTCGAGGAGAACGGTTC	31206154 (Anopheles gambiae str. PEST)
PX016	2288	TTCTTCAAGCAGGACTTCGAGGAGAACGGTTCCATGGAGAACGT	24646340 (Drosophila melanogaster)
PX016	2289	TTCTTGAACTTGGCCAATGACCC	9713 (Manduca sexta)
PX016	2290	TTCTTGGCCTACCAGTGCGAGAA	31206154 (Anopheles gambiae str. PEST) 67883622 (Drosophila pseudoobscura) 92231646 (Drosophila willistoni)

Table 4-AD

Target ID	SEQ ID NO	Sequence *	Example GI-number and species
AD001	2384	AAAGCATGGATGTTGGACAAA	73619372 (Aphis gossypii); 77325485 (Chironomus tentans); 22474232 (Helicoverpa armigera); 37951951 (Ips pini); 60305420 (Mycetophagus quadripustulatus); 84647995 (Myzus persicae)
AD001	2385	AAAGCATGGATGTTGGACAAACT	94432102 (Bombyx mori); 103790417 (Heliconius erato); 55904580 (Locusta migratoria); 101419954 (Plodia interpunctella)
AD001	2386	AAAGGTATTCCATTCTTGGTGACCCATGATGGCC GTACTATCCGTTATCCTGACCCAGTCATTAAAGT	109978109 (Gryllus pennsylvanicus)
AD001	2387	AACTGTGAAGTAACGAAGATTGTTATGCAGCGACT TATCAAAGTTGA	109978109 (Gryllus pennsylvanicus)
AD001	2388	AAGAAGCATTTGAAGCGTTTAAA	3658572 (Manduca sexta)
AD001	2389	AAGGGTAAGGGTGTGAAATTGAGTAT	109978109 (Gryllus pennsylvanicus)
AD001	2390	AATGTATTCATCATTGGAAAGC	55904577 (Locusta migratoria)
AD001	2391	AGAAGCATTTGAAGCGTTTAAA	98994282 (Antheraea mylitta); 73619372 (Aphis gossypii)
AD001	2392	AGAAGCATTTGAAGCGTTTAAATGC	27620566 (Anopheles gambiae)
AD001	2393	AGTACTGGCCCCCACAAATTGCG	109978109 (Gryllus pennsylvanicus)
AD001	2394	AGTGCAGAAGAAGCCAAGTACAAGCT	109978109 (Gryllus pennsylvanicus)
AD001	2395	ATCGCCGAGGAGCGCGGGACAAGC	3953837 (Bombyx mandarina); 94432102 (Bombyx mori)
AD001	2396	CAAGGACATACTTTTGCCACAAGATTGAATAATGT ATTCATCATTGGAAA	109978109 (Gryllus pennsylvanicus)
AD001	2397	CAGAAGAAGCCAAGTACAAGCT	42764924 (Armigeres subalbatus)
AD001	2398	CATGATGGCCGTACTATCCGTTA	73613065 (Aphis gossypii)
AD001	2399	CATGATGGCCGTACTATCCGTTATCCTGACCC	311365398 (Toxoptera citricida)
AD001	2400	CATTTGAAGCGTTTAAATGCTCC	27557322 (Anopheles gambiae)

AD001	2401	CCTAAAGCATGGATGTTGGAC	77324536 (Chironomus tentans)
AD001	2402	CCTAAAGCATGGATGTTGGACAA	58371410 (Lonomia obliqua)
AD001	2403	CCTAAAGCATGGATGTTGGACAAA	60311985 (Papilio dardanus)
AD001	2404	CCTAAAGCATGGATGTTGGACAAACT	30031258 (Toxoptera citricida)
AD001	2405	CGTACTATCCGTTATCCTGACCC	98994282 (Antheraea mylitta)
AD001	2406	GAATGTTTACCTTTGGTGATTTTTCTTCGCAATCGGCT	37804548 (Rhopalosiphum padi)
AD001	2407	GCAGAAGAAGCCAAGTACAAGCT	109978109 (Gryllus pennsylvanicus)
AD001	2408	GCATGGATGTTGGACAAACTCGG	37953169 (Ips pini)
AD001	2409	GCTGGTTTCATGGATGTTGTCAC	83935968 (Lutzomyia longipalpis)
AD001	2410	GGCCCCAAGAAGCATTTGAAGCGTTTAA	109978109 (Gryllus pennsylvanicus)
AD001	2411	GGTTTCATGGATGTTGTCACCAT	14693528 (Drosophila melanogaster)
AD001	2412	TATGATGTGAAAGGCCGTTTCACAATTCACAGAAT	25958683 (Curculio glandium)
AD001	2413	TCATTGCCAAGGGTAAGGGT	109978109 (Gryllus pennsylvanicus)
AD001	2414	TGGATATTGCCACTTGTAAAATCATGGACCACATCAGATTTGAATCTGG	77324972 (Chironomus tentans)
AD001	2415	TTAAATGCTCCTAAAGCATGGATGTTGGACAAACT	109978109 (Gryllus pennsylvanicus)
AD001	2416	TTTGAATCTGGCAACCTGTGTATGAT	60311985 (Papilio dardanus)
AD001	2417	TTTGATATTGTTCATATCAAGGATAC	109978109 (Gryllus pennsylvanicus)
AD002	2418	AAGAAAATCGAACAAGAAATC	55902553 (Locusta migratoria)
AD002	2419	CAGCACATGGATGTGGACAAGGT	67899569 (Drosophila pseudoobscura)
AD002	2420	GAGTTTCTTTAGTAAAGTATTCGGTGG	110762684 (Apis mellifera)
AD009	2421	CACTACAACTACCACAAGAGC	84226228 (Aedes aegypti) 18941376 (Anopheles gambiae)
AD009	2422	CAGAACATCCACAACTGTGACT	29534871 (Bombyx mori)
AD009	2423	GGTGTGGGGTGTCGTCGCGAGGG	83926368 (Lutzomyia longipalpis)
AD009	2424	TGGATCCCTGAATACTACAATGA	83926506 (Lutzomyia longipalpis)
AD015	2425	GAGCAGTAGAATTCAAAGTAGT	99012451 (Leptinotarsa decemlineata)
AD015	2426	GCAATTATATTTATTGATGAA	83936542 (Lutzomyia longipalpis)
AD015	2427	TCACCATATTGTATTGTTGCT	31366806 (Toxoptera citricida)
AD015	2428	TTGTCCTGATGTTAAGTATGG	84114691 (Blomia tropicalis)
AD016	2429	ACGATGCCCAAGCAGCGACACATCACCCATCC	101406307 (Plodia interpunctella)

Target ID	SEQ ID No	Sequences	Example Gi-number and species
AD016	2430	ATGCCCAACGACGAGACATCACCCA	53883819 (Plutella xylostella)
AD016	2431	ATGCCCAACGACGAGACATCACCCATCCTATT	110240379 (Spodoptera frugiperda), 27372076 (Spodoptera littoralis)
AD016	2432	CAGAAGATCCCCATCTTCTCGG	91827264 (Bombyx mori), 22474331 (Helicoverpa armigera), 60295607 (Homalodisca coagulata)
AD016	2433	CGGCTCCATCACTCAGATCCCCAT	67896654 (Drosophila pseudoobscura)
AD016	2434	GCCAACGACCCCACCATCGAG	101406307 (Plodia interpunctella)
AD016	2435	GCCCGTGTCCGAGGACATGCTGGG	83937868 (Lutzomyia longipalpis), 75473525 (Tribolium castaneum)
AD016	2436	GGCAGAAGATCCCCATCTTCTC	2286803 (Drosophila melanogaster)
AD016	2437	GTTCACCGGCGGATATTCTGCG	92997483 (Drosophila grimshawi)
AD016	2438	GTTCACCGGCGGGATATTCTGCGC	92953552 (Drosophila ananassae), 92042621 (Drosophila willistoni)

Table 5-LD

Target ID	SEQ ID No	Sequences*	Example Gi-number and species
LD001	124	AAGAAGCATTTGAAGCGTTTG	8005678 (Meloidogyne incognita), 9829015 (Meloidogyne javanica)
LD003	125	GTTCTTCCTCTTGACGCGTCC	7710484 (Zeldia punctata)
LD003	126	GCAGCTTTACGGGATTTTTGCCAA	32183696 (Meloidogyne chitwoodi)
LD003	127	TTTCAACTCCTGATCAAGACGT	1662318 (Brugia malayi), 31229562 (Wuchereria bancrofti)
LD006	128	GCTATGGGTAAGCAAGCTATGGG	520506 (Caenorhabditis elegans)
LD007	129	AAAGAATAAAAAATTATTTGA	17539725 (Caenorhabditis elegans)
LD007	130	AAGCAAGTGATGATGTTCAGTGC	7143515 (Globodera pallida)
LD014	131	ATGATGGCTTTCATTGAACAAGA	10122191 (Haemonchus contortus)
LD015	132	AACGCCCCAGTCTCATTAGCCAC	20064339 (Meloidogyne hapla)
LD016	133	TTTTGGCGTCGATTCCTGATG	71999357 (Caenorhabditis elegans)
LD016	134	GTGTACATGTAACCTGGGAAACC	13418283 (Necator americanus)
LD016	135	GTGTACATGTAACCTGGGAAACCACGACG	10819046 (Haemonchus contortus)

Table 5-PC

Target ID	SEQ ID NO	Sequence *	Example Gi-number and species
PC001	435	ATGGATGTTGGACAAATTGGG	7143612 (Globodera rostochiensis)
PC003	436	GCTAAAATCCGTAAAGCTGCTCGTGAACT	9831177 (Strongyloides stercoralis)
PC003	437	GAGTAAAGTACACTTTGGCTAAA	28914459 (Haemonchus contortus)
PC003	438	AAAATCCGTAAAGCTGCTCGTGAACT	32185135 (Meloidogyne chitwoodi)
PC003	439	CTGGACTCGCAGAAGCACATCGACTT	51334250 (Radopholus similis)
PC003	440	CGTCTGGATCAGGAATTGAAA	61115845 (Litomosoides sigmodontis)
PC005	441	TGGTTGGATCCAAATGAAATCAA	5430825 (Onchocerca volvulus)
PC005	442	GTGTGGTTGGATCCAAATGAAATCAA	6845701 (Brugia malayi); 45215079 (Wuchereria bancrofti)
PC014	443	CACATGATGGCTTTCATTGAACAAGAAGC	10122191 (Haemonchus contortus)
PC014	444	TACGAGAAAAAGGAGAAGCAAGT	21265518 (Ostertagia ostertagi)
PC016	445	GTCTGGATCATTTCCTCGGGATAAAT	18081287 (Globodera rostochiensis)
PC016	446	CCAGTCTGGATCATTTCCTCGGGATA	108957716 (Bursaphelenchus mucronatus); 108962248 (Bursaphelenchus xylophilus)

Table 5-EV

Target ID	SEQ ID NO	Sequence *	Example Gi-number and species
EV005	563	TTAAAGATGGTCTTATTATTAA	21819186 (Trichinella spiralis)
EV016	564	GCTATGGGTGTCAATATGGAAAC	54554020 (Xiphinema index)

Table 5-AG

Target ID	SEQ ID NO	Sequence *	Example Gi-number and species
AG001	739	GCTGGATTCATGGATGTGATCA	15666884 (Ancylostoma ceylanicum)
AG001	740	ATGGATGTTGGACAAATTGGG	18081843 (Globodera rostochiensis)
AG001	741	TTCATGGATGTGATCACCATTGA	27002091 (Ascaris suum)
AG005	742	GTCTGGTTGGATCCAAATGAAATCAATGA	2099126 (Onchocerca volvulus)
AG005	743	GGATCCAAATGAAATCAATGA	2099309 (Onchocerca volvulus)
AG005	744	TGATCAAGGATGGTTTGATCAT	2130916 (Brugia malayi)
AG005	745	TGGTTGGATCCAAATGAAATCAATGA	6845701 (Brugia malayi)
AG005	746	CCAAGGGTAACGTGTTCAAGAACAAG	2964728 (Heterodera glycines)

AG005	747	TGGTTGGATCCAAATGAAATCAATGA	45215079 (Wuchereria bancrofti)
AG005	748	TGGATCCAAATGAAATCAATGA	61116961 (Litomosoides sigmodontis)
AG014	749	GAAGAATTAACATTGAAAAGGG	10122191 (Haemonchus contortus)
AG014	750	GAATTAACATTGAAAAGGGCCG	28252967 (Trichuris vulpis)
AG016	751	GGTTACATGTACACCGATTTGGC	54552787 (Xiphinema index)

Table 5-TC

Target ID	SEQ ID NO	Sequence *	Example Gi-number and species
TC014	853	ATCATGGAATATTACGAGAAGAA	6562543 (Heterodera schachtii); 15769883 (Heterodera glycines)
TC015	854	AACGGTCCCGAAATTATGAGTAAATT	10896476 (Bursaphelenchus xylophilus)

Table 5-MP

Target ID	SEQ ID NO	Sequence *	Example Gi-number and species
MP001	1011	GATCTTTTGATATTGTTCACATTAA	13099294 (Strongyloides ratti)
MP001	1012	ACATCCAGGATCTTTTGATATTGTTCAC	15275671 (Strongyloides ratti)
MP001	1013	TCTTTTGATATTGTTCACATTAA	32183548 (Meloidogyne chitwoodi)
MP016	1014	TATTGCTCGTGGACAAAAAT	9832367 (Strongyloides stercoralis)
MP016	1015	TCTGCTGCTCGTGAAGAAGTACCTGG	13418283 (Necator americanus)
MP016	1016	GCTGAAGATTATTTGGATATT	20064440 (Meloidogyne hapla)
MP016	1017	GGTTACCACCATAATGAGATTGCTGC	20064440 (Meloidogyne hapla)
MP016	1018	AAGAAATGATTCAAACTGGTATTTCAGCTATTGAT	31545172 (Strongyloides ratti)
MP016	1019	TATTGCTCGTGGACAAAAAATTCCAAT	31545172 (Strongyloides ratti)
MP016	1020	GTTTCTGCTGCTCGTGAAGAAGT	31545172 (Strongyloides ratti)
MP016	1021	CGTGGTTTCCCTGGTTACATGTACAC	31545172 (Strongyloides ratti)
MP016	1022	CCTGGTTACATGTACACCGATTT	54552787 (Xiphinema index)
MP027	1023	TTTAAAAATTTAAAGAAAA	27540724 (Meloidogyne hapla)
MP027	1024	CTATTATGTTGGTGGTGAAGTTGT	34026304 (Meloidogyne arenaria)
MP027	1025	AAAGTTTTTAAAAATTTTAAA	34028558 (Meloidogyne javanica)

Table 5-NL

Target ID	SEQ ID No	Sequence *	Example Gi-number and species
NL001	1438	AGTACAAGCTGTGCAAAGTGAAGA	18087933 (Globodera rostochiensis), 54547517 (Globodera pallida)
NL001	1439	ATGGATGTTGGACAAATTGGGTGG	7143612 (Globodera rostochiensis)
NL001	1440	TGGATGTTGGACAAATTGGGTGG	7235910 (Meloidogyne incognita)
NL001	1441	AGTACAAGCTGTGCAAAGTGAAGA	111164813 (Globodera rostochiensis)
NL003	1442	AGTCCATCCATCACGCCCGTGT	6081031 (Pristionchus pacificus)
NL003	1443	CTCCGTAACAAGCGTGAGGTGTGG	5815927 (Pristionchus pacificus)
NL003	1444	GACTCGCAGAAGCACATTGACTTCTC	5815618 (Pristionchus pacificus)
NL003	1445	GCAGAAGCACATTGACTTCTC	6081031 (Pristionchus pacificus)
NL003	1446	GCCAAGTCCATCCATCACGCCC	6081133 (Pristionchus pacificus)
NL003	1447	GCCAAGTCCATCCATCACGCCCGTGT	1783663 (Pristionchus pacificus)
NL003	1448	TCGCAGAAGCACATTGACTTCTC	10804008 (Ascaris suum)
NL003	1449	TCGCAGAAGCACATTGACTTCTCGCTGAA	18688500 (Ascaris suum)
NL003	1450	GCCAAGTCCATCCATCACGCCCGTGT	91102596 (Pristionchus pacificus)
NL003	1451	GACTCGCAGAAGCACATTGACTTCTC	91102596 (Pristionchus pacificus)
NL003	1452	CTCCGTAACAAGCGTGAGGTGTGG	91102596 (Pristionchus pacificus)
NL004	1453	AAGAACAAGGATATTCGTAAATT	3758529 (Onchocerca volvulus), 6200728 (Litomosoides sigmodontis)
NL004	1454	AAGAACAAGGATATTCGTAAATTCTTGGA	21056283 (Ascaris suum), 2978237 (Toxocara canis)
NL004	1455	CCGTGTACGCCCATTTCCCCATCAAC	1783477 (Pristionchus pacificus)
NL004	1456	TACGCCCATTTCCCCATCAAC	2181209 (Haemonchus contortus)
NL007	1457	CAACATGAATGCATTCCTCAAGC	39747064 (Meloidogyne paranaensis)
NL007	1458	GAAGTACAACATGAATGCATTCC	6721002 (Onchocerca volvulus)
NL007	1459	GCTGTATTTGTGTTGGCGACA	27541378 (Meloidogyne hapla)
NL008	1460	AGAAAAGGTTGTGGGTTGGTA	108958003 (Bursaphelenchus mucronatus)
NL011	1461	GGACTTCGTGATGGATATTACATTCAGGGACAATG	33138488 (Meloidogyne incognita)
NL011	1462	CAACTACAACTTCGAGAAGCC	108984057 (Bursaphelenchus xylophilus)
NL014	1463	GAAGAATTCAACATTGAAAAGGG	11927908 (Haemonchus contortus)

NL014	1464	GAGCAAGAAGCCAATGAGAAAGC	108985855 (Bursaphelenchus mucronatus)
NL014	1465	TTTCATTGAGCAAGAAGCCAATGAGAAAGCCGAAGA	108979738 (Bursaphelenchus xylophilus)
NL015	1466	ATGAGCAAATTGGCCGGCGAGTCGGAG	18090737 (Globodera rostochiensis)
NL015	1467	CACACCAAGAAACATGAAGTTGGCTGA	68276872 (Caenorhabditis remanei)
NL015	1468	CAGGAAATCTGTTCGAAGTGT	45564676 (Meloidogyne incognita)
NL015	1469	CTGGCGCAGATCAAAGAGATGGT	18090737 (Globodera rostochiensis)
NL015	1470	TGGCGCAGATCAAAGAGATGGT	27428872 (Heterodera glycines)
NL016	1471	TATCCCGAGGAAATGATCCAGAC	18081287 (Globodera rostochiensis)
NL016	1472	CGTATCTATCCCGAGGAAATGATCCAGACTGGAATTTC	108957716 (Bursaphelenchus mucronatus) 108962248 (Bursaphelenchus xylophilus)
NL023	1473	TGGATGGGAGTCATGCATGGA	13959786 (Nippostrongylus brasiliensis)

Table 5-CS

Target ID	SEQ ID NO	Sequence *	Example Gi-number and species
CS001	1988	ATACAAGCTGTGCAAGGTGCG	10803803 (Trichuris muris)
CS003	1989	AAGCACATTGACTTCTCGCTGAA	18850138 (Ascaris suum)
CS003	1990	CGCAACAAGCGTGAGGTGTGG	40305701 (Heterodera glycines)
CS003	1991	CGTCTCCAGACTCAGGTGTTCAAG	91102965 (Nippostrongylus brasiliensis)
CS011	1992	TTTAATGTATGGGATACTGCTGG	9832495 (Strongyloides stercoralis)
CS011	1993	CACTTGACTGGGAGAGTTCGAGAAAA	1808274 (Globodera rostochiensis)
CS011	1994	CTCGTGTCACCTACACAAAAATGTACC	71182695 (Caenorhabditis remanei)
CS011	1995	CACTTGACTGGGAGAGTTCGAGAA	108987391 (Bursaphelenchus xylophilus)
CS013	1996	TAGGTGAATTTGTTGATGATTA	40305096 (Heterodera glycines)
CS014	1997	AAGAAAGAGAAACAAGTGGAACT	51871231 (Xiphinema index)
CS016	1998	GTGTACATGTAACCTGGGAAACCACG	10819046 (Haemonchus contortus)
CS016	1999	GTGTACATGTAACCTGGGAAACC	13418283 (Necator americanus)
CS016	2000	GCCAAATCGGTGTACATGTAACC	54552787 (Xiphinema index)
CS016	2001	AAGTTCTTCTCGAACTTGGTGAGGAACTC	111163626 (Globodera rostochiensis)

Table 5-PX

Target ID	SEQ ID NO	Sequence *	Example Gi-number and species
PX001	2291	CTCGACATCGCCACCTGCAAG	11069004 (Haemonchus contortus); 27770634 (Teladorsagia circumcincta)
PX001	2292	GACGGCAAGGTCCGCACCGAC	32320500 (Heterodera glycines)
PX001	2293	CCCGGCTGGATTCATGGATGT	51334233 (Radopholus similis)
PX001	2294	ATCAAGGTGGACGGCAAGGTCCGCAC	108959807 (Bursaphelenchus xylophilus)
PX001	2295	ACAACGTGTTCATCATCGGCAA	111166840 (Globodera rostochiensis)
PX016	2296	CGTGGTTTCCCAGGTTACATGTACACGGATTTGGC	10819046 (Haemonchus contortus)
PX016	2297	GGTTTCCCAGGTTACATGTACAC	13418283 (Necator americanus)
PX016	2298	GAGTTCCTCACCAAGTTCGAGAAGAACTT	111163626 (Globodera rostochiensis)

Table 5-AD

Target ID	SEQ ID NO	Sequence *	Example Gi-number and species
AD015	2439	ATAAATGGTCCTGAAATTATGA	9832193 (Strongyloides stercoralis)
AD016	2440	GTCAACATGGAGACGGCGCGCTT	30220804 (Heterodera glycines)

Table 6-LD

Target ID	SEQ ID No	Sequences*	Example Gi-number and species
LD001	136	TAGCGGATGGTGCGGCCGTCGTG	54625255 (Phlebiopsis gigantea)
LD003	137	TTCCAAGAAATCTTCAATCTTCAAA	50294437 (Candida glabrata CBS 138)
LD007	138	GACTGCGGTTTGAACACCCTTCAGAAGTTCA	110463173 (Rhizopus oryzae)
LD007	139	TGTCAAGCCAAATCTGGTATGGG	110463173 (Rhizopus oryzae)
LD011	140	GGCTTCTCAAAGTTGTAGTTA	48898288 (Aspergillus flavus)
LD011	141	CCATCACGGAGACCACCAAACTT	60673229 (Alternaria brassicicola)
LD011	142	AAAGGCTTCTCAAAGTTGTAGTTA	58157923 (Phytophthora infestans)
LD011	143	TGTGCTATTATCATGTTTGATGT	110458937 (Rhizopus oryzae)
LD011	144	ACTGCCGGTCAGGAGAAGTTTGG	90638500 (Thermomyces lanuginosus)
LD011	145	AATACAACTTTGAGAAGCCTTTCCT	90549582 (Lentinula edodes), 90381505 (Amorphotheca resinae)

LD011	146	CAGGAGAAGTTTGGGTGGTCTCCG	90544763 (Gloeophyllum trabeum)
LD011	147	ACCACCAAACTTCTCCTGACC	90368069 (Aureobasidium pullulans)
LD011	148	GGTCAGGAGAAGTTGGTGGTCTCCG	90355148 (Coprinopsis cenerea)
LD016	149	GCAGCAATTTCATTGTGAGGCAGACCAG	50285562 (Candida glabrata CBS 138)
LD016	150	ATGGAGTTCATCACGTCAATAGC	68419480 (Phytophthora parasitica)
LD016	151	GGTCTCGCCTCACAATGAAATTGCTGCCCAGAT	85109950 (Neurospora crassa)
LD016	152	CTATTGTTTCGCTGCTATGGGTGGTGTTAACATG GA	50423336 (Debaryomyces hansenii), 90540142 (Gloeophyllum trabeum)
LD016	153	ATGAACTCCATTGCTCGTCGTGGTCAGAAGAT	84573655 (Aspergillus oryzae)
LD016	154	ATAGGAATCTGGGTGATGGATCCGTT	90562068 (Leucosporidium scottii), 90359845 (Aureobasidium pullulans)
LD016	155	TCCTGTTTCTGAAGATATGTTGGG	90388021 (Cunninghamella elegans)
LD016	156	TTTGAAGATTGAAGATTTCTTGGAACG	50294437 (Candida glabrata CBS 138), 110468393 (Rhizopus oryzae), 90388664 (Cunninghamella elegans), 90376235 (Amorphotheca resinae)
LD027	157	TCACAGGCAGGCGAAGATGGTACC	90546087 (Gloeophyllum trabeum)
LD027	158	TTCTTTGAAGTTTTTGAATAT	50292600 (Candida glabrata CBS 138)

Table 6-PC

Target ID	SEQ ID NO	Sequence *	Example GI-number and species
PC001	447	CCCTGCTGGTTCATGGATGTCAT	110469463 (Rhizopus oryzae)
PC003	448	ATTGAAGATTTCTTGGAAAGAAG	50294437 (Candida glabrata CBS 138)
PC003	449	TTGAAGATTTCTTGGAAAGAAG	50310014 (Kluyveromyces lactis NRRL Y-1140)
PC003	450	CTTCTTTCCAAGAAATCTTCAA	622611 (Saccharomyces cerevisiae)
PC003	451	GACTCGCAGAAGCACATCGACTT	110744873 (Allomyces macrogynus); 59284959 (Blastocladiella emersonii); 90623359 (Corynascus heterothallicus); 29427071 (Verticillium dahliae)
PC003	452	GACTCGCAGAAGCACATCGACTTC	59298648 (Blastocladiella emersonii); 90565029 (Leucosporidium scottii)
PC003	453	TCGCAGAAGCACATCGACTTC	47032157 (Mycosphaerella graminicola)
PC003	454	CAGAAGCACACATCGACTTCTCCCT	34332427 (Ustilago maydis)

	SEQ ID NO	Sequence	Gi-number and species
PC005	455	CTTATGGGAGTACATCCACAAG	98997063 (Spizellomyces punctatus)
PC005	456	AAGAAGAAGGCAGAGAAGGCCA	84572408 (Aspergillus oryzae)
PC010	457	GTGTTCAATAATTCTCCTGATGA	50288722 (Candida glabrata CBS 138)
PC010	458	ATTTTCCATGGAGAGACCATTGC	70990481 (Aspergillus fumigatus)
PC010	459	GGGCAGAATCCCCAAGCTGCC	90631635 (Thermomyces lanuginosus)
PC014	460	AATACAAGGACGCCACCGGCA	30394561 (Magnaporthe grisea)
PC016	461	ATGCCCAACGACGACATCACCCA	59281308 (Blastocladiella emersonii)
PC016	462	TGGGTGATGTCGTTGGGCAT	38353161 (Hypocrea jecorina)
PC016	463	GGTTTCCCCGGTTACATGTACAC	34447668 (Cryphonectria parasitica)
PC016	464	ACTATGCCCAACGACGACATCAC	34447668 (Cryphonectria parasitica)
PC016	465	CCGGGCACTTCTTCTCGAGCGGC	38353161 (Hypocrea jecorina)
PC016	466	CCGACCATGGCCGCATCATCAC	59281308 (Blastocladiella emersonii)
PC016	467	TTCTTGAACTTGGCCAACGATCC	50285562 (Candida glabrata CBS 138)
PC016	468	TGTTCTTGAACTTGGCCAACGA	66909391 (Phaeosphaeria nodorum)
PC016	469	GCTATGGGGTGTCAACATGGAAACTGC	110463410 (Rhizopus oryzae)
PC016	470	TGCTATGGGGTGTCAACATGGA	71006197 (Ustilago maydis)
PC016	471	CTATTGTGTTTGCTGCTATGGGGTGT	68488910 (Candida albicans)
PC016	472	TACGAGCGGCGCCGGTCGTGTGGA	90347883 (Coprinopsis cinerea)

Table 6-EV

Target ID	SEQ ID NO	Sequence*	Example Gi-number and species
EV010	565	TTCAATAATTCACCAGATGAAAC	50405834 (Debaryomyces hansenii)
EV015	566	CGATCGCCTTGAACAGCGACG	22502898 (Gibberella zeae)
EV015	567	GTTACCATGGAGAACTTCCGTTA	67900533 (Aspergillus nidulans FGSC A4)
EV015	568	GTTACCATGGAGAACTTCCGTTACGCC	70820241 (Aspergillus niger)
EV015	569	ACCATGGAGAACTTCCGTTACGCC	84573628 (Aspergillus oryzae)
EV015	570	ATGGAGAACTTCCGTTACGCC	71002727 (Aspergillus fumigatus)
EV016	571	TCTGAAGATATGTTGGGTCGTGT	90396765 (Cunninghamella elegans)
EV016	572	CAAAAGATTCCAATTTTCTCTGCA	50306984 (Kluyveromyces lactis NRRL Y-1140)
EV016	573	CCCCACAATGAAATCGCTGCTCAAAT	68001221 (Schizosaccharomyces pombe 972h-)
EV016	574	ATCGTTTTCGCCGCTATGGGTGT	58271359 (Cryptococcus neoformans var.)
EV016	575	TTCAAGCAAGATTTTGAAGAGAATGG	50285562 (Candida glabrata CBS 138)

Table 6-AG

Target ID	SEQ ID NO	Sequence *	Example Gi-number and species
AG001	752	CGTAACAGGTTGAAGTACGCCCT	16931515 (Coccidioides posadasii)
AG001	753	AAGGTCGACGGCAAAGTCAGGACTGAT	33515688 (Cryptococcus neoformans var.)
AG001	754	CCATTCTTGGTCACCCACGATG	38132640 (Hypocrea jecorina)
AG001	755	ATCAAGGTAAACGACACCATC	56939474 (Puccinia graminis f. sp.)
AG005	756	TGTACATGAAGGCCAAGGGTAACGTGTTCAAGAACAAG	98997063 (Spizellomyces punctatus)
AG005	757	CCAAGGGTAACGTGTTCAAGAACAAG	109744763 (Allomyces macrogynus); 59297176 (Blastocladiella emersonii)
AG005	758	AAGGGTAACGTGTTCAAGAACAAG	109741162 (Allomyces macrogynus)
AG005	759	CAAGAAGAAGGCTGAGAAGGC	67903433 (Aspergillus nidulans FGSC A4)
AG005	760	CAAGAAGAAGGCTGAGAAGGC	4191107 (Emericella nidulans)
AG005	761	AAGAAGAAGGCTGAGAAGGCC	66909252 (Phaeosphaeria nodorum)
AG005	762	CAAAACATCCGTAAATTGATCAAGGATGGTTT	21649803 (Conidiobolus coronatus)
AG016	763	TTCGCCGCCATGGGTGTCAAC	50554108 (Yarrowia lipolytica)
AG016	764	ATGGGTGTCAACATGGAAACCGC	90639144 (Trametes versicolor)
AG016	765	TGGAAACCGCCCGTTTCTTCA	85109950 (Neurospora crassa)
AG016	766	GGTTACATGTACACCGATTTG	32169825 (Mucor circinelloides)
AG016	767	GTCAAGATGGGAATCTGGGTGATGGA	38353161 (Hypocrea jecorina)

Table 6-TC

Target ID	SEQ ID NO	Sequence *	Example Gi-number and species
TC001	855	AACAGGCTGAAGTATGCCCTTGACC	90545567 (Gloeophyllum trabeum)
TC015	856	TTCATCGTCCGTGGTGGCATG	46122304 (Gibberella zeae PH-1)
TC015	857	AGTTTTACCGGTACCTGGAGG	50310636 (Kluyveromyces lactis NRRL Y-1140)
TC015	858	CCTCCAGGTACCGGTAAAACT	85114224 (Neurospora crassa)
TC015	859	CCTCCAGGTACCGGTAAAACTTT	50290674 (Candida glabrata CBS 138)
TC015	860	ATTAAAGTTTTACCGGTACCTGGAGG	3356460 (Schizosaccharomyces pombe)
TC015	861	GGTGCTTTCTTCTTCTTAATCAA	21649889 (Conidiobolus coronatus)
TC015	862	ATCAACGGTCCCGAAATTATG	82610024 (Phanerochaete chrysosporium)

Table 6-MP

Target ID	SEQ ID NO	Sequence *	Example Gi-number and species
MP002	1026	AATTTTTAGAAAAAAAAATTG	68026454 (Schizosaccharomyces pombe 972h-)
MP010	1027	GTCACCACATTAGCTAGGAAT	48564349 (Coccidioides posadasii)
MP016	1028	AAGAAATGATTCAAACTGGTAT	90396765 (Cunninghamella elegans)
MP016	1029	AAGAAATGATTCAAACTGGTATTTC	110463410 (Rhizopus oryzae)
MP016	1030	CATGAACTCTATTGCTCGTGG	50285562 (Candida glabrata CBS 138)
MP016	1031	GCTGCTATGGGTGTTAATATGGA	90348219 (Coprinopsis cinerea)
MP016	1032	TGCTATGGGTGTTAATATGGAAAC	90396964 (Cunninghamella elegans)
MP016	1033	CCTACTATTGAGCGTATCATTAC	90524974 (Geomyces pannorum)
MP016	1034	GAAGTTTCTGCTGCTCGTGAAGAAGTACCTGG	90396313 (Cunninghamella elegans)
MP016	1035	GTTTCTGCTGCTCGTGAAGAAGT	32169825 (Mucor circinelloides)
MP016	1036	GTGTACATGTAACCAGGGAAACCACG	45392344 (Magnaporthe grisea)
MP016	1037	CCTGGTTACATGTACACCGATTTA	32169825 (Mucor circinelloides)
MP016	1038	GGTTACATGTACACCGATTTA	47067814 (Eremothecium gossypii)
MP016	1039	CCTATTTTAACTATGCCTAACGA	90396313 (Cunninghamella elegans)
MP027	1040	ACTCTCCATCACCACACTACTA	60673889 (Alternaria brassicicola)

Table 6-NL

Target ID	SEQ ID No	Sequence *	Example Gi-number and species
NL001	1474	CCAAGGGGCAAGGGGTGTGAAGCTCA	30418788 (Magnaporthe grisea)
NL001	1475	TCTCTGCCCAAGGGGCAAGGGGTGT	22500578 (Gibberella zeae), 46128672 (Gibberella zeae PH-1), 70662858 (Gibberella moniliformis), 71000466 (Aspergillus fumigatus)
NL001	1476	TCTGCCCAAGGGGCAAGGGTGT	14664568 (Fusarium sporotrichioides)
NL001	1477	TCTCTGCCCAAGGGGCAAGGGT	50550586 (Yarrowia lipolytica)
NL001	1478	TCTCTGCCCAAGGGGCAAGGGTGT	71000466 (Aspergillus fumigatus) 92459259 (Gibberella zeae)
NL001	1479	CTGCCCAAGGGGCAAGGGTGTGAAG	90545567 (Gloeophyllum trabeum)
NL003	1480	ATGAAGCTCGATTACGTCTTGG	24446027 (Paracoccidioides brasiliensis)
NL003	1481	CGTAAGGCCGCTCGTGAGCTG	10229753 (Phytophthora infestans)

		Sequence	Organism
NL003	1482	CGTAAGGCCGCTCGTGAGCTGTTGAC	58082846 (Phytophthora infestans)
NL003	1483	GACTCGCAGAAGCACATTGACTT	21393181 (Pratylenchus penetrans), 34330401 (Ustilago maydis)
NL003	1484	TGAAGCTCGATTACGTCTTGG	46346864 (Paracoccidioides brasiliensis)
NL003	1485	TGGCCAAGTCCATCCATCACGCGCCGTGT	58113938 (Phytophthora infestans)
NL004	1486	CGTAACTTCCTGGGCGAGAAG	58127885 (Phytophthora infestans)
NL003	1487	ATGAAGCTCGATTACGTCTCTTGG	90366381 (Aureobasidium pullulans)
NL003	1488	TCGGTTTGGCCAAGTCCATCCA	90353540 (Coprinopsis cinerea)
NL003	1489	GACTCGCAGAAGCACATTGACTT	71012467 (Ustilago maydis)
NL003	1490	GACTCGCAGAAGCACATTGACTTCTC	90616286 (Ophiostoma piliferum)
NL004	1491	TACGCCCATTTCCCCATCAAC	15771856 (Gibberella zeae), 29426217 (Verticillium dahliae), 30399988 (Magnaporthe grisea), 34330394 (Ustilago maydis), 39945691 (Magnaporthe grisea 70-15), 46108543 (Gibberella zeae PH-1), 70660620 (Gibberella moniliformis)
NL004	1492	CGTGTACGCCCATTTCCCCATCAAC	90615722 (Ophiostoma piliferum)
NL004	1493	TACGCCCATTTCCCCATCAAC	90367524 (Aureobasidium pullulans) 90372622 (Cryptococcus laurentii) 109654277 (Fusarium oxysporum f. sp.) 90535059 (Geomyces pannorum) 46108543 (Gibberella zeae PH-1) 90566138 (Leucosporidium scottii) 39945691 (Magnaporthe grisea 70-15) 110115733 (Saitoella complicata) 110081735 (Tuber borchii) 71021510 (Ustilago maydis) 50554252 (Yarrowia lipolytica)
NL004	1494	TACGCCCATTTCCCCATCAACTG	90640952 (Trametes versicolor)
NL004	1495	CGTGTACGCCCATTTCCCCATCAAC	90615722 (Ophiostoma piliferum)
NL005	1496	AAAAGGTCAAGGAGGCCAAGA	14662414 (Fusarium sporotrichioides)
NL005	1497	TTCAAGAACAAGCGTGTATTGATGGA	90395504 (Cunninghamella elegans)
NL005	1498	TTCAAGAACAAGCGTGTATTGATGGAGT	90542553 (Gloeophyllum trabeum)
NL006	1499	CCTGGAGGAGGAGCGACCAT	70998503 (Aspergillus fumigatus)
NL006	1500	TCCCATCTCGTATGACAATTGG	68471154 (Candida albicans)

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NL006	1501	ATGGTCGTCTCCTCCTCCAGG	70998503 (Aspergillus fumigatus)
NL006	1502	TCCCATCTCGTATGACAATTGG	68471154 (Candida albicans), 50425488 (Debaryomyces hansenii)
NL007	1503	CAAGTCATGATGTTCAGTGCAAC	70984614 (Aspergillus fumigatus)
NL007	1504	TGACGCTTCACGGCCTGCAGCAG	10229203 (Phytophthora infestans)
NL007	1505	CAAGTCATGATGTTCAGTGCAAC	70984614 (Aspergillus fumigatus)
NL010_2	1506	CAATTCTTGCAAGTGTTCAACAA	68478799 (Candida albicans)
NL010_2	1507	TTCAACAACAGTCCTGATGAAAC	21649260 (Conidiobolus coronatus)
NL010_2	1508	TTCTTGCAAGTGTTCAACAAC	47031965 (Mycosphaerella graminicola)
NL011	1509	AAGAACGTTCCCAACTGGCAC	68132303 (Trichophyton rubrum)
NL011	1510	ACAAGAACGTTCCCAACTGGCA	68132303 (Trichophyton rubrum)
NL011	1511	ACCTACAAGAACGTTCCCAACT	68132303 (Trichophyton rubrum)
NL011	1512	ACCTACAAGAACGTTCCCAACTGGCAC	70674996 (Gibberella moniliformis)
NL011	1513	CAACTACAACTTCGAGAAGCC	22500425 (Gibberella zeae), 34331122 (Ustilago maydis), 46108433 (Gibberella zeae PH-1), 47029512 (Mycosphaerella graminicola), 56236507 (Setosphaeria turcica), 62926335 (Fusarium oxysporum f. sp.), 70674996 (Gibberella moniliformis), 70992714 (Aspergillus fumigatus)
NL011	1514	CAAGAACGTTCCCAACTGGCAC	68132303 (Trichophyton rubrum)
NL011	1515	CACCTACAAGAACGTTCCCAAC	68132303 (Trichophyton rubrum)
NL011	1516	CCTACAAGAACGTTCCCAACTG	68132303 (Trichophyton rubrum)
NL011	1517	CTACAAGAACGTTCCCAACTGG	68132303 (Trichophyton rubrum)
NL011	1518	GCAACTACAACTTCGAGAAGCC	22505588 (Gibberella zeae)
NL011	1519	TACAAGAACGTTCCCAACTGGC	68132303 (Trichophyton rubrum)
NL011	1520	TCAACTACAAGAACGTTCCCA	68132303 (Trichophyton rubrum)
NL011	1521	TCACCTACAAGAACGTTCCCAA	68132303 (Trichophyton rubrum)
NL011	1522	TCACCTACAAGAACGTTCCCAACT	30405871 (Magnaporthe grisea)
NL011	1523	TCACCTACAAGAACGTTCCCAACTGGCAC	13903501 (Blumeria graminis f. sp.), 3140444 (Emericella nidulans), 34331122 (Ustilago maydis), 49096317 (Aspergillus nidulans FGSC A4)
NL011	1524	TGGGACACAGCTGGCCAGGAAA	14180743 (Magnaporthe grisea), 39950145 (Magnaporthe grisea 70-15)

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NL011	1525	TTCGAGAAGCCGTTCCTGTGG	38056576 (Phytophthora sojae), 45244260 (Phytophthora nicotianae), 58091236 (Phytophthora infestans)
NL011	1526	TTCGAGAAGCCGTTCCTGTGGTTGGC	58090083 (Phytophthora infestans)
NL011	1527	TGGGACACAGCTGGCCAGGAAA	39950145 (Magnaporthe grisea 70-15)
NL011	1528	TATTACATTCAGGGACAATGCG	110134999 (Taphrina deformans)
NL011	1529	TCACCTACAAGAAGAACGTTCCCAACTGGCAC	84573903 (Aspergillus oryzae), 90355199 (Coprinopsis cinerea), 90624693 (Corynascus heterothallicus), 90638500 (Thermomyces lanuginosus)
NL011	1530	ACCTACAAGAAGAACGTTCCCAACTGGCAC	113544700 (Cordyceps bassiana), 85114463 (Neurospora crassa)
NL011	1531	TACAAGAACGTTCCCAACTGGCA	110269748 (Hypocrea lixii)
NL011	1532	TACAAGAACGTTCCCAACTGGCAC	110458937 (Rhizopus oryzae)
NL011	1533	AGGAAGAAGAACCTTCAGTACT	90557551 (Leucosporidium scottii)
NL011	1534	AAGAAGAACCTTCAGTACTACGA	113551594 (Cordyceps bassiana)
NL011	1535	AAGAAGAACCTTCAGTACTACGACATC	90036917 (Trichophyton rubrum)
NL011	1536	AAGAACCTTCAGTACTACGACACATC	90624693 (Corynascus heterothallicus)
NL011	1537	GGCTTCTCGAAGTTGTAGTTGC	89975123 (Hypocrea lixii)
NL011	1538	CAACTACAACTTCGAGAAGCC	70992714 (Aspergillus fumigatus), 90368808 (Aureobasidium pullulans), 90629512 (Corynascus heterothallicus), 109656121 (Fusarium oxysporum f. sp.), 90532849 (Geomyces pannorum), 110272576 (Hypocrea lixii), 47029512 (Mycosphaerella graminicola), 85114463 (Neurospora crassa), 90617165 (Ophiostoma piliferum), 90036917 (Trichophyton rubrum)
NL011	1539	GGCTTCTCGAAGTTGTAGTTG	92233975 (Gibberella zeae)
NL013	1540	CCCGAGATGGTGGTGGGCTGGTACCA	49069733 (Ustilago maydis)
NL013	1541	GGTACCACTCGCACCCGGGCTT	58134950 (Phytophthora infestans)
NL013	1542	GTGGGCTGGTACCACTCGCACCCGGGGCTTCGG CTGCTGGCTGTCGGGG	38062327 (Phytophthora sojae)
NL013	1543	TGGTACCACTCGCACCCGGGCTT	58084933 (Phytophthora infestans)

NL013	1544	CCCGAGAGATGGTGGTGGGCTGGTACCA	71006043 (Ustilago maydis)
NL015	1545	ATCCACACCAAGAACATGAAG	10181857 (Aspergillus niger), 22505190 (Gibberella zeae), 30394634 (Magnaporthe grisea), 33507832 (Cryptococcus neoformans var.), 3773467 (Emericella nidulans), 39940093 (Magnaporthe grisea 70-15), 46122304 (Gibberella zeae PH-1), 47032030 (Mycosphaerella graminicola), 49106059 (Aspergillus nidulans FGSC A4)
NL015	1546	CACACCAAGAACATGAAGTTGG	21649889 (Conidiobolus coronatus)
NL015	1547	GCCTTCTTCTTCCTCATCAACGG	46122304 (Gibberella zeae PH-1.)
NL015	1548	TTGGAGGCTGCAGAAAGCAGCT	90369178 (Cryptococcus laurentii)
NL015	1549	GCCTTCTTCTTCCTCATCAACGG	46122304 (Gibberella zeae PH-1)
NL015	1550	ATCCACACCAAGAACATGAAG	70820941 (Aspergillus niger), 58260307 (Cryptococcus neoformans var.), 85691122 (Encephalitozoon cuniculi GB-M1), 46122304 (Gibberella zeae PH-1), 39940093 (Magnaporthe grisea 70-15), 85082882 (Neurospora crassa), 50555821 (Yarrowia lipolytica)
NL015	1551	CACACCAAGAACATGAAGTTGGC	110272618 (Hypocrea lixii)
NL016	1552	CATGAACTCGATTGCTCGTGG	30418452 (Magnaporthe grisea), 39942327 (Magnaporthe grisea 70-15)
NL016	1553	CCACCATCTACGAGCGCGCCGGACG	39942327 (Magnaporthe grisea 70-15), 45392344 (Magnaporthe grisea)
NL016	1554	CATGAACTCGATTGCTCGTGG	90367610 (Aureobasidium pullulans), 39942327 (Magnaporthe grisea 70-15)
NL016	1555	CATGTCGGTGAGGATGACGAG	90562068 (Leucosporidium scottii)
NL016	1556	CCACCATCTACGAGCGCGCCGGGACG	39942327 (Magnaporthe grisea 70-15)
NL019	1557	CAGATTTGGGACACGGCCGGCCAGGAGCG	9834078 (Phytophthora sojae)
NL019	1558	GACCAGGAGTCGTTCAACAAC	9834078 (Phytophthora sojae)
NL019	1559	TGGGACACGGCGCGGCCGGCCAGGAG	38056576 (Phytophthora sojae), 40545332 (Phytophthora nicotianae), 58083674 (Phytophthora infestans)
NL019	1560	TGGGACACGGCCGGCCGGCCAGGAGCG	29426828 (Verticillium dahliae), 38057141 (Phytophthora sojae)
NL019	1561	TGGGACACGGCCGGCCAGGAGCGGTT	70981934 (Aspergillus fumigatus)
NL019	1562	TTCCTGGAGACGTCGGGCGAAGAACGC	90643518 (Trametes versicolor)

NL019	1563	CAGATTTGGGACACGGCCGGCCAGGAGCG	90616605 (Ophiostoma piliferum)
NL019	1564	TGGGACACGGCCGGCCAGGAG	110272626 (Hypocrea lixii)
NL019	1565	TGGGACACGGCCGGCCAGGAGCG	50550714 (Yarrowia lipolytica)
NL019	1566	TGGGACACGGCCGGCCAGGAGCGGTT	70981934 (Aspergillus fumigatus)
NL019	1567	TGGGACACGGCCGGCCGGCCAGGAGCGGGTTCCG	50553761 (Yarrowia lipolytica)
NL022	1568	CAGGCAAAGATTTTCCTGCCCA	58124185 (Phytophthora infestans)
NL022	1569	GGCAAGTGCTTCCGTCTGTACAC	58124872 (Phytophthora infestans)
NL023	1570	GGATGACCAAAAACGTATTCT	46137132 (Gibberella zeae PH-1)
NL023	1571	AGAATACGTTTTGGTCATCC	46137132 (Gibberella zeae PH-1)

Table 6-CS

Target ID	SEQ ID NO	Sequence *	Example Gi-number and species
CS003	2002	TGGTCTCCGCAACAAGCGTGA	46356829 (Paracoccidioides brasiliensis)
CS003	2003	GGTCTCCGCAACAAGCGTGAG	71012467 (Ustilago maydis)
CS003	2004	TGGTCTCCGCAACAAGCGTGAGGT	5832048 (Botryotinia fuckeliana)
CS003	2005	TGGTCTCCGCAACAAGCGTGAGGT	40545704 (Sclerotinia sclerotiorum)
CS003	2006	GGTCTCCGCAACAAGCGTGAGGT	21907821 (Colletotrichum trifolii); 90623359 (Corynascus heterothallicus); 94331331 (Pyronema omphalodes); 29427071 (Verticillium dahliae)
CS003	2007	TGGTCTCCGCAACAAGCGTGAGGTGTGG	27439041 (Chaetomium globosum); 47032270 (Mycosphaerella graminicola)
CS003	2008	CGCAACAAGCGTGAGGTGTGG	71000428 (Aspergillus fumigatus); 67537265 (Aspergillus nidulans FGSC A4); 70825441 (Aspergillus niger); 84573806 (Aspergillus oryzae); 3773212 (Emericella nidulans); 90632673 (Thermomyces lanuginosus); 34332427 (Ustilago maydis)
CS006	2009	TCCCCTCTCGTATGACAATTGGT	68011927 (Schizosaccharomyces pombe 972h-)
CS007	2010	ATTTAGCTTTGACAAAGAATA	50305206 (Kluyveromyces lactis NRRL Y-1140)
CS007	2011	GAGCACCCTTCAGAAGTTCAACA	90553133 (Lentinula edodes)
CS011	2012	TGGGATACTGCTGGCCAAGAA	90385536 (Amorphotheca resinae); 68475609 (Candida albicans); 50304104 (Kluyveromyces

			lactis NRRL Y-1140); 85105150 (Neurospora crassa)
CS011	2013	AAGTTTGGTGGTCTCCGAGATGGTTACTA	90355199 (Coprinopsis cinerea)
CS011	2014	CAATGTGCCATCATCATGTTCGA	15276938 (Glomus intraradices)
CS011	2015	CATCATCATGTTCGATGTAAC	28268268 (Chaetomium globosum)
CS011	2016	CACTTGACTGGAGAGTTCGAGAA	90368808 (Aureobasidium pullulans); 34331122 (Ustilago maydis)
CS011	2017	TGAAGGTTCTTTTTCTGTGGAA	6831345 (Pneumocystis carinii)
CS013	2018	GGATGGTACCACTCGCATCCTGG	109651225 (Fusarium oxysporum f. sp.)
CS015	2019	AACGAGAGGAAGAAGAAGAAG	39944615 (Magnaporthe grisea 70-15)
CS015	2020	AGGGCTTCTTCTTCTTCCTCTC	14662870 (Fusarium sporotrichioides)
CS015	2021	TAGGGCTTCTTCTTCTTCCTC	85112692 (Neurospora crassa)
CS015	2022	GAGATGGTCGAGTTGCCCTCTA	71005073 (Ustilago maydis)
CS016	2023	GCTGAAGACTTTTGGACATC	30418452 (Magnaporthe grisea)
CS016	2024	CCTCACCAAGTTCGAGAAGAACTTC	90566317 (Leucosporidium scottii)
CS016	2025	GTCGTCGGTGGGTGAGGAAGCCCTG	84573655 (Aspergillus oryzae)
CS016	2026	TCCTCACCGACGACAGCCTTCATGGCC	29427786 (Verticillium dahliae)
CS016	2027	GATGTTTCCAACCAGCTGTACGCC	90368806 (Aureobasidium pullulans)
CS016	2028	GGCGTACAGCTGGTTGGAAACATC	29427786 (Verticillium dahliae)
CS016	2029	TGATGTTTCCAACCAGCTGTACGCC	46107507 (Gibberella zeae PH-1)
CS016	2030	ATGGCAGAACTTCATGAGACGAGA	29427786 (Verticillium dahliae)
CS016	2031	ATGCCCAACGACGACATCACCCA	59281308 (Blastocladiella emersonii)
CS016	2032	TGGGTGATGTCGTCGTTGGGCAT	38353161 (Hypocrea jecorina)
CS016	2033	ACTATGCCCAACGACGACATCAC	34447668 (Cryphonectria parasitica)
CS016	2034	GGTTACATGTACACCGATTTG	32169825 (Mucor circinelloides)
CS016	2035	CCCAGGTTACATGTACACCGATTT	47067814 (Eremothecium gossypii)
CS016	2036	ACACCACGTTTGGCCTTGACT	68488910 (Candida albicans)
CS016	2037	GCCATGGGTGTGAACATGGAGAC	82608508 (Phanerochaete chrysosporium)
CS016	2038	GACGACCACGAGGACAACTTTGCCATCGTGTTCG	59277641 (Blastocladiella emersonii)
CS016	2039	AAGATCCCCATTTTCTCGGCTGC	90348219 (Coprinopsis cinerea)

Table 6-PX

Target ID	SEQ ID NO	Sequence *	Example Gi-number and species
PX001	2299	CTCATCAAGGTGGACGGCAAGGT	85080580 (Neurospora crassa)
PX001	2300	TCGGTGCGGACCTTGCCGTCCACCTTGA	70768092 (Gibberella moniliformis)
PX001	2301	GACGGCAAGGTCCGCACCGAC	109745014 (Allomyces macrogynus); 60673542 (Alternaria brassicicola); 90368699 (Aureobasidium pullulans); 59299145 (Blastocladiella emersonii); 27438899 (Chaetomium globosum); 90623992 (Corynascus heterothallicus); 89975695 (Hypocrea lixii); 99039195 (Leptosphaeria maculans); 39970560 (Magnaporthe grisea); 47731115 (Metarhizium anisopliae); 90036859 (Trichophyton rubrum); 29427127 (Verticillium dahliae)
PX001	2302	GACGGCAAGGTCCGCACCGACCC	70823112 (Aspergillus niger); 90633197 (Thermomyces lanuginosus)
PX001	2303	AAGGTCCGCACCGACCCCACCTACCC	71015993 (Ustilago maydis)
PX001	2304	CGCTTCACCATCCACCGCATCAC	90639458 (Trametes versicolor)
PX001	2305	CGAGGAGGCCAAGTACAAGCTG	78177454 (Chaetomium cupreum); 27438899 (Chaetomium globosum)
PX001	2306	GAGGCCAAGTACAAGCTGTGCAAGGT	109745014 (Allomyces macrogynus)
PX001	2307	GCCAAGTACAAGCTGTGCAAG	45923813 (Coccidioides posadasii)
PX001	2308	CCCGACCCGCTCATCAAGGTCAACGAC	78177454 (Chaetomium cupreum)
PX001	2309	CGACATCGTCCACATCAAGGAC	82603501 (Phanerochaete chrysosporium)
PX001	2310	CCGCACAAGCTGCGCGAGTGCCTGCCGCTC	109745014 (Allomyces macrogynus)
PX010	2311	TTCGACCAGGAGGCGGCGGCGGT	90542152 (Gloeophyllum trabeum)
PX010	2312	CACCACCGCGCGGCGCCTCCTG	84578035 (Aspergillus oryzae)
PX010	2313	TGCAGGTCTTCAACAACTCGCCCGACGA	39978050 (Magnaporthe grisea)
PX010	2314	TTCAACAACTCGCCCGACGAGAC	90618424 (Corynascus heterothallicus)
PX015	2315	CATGCGCGCCGTCGAGTTCAAGGTGGT	59282860 (Blastocladiella emersonii)
PX015	2316	GCATTCTTCTTCCTCATCAACGG	68323226 (Coprinopsis cinerea)
PX015	2317	ATCAACGCCCCGAGATCATGTC	85082882 (Neurospora crassa)
PX015	2318	TGCGCAAGGGCGTTCGAGGAGGC	71002727 (Aspergillus fumigatus)
PX016	2319	CCTCACCAAGTTCGAGAAGAACTTC	90566317 (Leucosporidium scottii)

Target ID	SEQ ID NO	Sequence	Example Gi-number and species
PX016	2320	GAGGAGATGATCCAGAACTGGTAT	90639144 (Trametes versicolor)
PX016	2321	GAGGAGATGATCCAGAACTGGTATCTC	58271359 (Cryptococcus neoformans)
PX016	2322	ATGAACTCCATCGCCCGTGGTCAGAAGATCCC	90545177 (Gloeophyllum trabeum)
PX016	2323	GTCAGAAGATCCCCATCTTCTCCGCC	9651842 (Emericella nidulans)
PX016	2324	CAGAAGATCCCCATCTTCTCCGC	70825597 (Aspergillus niger); 90611576 (Ophiostoma piliferum); 90639144 (Trametes versicolor)
PX016	2325	CAGAAGATCCCCATCTTCTCCGCC	67540123 (Aspergillus nidulans)
PX016	2326	CAGAAGATCCCCATCTTCTCCGCGCCGCCGG	59283275 (Blastocladiella emersonii)
PX016	2327	AAGATCCCCATCTTCTCCGCGCCGCCGGTCT	34447668 (Cryphonectria parasitica)
PX016	2328	CCCATCTTCTCCGCGCCGCCGGTCTGCC	90621827 (Corynascus heterothallicus)
PX016	2329	GGTCTGCCCCACAACGAGATTGCTGC	90367610 (Aureobasidium pullulans); 66909391 (Phaeosphaeria nodorum)
PX016	2330	TTCGCCGCCATGGGAGTCAACATGGAGAC	90562163 (Leucosporidium scottii)
PX016	2331	ACCGCCAGGTTCTTCAAGCAGGA	47067814 (Eremothecium gossypii)
PX016	2332	CTGTTCTTGAACTTGGCCAATGA	90545177 (Gloeophyllum trabeum)
PX016	2333	GGTTACATGTACACGGATTTG	34447668 (Cryphonectria parasitica); 90545177 (Gloeophyllum trabeum); 39942327 (Magnaporthe grisea); 82608506 (Phanerochaete chrysosporium); 71006197 (Ustilago maydis)
PX016	2334	GGCAAGCCCATCGACAAGGGGCCC	59283275 (Blastocladiella emersonii)
PX016	2335	ATGGGGTGGGTGATGTCGTCGTTGGGCATGGTCA	38353161 (Hypocrea jecorina)
PX016	2336	ACCATGCCCAACGACGACATCACCCACCC	59281308 (Blastocladiella emersonii)
PX016	2337	TGCACAACAGGCAGATCTACCC	107889579 (Encephalitozoon cuniculi)
PX016	2338	CCGTCGCTATCTCTGTCTCATGAA	48521040 (Coccidioides posadasii)

Table 6-AD

Target ID	SEQ ID NO	Sequence*	Example Gi-number and species
AD001	2441	CCCGCTGGTTTCATGGATGTT	58259586 (Cryptococcus neoformans)
AD001	2442	GACAACATCCATGAAACCAGCGGG	21649877 (Conidiobolus coronatus)
AD001	2443	TTCATGGATGTTGTCACCATTG	90616000 (Ophiostoma piliferum)
AD001	2444	GAAGAAGCCAAGTACAAGCTCTG	110469512 (Rhizopus oryzae)
AD001	2445	AAGAAGCCAAGTACAAGCTCTG	110469518 (Rhizopus oryzae)

AD001	2446	GCCAAGTACAAGCTCTGCAAGGT	98996590 (Spizellomyces punctatus)
AD001	2447	GCCAAGTACAAGCTCTGCAAGGTCA	109743129 (Allomyces macrogynus)
AD001	2448	AGTACAAGCTCTGCAAGGTCA	71000466 (Aspergillus fumigatus); 67537247 (Aspergillus nidulans); 70823112 (Aspergillus niger); 40886470 (Emericella nidulans)
AD015	2449	TATGGACCCCCTGGAACTGGTAAAACC	46349704 (Paracoccidioides brasiliensis)
AD016	2450	TGCCCGTGTCCGAGGACATGCTGGGCCG	109743322 (Allomyces macrogynus)
AD016	2451	TGCCCGTGTCCGAGGACATGCTGGGCCGC	59283275 (Blastocladiella emersonii)
AD016	2452	CGTGTCCGAGGACATGCTGGGCCGCA	90612905 (Ophiostoma piliferum)
AD016	2453	ATGGGCGTCAACATGGAGACGGGC	59277641 (Blastocladiella emersonii)
AD016	2454	TGGAGACGGGCGGCTTCTTCA	90611376 (Ophiostoma piliferum)
AD016	2455	TTCCTCAACCTGGCCAACGACCCCAC	90611376 (Ophiostoma piliferum)
AD016	2456	ACCATCGAGCGCATCATCACCCCGCGCCTCGC	59281308 (Blastocladiella emersonii)
AD016	2457	TCCACCATCTACGAGCGCGCTGG	90368806 (Aureobasidium pullulans)
AD016	2458	CTGACGATGCCCAACGACGACATCAC	90611301 (Ophiostoma piliferum)
AD016	2459	ATGCCCAACGACGACATCACCCA	59281308 (Blastocladiella emersonii)
AD016	2460	TGGGTGATGTCGTTGGGCAT	38353161 (Hypocrea jecorina)

Table 7-LD

Target ID	SEQ ID NO and DNA Sequence (sense strand) 5' → 3' of fragments and concatemer constructs
LD014_F1	SEQ ID NO: 159 TCTAGAATGTTGAATCAGGCTCGATTGAAAGTATTGAAGGTTAGGGAAGATCACGTTCGTACCGTACTAGAGGAGGCGCGTAAACGACTTGGTCAGGTCACAAACGCCCGGG
LD014_F2	SEQ ID NO: 160 TCTAGAAAGATCACGTTCGTACCGTACTAGAGGAGGCGCGTAAACGACTTGGTCAGGTCACAAACGCCCGGG
LD014_C1	SEQ ID NO: 161 TCTAGAATGTTGAATCAGGCTCGATTGAAAGTATTGAAGGTTAGGGAAGATCACGTTCGTACCGTACTAGAGGAGGCGCGTAAACGACTTGGTCAGGTCACAAACGATGTTGAATCAGGCTCGATTGAAAGTATTGAAGGTTAGGGAAGTATTGAAGGCTCGATTGAATCAGGCTCGATGTTGAATCAGGCTCGATTGAAGGTTGATTGAAGGTTGATTGGGAAGATCAGGCTCGAAACGATGTTGGTCAGGTCAAACGCCCGGG
LD014_C2	SEQ ID NO: 162 TCTAGAAAGATCACGTTCGTACCGTACTAGAGGAGGCGCGTAAACGACTTGGTCAGGTCACAAACGAAGATCACGTTCGTACCGT

ACTAGAGAGGAGGGCGCGTAAACGACTTGGTCAGGTCACAAACGAAGATCACGTTCGTACCGTACTAGAGAGGAGGGGCGTAAACGACTT GGTCAGGTCACAAACGAAGATCACGTTCGTACCGTACTAGAGAGGAGGGGCGTAAACGACTTGGTCAGGTCACAAACGAAGATCACG TTCGTACCGTACTAGAGAGGAGGGGCGTAAACGACTTGGTCAGGTCACAAACGCCCGGG			

Table 8-LD

Target ID	Primers Forward 5' → 3'	Primers Reverse 5' → 3'	dsRNA DNA Sequence (sense strand) 5' → 3'
LD001	SEQ ID NO: 164 GCGTAATACGACTC ACTATAGGGGCCCC AAGAAGCATTTGAA GCG SEQ ID NO: 166 GGCCCCAAGAAGCA TTTGAAGCG	SEQ ID NO: 165 CCTTTGGGGCCCAGT TTGCATC SEQ ID NO: 167 GCGTAATACGACTC ACTATAGGCCTTTG GGGCCCAGTTTGCAT C	SEQ ID NO: 163 GGCCCCAAGAAGCATTTGAAGCGTTTGAATGCCCCAAAAGCATGGATGTTGG ATAAATTGGGAGGTGTTTTCGCACCTCGCCCATCTACAGGACCTCACAAATTG CGAGAGTCTTGCCCTTGGTGATCTTCCTACGTAACCGATTGAAGTATGCTTT GACTAACAGCGAAGTTACTAAGATTGTTATGCAAGGTTAATCAAAGTAGATG GAAAAGTGAGGACCGACTCCAATTACCCTGCTGGGTTTATGGATGTTATTACC ATTGAAAAAACTGGTGAATTTTCCGACTCATCTATGATGTTAAAGGACGATTT GCAGTGCATCGTATTACTGCTGAGGAAGCAAGTACAAACTATGCAAAGTCAG GAGGATGCAAACTGGCCCCAAAGG
LD002	SEQ ID NO: 169 GCGTAATACGACTC ACTATAGGGTCCAC GTCCAAGTTTTTATG GGC SEQ ID NO: 171 GTCCACGTCCAAGT TTTTATGGGC	SEQ ID NO: 170 AAGCGATTAGAAAA AAATCAGTTGC SEQ ID NO: 172 GCGTAATACGACTC ACTATAGGAAGCGA TTAGAAAAAAATCAG TTGC	SEQ ID NO: 168 GTCCACGTCCAAGTTTTTATGGGCTTTCTTAAGAGCTTCAGCTGCATTTTCAT AGATTCCAATACTGTGGTGTTCGTACTAGCTCCCTCCGAGCTTCTCGTTGAA GTTCAATAGTAGTTAAAGTGCCATCTATTTGCAACTGATTTTTTTCTAATCGCTT
LD003	SEQ ID NO: 174 GCGTAATACGACTC ACTATAGGGCCCAGG CGACCTTATGAAAA GGC SEQ ID NO: 176	SEQ ID NO: 175 GGTGACCACCACCG AATGGAG SEQ ID NO: 177 GCGTAATACGACTC ACTATAGGGGTGAC	SEQ ID NO: 173 GGTGACCACCACCGAATGGAGTGGAGAAGTCAATATGCTTCTGGGA ATCAAGTCTCACAATGAAGCTTGAATATTCGACCTGCTTACGACCCTGA TATGTCTTTGACGGACCAGCACAGAGCATGATGATTGATTTGCAAGCCCC AACTTGAAAACTTGTGTTTGGAGACGTCGTTCCAAGAAATCTTCAATCTTCAAA CCCAAGACGTAATCAAGCTTCATCCAACACTCCAATACGCAC CAACCGAGCAGAAGAGAGCATTGCCTTTCAAACAACCTGCGCTGATCTTTCTCTT

LD006	CCCAGGCGACCTTATGAAAAGGC	CACCACCGAATGGAG	SEQ ID NO: 178 GGTGTTGGTTGCTTCTGGTGTGGTGGAATACATCGACACTCTTGAAGAAGAAACTGTCATGATTGCGATGAATCCTGAGGATCTTGGGCAGGACAAAGAATATGCTTATTGTACGACCTACACCCACTGCGAAATCCACCCGGCCAATCCAGAGACCCTTTGGCGCGTCTATTATACCTTTCCCCGATCATAAACCAGAGCCCAAGGAACACCTACCAGAGACGGCTATGGGTAAGCAAGCTATGGGGGTCTACATTACGAATTTCCACGTGCGGATGGACACCCTGGCCCACGTGCTATACTACCCGCACAAACCTCTGGTCACTACCAGGTCTATGGAGTATCGGCGGTTCAGAGAATTACCAGCCGGGATCAACAGTAGTTGCTATTGCTGTTATACTGGTTATATCAAGAAGAGATTCTGTTATTCTGAAGACGGTCTGCTGTGGTGGAAGAGGATTTTTCCGATCCGTGTTTTATCGTTCCTATAAAGAATGCCGAATCGAAGC
	SEQ ID NO: 179 GCGTAATACGACTCACTATAGGGGTGTTGGTTGCTTCTGGTGTG	SEQ ID NO: 180 GCTTCGATTCGGCATCTTTATAGG	
	SEQ ID NO: 181 GGTGTTGGTTGCTTCTGGTGTG	SEQ ID NO: 182 GCGTAATACGACTCACTATAGGGCTTCGATTCGGCATCTTTATAGG	
LD007	SEQ ID NO: 184 GCGTAATACGACTCACTATAGGGACTGGCGGTTTTGAACACCC	SEQ ID NO: 185 CCTTTCAATGTCCATGCCACG	SEQ ID NO: 183 GACTGGCGGTTTTGAACACCCTTCAGAAGTTCAGCACGAATGTATTCCTCAAGCTGTCATTGGCATGGCATGGACATTTATGTCAAGCCAAATCTGGTATGGGCAAAACGGGAGTGTTTGTTCTCGGCGACACTGCAACAATTGGAACCAGCGGACAATGTTGTTTACGTTTTGGTGATGTGTCACACTCGTGACTGGCCTTTCCAAATCAGCAAAGAGTACGAGAGGTTCAGTAATATATGCTGACCAGTGTCCAGTGTCTTTTTCGGAGGAATGCCTATTGTGGGGACGCCTGGGTATTTTGGCGCTTGTCAAGTCTAGGAAACATTGTTGTGGGGAAGAACCTGAAACACTTCATTCTTGATGAGTGCGATAAAATGTGCTAGTCCTCAAGAAGACTTGAAACACTTCATTCTTGATGAGTCGATAAAATGTTAGAACTGTTGGATATGAGGAGAGACGTGTCAAGATCCAGCGAGTGTATGTAGACGATGTCACACCAAGCAAGTGATGATGTTCATGCAAGATCCAGCGAGTGTATGTAGACGATGCCGGTGTGCAAGAAATTGACGTTGCACGGATTACAACAGCATTACGTTAAACTCAAAGAAAAGCCAAATTGACGTTGCACGGATTACAACAGCATTATTGAGTTGCTCGATGTTCTCGAATTTAATCAGAATGAAAAGAAATAAAAATTATTTGAGTTGCTCGATGTTCTCGAATTTAATCAGGTGGTCATTTTGTGAGTCCGTTCAAAGGTGTGTGGCTTTGGCACAGTTGCTGACTGAACAGAATTTCCCAGCCATAGGAATTCACAGAGGAATGGACCAGAAAGAGAGGTTGTCTCGGTATGAGCAGTTCAAAGATTTCCAGAAGAGAATATTGGTAGCTACGAATCTCTTTGGGCGTGGCATGGACATTGAAAGG
	SEQ ID NO: 186 GCGTAATACGACTCACTATAGGGCCTTTCAGACTGGCGGGTTTGAACACCC	SEQ ID NO: 187 GCGTAATACGACTCACTATAGGCCTTTCAATGTCCATGCCACG	
LD010	SEQ ID NO: 189 GCGTAATACGACTCACTATAGGGGATGGATGCCCCCGAATGC	SEQ ID NO: 190 CTATCGGGTTGGATGGAACTCG	SEQ ID NO: 188 GCTTGTTGCCCCGAATGCCTTGATAGGGTTGATTACCTTTGGGAAGATGGTCCAAGTGCACGAACTAGGTACCGAGGGCTGCAGCAAATCTTACGTTTTCCGAGGGACGAAAGACCTCACAGTCAAGCAAGTTCAAGAGATGTTGGAAGTGGGGCAG

	SEQ ID NO: 192 GCGTAATACGACTCACTATAGGCTATCGGGTTGGATGGAACTCG	AGCCGCAGTAAGTGCTCAACCTGCTCCTCAACAACCAGGACAACCCATGAGGCCTGGAGCACTCCAGCAGCTCCTACGCCACCAGGAGCAAGCAGGTTCCTTCAACCCATCTCGAAATGCGACATGAACCTCACTGACTCTTATTGGAGAGTTGCAAGAGACCCATGGCCGCTGTCCACCAAGGCAAATGCGCCCTTAGATCGACCGGGACAGCTTTATCGATAGCCATTGGGGTTGTTGGAGTGCACATACGCCAATACTGGTGCCAGGGTCATGTCATTCGTTCGGGAGACCTTGCTCTCAAGGCCCTGGTCAAGTCTTGAATGATGATCTGAAGCAACCTATCAGATCTCACCACGACATCCAAAAAGACAATGCCAAATACATGAGAAAGCAATCAAGCACTATGATAATTTAGCGATGAGAGCAGCAACGAATGGCCACTGCGTTGACATATATTCATGCGCTTTGGATCAGACAGGATTGATGGAGATGAAACAGTGTTGTAATTCAACAGGGGGACATATGGTCATGGGCGACTCGTTCAATTCTTCCCGTTCAAGCAAACGTTCCAGCGCATATTTTCGAAAGATCAGAAAAACGAGCTGAAGATGCATTTAATGGTACTCTGGAGGGTCAAGTGTTCCAGGGAGTTGAAAATTCAAGGCGGTATTGGATCTTGTGTTTCGTTGAATGTGAAGAATCCTTTGGTTTCCGACACCGAAAATAGGAATGGGTAACACGGTCCAGTGGAAATGTGTACGGTAACTCCAAGTACTACCATGGCCTTGTTCTTCGAGGTCGTCAACCAACATTCCGCTCCCATACCTCAAGGGGGAAGGGGCTGCATACAGTTCATCACGCAATATCAGCATGCTAGTGCCAGAAGAGGATCCGAGTAACGACAGTTGCTAGAAACTGGGCCGATGCTTCCGCTAATATACATCATGTCAGTGCTGATTCGACAGGAGCAGCCGCAGTGATAATGGCGAGGATGGCAGTTTACAGAGCGGAATCAGACAGATAGCCCTGATGTTTTGAGATGGGTCGATAGGATGTTGATACGTCTGTGCCAGAAATTCGGCGAATATAACAAGGACGACCCGAATTCGTTCCGCTTGTGCCGGGCAAAACTTCAGCCTCTCACCCGCAGTTCATGTACCATTTGAGAAGGTCACAGTTCCTGCAGGTGTTTAACAATTCTCCCGACGAAACGTCCTTCTCACAGGCACATGCTTATGCGGCGAAGACCTCACGCAGTCGCTGATCATGATCCAGCCGATACTCTACAGCTACAGTTTCAATGGACCACCAGAACCTGTGCTTTGGATACGAGTTCCATCCAACCCGATAG
	SEQ ID NO: 191 GCTTGTTGCCCCCGAATGC	
LD011	**SEQ ID NO:194** GCGTAATACGACTCACTATAGGCCATAGGAAAGGCCTTCTCAAAG	**SEQ ID NO: 195** GGAAAAACGACATTTGTGAAACGTC
	SEQ ID NO: 196 GCCATAGGAAAGGCTTCTCAAAG	**SEQ ID NO: 197** GCGTAATACGACTCACTATAGGGGGAAAAACGACATTTGTGAAACGTC
		SEQ ID NO: 193 GCCATAGGAAAGGCTTCTCAAAGTTGTAGTTAGATTTGGCAGAGATATCATAGTACTGCAAATTCTTCTCCTATGAAAGACAATACTTTTCGCTTTACTTTTCTGTCTTTGATGTCAACCTTGTTCCCGCAAAGTACTATCGGGATATTTTCACAGACTCTGACAAGATCTCTGTCTGTGCCAATTTGGTACATTCTTGTATGTAACTCTGGAAGTTACATCAAACATGATAATAGCACACTGTCCCTGAATGTAATATCCATCACGGAGACCACCAAACTTCTCCTGACCGGCAGTGTCCCATACACATTGAACCGAATAGGGCCCCTGTTTGTATGGAGAACCAGAGGATGGACTTCAACTCCCAAGTAGCTACATATCTTTTTCAAATTCACCAGTCATATGACGTTTCACAAATGTCGTTTTCC
LD014	**SEQ ID NO: 199**	**SEQ ID NO: 200**	**SEQ ID NO: 198**

		TTTCATTGAACAAGAGAGGCAAACGAAACGAAAAGGCAGAAGAAATCGATGCCAAGGCC GAGGAAGAAATTAATATTGAAGAGGGGGCGCCCTTGTTCAGCAACAACGTCTCAA GATTATGGAATATTATGAGAAGAAAGAGAAGAGAAACAGTCGAAGTCGAAAGTATTGAAGGTTAGG TCCAATCGTCTAACATGTTGACCGTACCTAGAGGAGGCGCGTAAACGACTTGGTCAGG GAAGATCACGTTCGTACCGTACTAGAGGAGGAAATATTCCCAAATCCTGAAAGCCTCATTTTGCAG GGATTATATCAGCTTTTTGAGAAAGATGTTACCATTCGAGTTGGCCCCCAGGA CCGAGAACTGGTCAAATCCATCCATCCCACCGTCACGAACAAGTATAAAGATG CCACCGGTAAGGACATCCATCTGAAAATTGATGACGAAATCCATCTGTCCCAA GAAACCACCGGGGAATCGACCTGCTCGGCGCAGAAAAACAAAATCAAGATCA GCAATACTATGTGGAGGCTCGTCGTCTGGAGCTGATTTCGC
GCGTAATACGACTC ACTATAGGTTTCATT GAACAAGAGGCAAA CG SEQ ID NO: 201 TTTCATTGAACAAGA GGCAAACG	GCGAAATCAGCTCC AGACGGAGC SEQ ID NO: 202 GGCTAATACGACTC ACTATAGGGCGAAA TCAGCTCCAGACGA GC	
LD014_F1 SEQ ID NO: 204 GCGTAATACGACTC ACTATAGGATGTTGA ATCAGGCTCGATTG SEQ ID NO: 206 GGCTAATACGACTC ACTATAGGCCGTTTGT GACCTGACCAAGTC ATGTTGAATCAGGC TCGATTG	SEQ ID NO: 205 CGTTTGTGACCTGA CCAAGTC SEQ ID NO: 207 GGCTAATACGACTC ACTATAGGCCGTTTGT GACCTGACCAAGTC	SEQ ID NO: 203 ATGTTGAATCAGGCTCGATTGAAAGTATTGAAGGTTAGGGAAGATCACGTTCG TACCGTACTAGAGAGGAGGCGCGTAAACGACTTGGTCAGGTCACAAACG
LD014_F2 SEQ ID NO: 209 GCGTAATACGACTC ACTATAGGAAGATC ACGTTCGTACCGTA C SEQ ID NO: 211 AAGATCACGTTCGT ACCGTAC	SEQ ID NO: 210 CGTTTGTGACCTGA CCAAG SEQ ID NO: 212 GGCTAATACGACTC ACTATAGGCCGTTTGT GACCTGACCAAG	SEQ ID NO: 208 AAGATCACGTTCGTACCGTACTAGAGAGGAGGCGCGTAAACGACTTGGTCAGGT CACAAACG
LD014_C1		SEQ ID NO: 213 AATGTTGAATCAGGCTCGATTGAAAGTATTGAAGGTTAGGGAAGATCACGTTC GTACCGTACTAGAGAGGAGGCGCGTAAACGACTTGGTCAGGTCACAAACGATGT TGAATCAGGCTCGATTGAAAGTATTGAAGGTTAGGGAAGATCACGTTCGTACC GTACTAGAGAGGAGGCGCGTAAACGACTTGGTCAGGTCACAAACGATGTTGAAT CAGGCTCGATTGAAAGTATTGAAGGTTAGGGAAGATCACGTTCGTACCGTACT

AGAGGAGGCGCGTAAACGACTTGGTCAGGTCACAAACGC

LD014_C2			SEQ ID NO: 214 AAGATCACGTTCGTACCGTACTAGAGGAGGCGCGTAAACGACTTGGTCAGG TCACAAACGAAGATCACGTTCGTACCGTACTAGAGGAGGCGCGTAAACGACT TGGTCAGGTCACAAACGAAGATCACGTTCGTACCGTACTAGAGGAGGCGCGT AAACGACTTGGTCAGGTCACAAACGAAGATCACGTTCGTACCGTACTAGAGG AGGCGCGTAAACGACTTGGTCAGGTCACAAACGAAGATCACGTTCGTACCGT ACTAGAGGAGGCGCGTAAACGACTTGGTCAGGTCACAAACGC
LD015	SEQ ID NO: 216 GGGTAATACGACTC ACTATAGGGCCGG AGAGTTTTGTCAGC SEQ ID NO: 218 CGCCGGAGAGTTT TGTCAGC	SEQ ID NO: 217 CTATCGGCGTGAAG CCCCC SEQ ID NO: 219 GCGTAATACGACTC ACTATAGGCTATCG GCGTGAAGCCCCC	SEQ ID NO: 215 CGCCGGAGAGTTTTTGTCAGCTTCTTCAAAAGCTTTGCGCAAGTTACTCTCAG ACTCGCCCAGCGAGTTTGCTCATGATCTCCGGCCCGTTATCAAGAAGAAGAA CGCCCCAGTCTCATTAGCCACGGCCGGAGCAATCAGGGTCTTACCCGTACCA GGGGGACCACACAGCAGTATACCCCTAGGGGGGCTTCACGCCGGATAG
LD016	SEQ ID NO: 221 GGGTAATACGACTC ACTATAGGGGCATA GTCAATATAGGAATC TGGGTG SEQ ID NO: 223 GGCATAGTCAATATA GGAATCTGGGTG	SEQ ID NO: 222 GGTAATCCTCGAAG ATGTTAAGTTCC SEQ ID NO: 224 GGGTAATACGACTC ACTATAGGGGTAAT CCTCGAAGATGTTA AGTTCC	SEQ ID NO: 220 GGCATAGTCAATATAGGAATCTGGGTGATGGGATCCGTTACGTCCTTCAACACG GCCGGGCACGTTCATAGATGGTAGCTAAATCGGTGTACATGTAACCTGGGGAAA CCACGACGACCAGGCACCTCTTCTCTGGCAGCAGATACCTCACGCAAAGCTT CTGCATACGAAGACATATCTGTCAAGATGACCAAGACGGTGCTTCTCACATTGG TAAGCCAAGAATTCGGCAGCTGTCAAAGTCAGGAACAGGCAGACATTCTCCATAGAAC AATGGTAGGATCGGTTGGCCAAATTCAAGAACCTAGCTGTTTCCATGTTAACACCCA CGTTCTCTTCGAAATCCTGTTTGAAGAACCTAGCTGTTTCCATGTTAACACCCA TAGCAGCGAAAACAATAGCAAAGTTATCTTCATGATCATCAAGTACAGATTTAC CAGGAATCTTGACTAAACCAGCCTGTCTACAGATCTGGGCAGCAATTTCATTG TGAGGCAGACCAGCTGCAGAGAAAATGGGGATCTTCTGACCACGAGCAATGG AGTTCATCACGTCAATAGCTGTAATACCCGTCTGGATCATTTCCTCAGGATAG ATACGGGGACCACGGATTGATTGGTTGACCCTGGATGTCCAAGAAGTCTTCAG CCAAAATTGGGGGACCTTTGTCGATGGTTTCCTGATCCATTGAAAACACGT CCCAACATATCTTCAGAAACAGGAGTCCTCAAAATATCTCCTGTGAATTCACAA GCGGTGTTTTGGCGTCGACTTCCAGAACTTGTCCCGAACGTATAGTGCCATCAGCC CTTTTGACCCACTGACTTCATTGTACGATTTCATTGTACTTGGGGAACTTAACATCTTCGAGGATT ACC

LD018	SEQ ID NO: 226	SEQ ID NO: 227	SEQ ID NO: 225
	GCGTAATACGACTC ACTATAGGGGGAGC GCAGAAATACGAGA GCAC	GTAGAGGCTCCACC GTCAATCGC	GGAGTCGCAGAAATACGAGAGCACCTTCTCGAACAACCAAGCCTCCTTGAGG GTAAAACAAGCCCAGTCTGAGGACTCGGGACTCACACTTTGTTGGCGGGAGA ACCCTCAAGGCTGCATAGTGTCATCTGCTTACTTAGCCATAGAACCGGTAACC ACCCAGGAAGGGTTGATCCACGAGTCCACCTTCAAGCAGCAACAGACCGAAA TGGAGCAAATCGACACCAGCAAGACCTTGGCGCCTAACTTCGTCAGGGTTTG CGGGGATAGAGACGGTGACCGAGGGCAAGATGACCCGCTTCGACTGTCGCGT CACTGGTCGTCCTTATCCAGACGTGACAGTGTACATAAACGGTCGACAAGTCA CCGACGACCAACCACAAGATTTGGTTAACGAATCCGGAAACCATGCCCT GATGATCACCACCGTGAGCAGGAACGACTCAGGAGTGACCTGACCTGCTCGC CAGGAACAAGACGGGAGAAACCTCCTTCCAGTCGCAACCTTAACGTCATCGAA AAGGAACACAGGTAGTCGCGCCCAAGTTCGTGCGCGGACGGGGCGCCCAACG TGGCAGAAGGAGAACCAGTGTCTCTGCGCGGACGGGGCGCCCTAGCCCAGGGGGCCC TGCCGCGAATCACTTGGCAGGAGGACGGGGCGCCCTAGCCCAGGGGGCCC GACGTTCGCATCGCCGATTGACGGGTGGGAGCCTCTAC
	SEQ ID NO: 228	SEQ ID NO: 229	
	GGAGTCGCAGAAAT ACGAGAGCAC	GCGTAATACGACTC ACTATAGGGTAGAG GCTCCACCGTCAAT CGC	

LD027	SEQ ID NO: 231	SEQ ID NO: 232	SEQ ID NO: 230
	GCGTAATACGACTC ACTATAGGGGGAGC AGACGATCGGTTGG	TCGGACAGACTCGT TCATTTCCC	GGGAGCAGACGATCGGTTGGTTAAAATCTGGGACTATCAAAACAAAACGTGT GTCAAACCTTGGAGGACACGCCCAAAACGTAACGCGGTTGTTCCACC CTGAACTACCTGTGCCTCTCACAGGCAGCGAAGATGGTACCGTTAGAGTTTG GCATACGAATACACACAGATTAGAGAATTGTTGAATTATGGGTTCGAGAGAG TGTGGACCATTGTTGCTTGAAGTGTTGAAGTTGGAAGAGAAGAACCGGCAGTTAGTATGG GAGGGCAGTATATTAGTGAAAGTTGAAAGTTGGGCAAGCCAGTTAGTATGG ATGCCAGTGGCGGTAAAATAATTTGGGCAAGCCAGTTAGTAGTAAACAAGC TAATTTGAAGGCGCTGCCAGAAGGTGGAGAAATAAGAGATGGGGAGCGTTTA CCTGTCTCTGTAAAAGATATGGGAGCATGTGTAGTATGCGGAGACGGGAATATCA ACATAATCCGAATGGAAGATTCGTTGTAGTATGCGGAGACGGGGAATATCA TTTACACAGCGATGGCTCTACGGAACCAAGGCTTTGGAAGCGCTCAAGAGTTT GTCTGGCTCAGGACTCCAGCGAGTATGCCATTCGCGAGTCTGGTTCCACAA TTCGGATATTCAAAAACTTCAAAGAAGAAGAACTTCAAGTCGGATTTCAGC GCGAAGGAATCTACGGGGGTTTTCTTGGGGATTAAATCGGTGTCCGGTT TAACGTTTTACGATTGGGAAACTTTGGACTTGGTGAGACGGATTGAAATACAA CCGAGGGCGGTTATTGGTCTGACAGTGAAAATTAGTCTGTCTCGCAACGG AGGACAGCTACTTCCTTTCATCCTTCTTATGATTCGGAGCAAGTTCAGAAGGCCAGG GAGAACAATCAAGTCGCAGAGGATGGGCGTAGAGGCGCGGCTTTCGGATGTGTTGGA GGGAAATGAACGAGTCTGTCCGA
	SEQ ID NO: 233	SEQ ID NO: 234	
	GGGAGCAGACGATC GGTTGG	GCGTAATACGACTC ACTATAGGTCGGAC AGACTCGTTCATTTC CC	

| gfp | SEQ ID NO: 236

GCGTAATACGACTC ACTATAGGAGATAC CCAGATCATATGAAA CGG

SEQ ID NO: 238

AGATACCCAGATCA TATGAAACGG | SEQ ID NO: 237

CAATTGTGTCCAAG AATGTTTCC

SEQ ID NO: 239

GCGTAATACGACTC ACTATAGGCAATTG TGTCCAAGAATGTTT CC | SEQ ID NO: 235

AGATACCCAGATCATATGAAACGGGCATGACTTTTTCAAGAGTGCCATGCCCGA AGGTTATGTACAGGAAGAACTATATTTTCAAGATGACGGGAACTACAAGA CACGTAAGTTTAAACAGTTCGGTACTAACTAACCATACATATTTAAATTTCAG GTGCTGAAGTCAAGTTGAAGGTGATACCCTGTTAATAGAATCGAGTAAAA GGTATTGATTTTAAAGAAGATGGAAACATTCTTGGACACAAATTG |

Table 8-PC

Target ID	Primers Forward 5' → 3'	Primers Reverse 5' → 3'	dsRNA DNA Sequence (sense strand) 5' → 3'
PC001	SEQ ID NO: 474 GCGTAATACGACTC GCATGGATGTTGGA CAAATTGGG SEQ ID NO: 476 GCGTAATACGACTC ACTATAGGGCATGG ATGTTGGACAAATTG GG	SEQ ID NO: 475 GCGTAATACGACTC ACTATAGGAGATTCA AATTTGATGTAGTCA AGAATTTTAG SEQ ID NO: 477 AGATTCAAATTTGAT GTAGTCAAGAATTTT AG	SEQ ID NO: 473 GCATGGATGTTGGACAAATTGGGGGGGTGTCTTCGCCCCTCGTCCATCCACCGGG CCTCACAAGTTGCGCGGACTCCCTGCCTTTAGTGATTTCCTTCGTAACAGGCTGAA GTATGCCCTTACAAACAGTGAAGTCACTAAAATTGTCATGCAAGGTTGATCAAAG TTGATGGTAAAGTGAGGACTGGTGAATTTTCCGTCTGATCTATGATGTCATT ACTATTGAGAAGACTGGTGAATTTTTCCGTCTGATCTATGATGTTAAAGGAAGATT TGCTGTGCCACCGTATTACAGCTGAAGAGGCAAAATACAAGTTGTGTAAAGTAAGG AGAGTCCAAACTGGTCCCAAAGGAATCCCCATTTTGGTAACACATGAGGCAGAA CCATTCGTTACCCTGACCCCAACATCAAAGTGAATGACACAATTCAAATGAAATT GCTACACATCTAAAATTCTTGACTACACTACACTCAAATTTGAATCT
PC003	SEQ ID NO: 479 CCCTAGACGTCCCT ATGAAAAGGCCC SEQ ID NO: 481 GCGTAATACGACTC ACTATAGGCCCCTAG ACGTCCCTATGAAA AGGCCC	SEQ ID NO: 480 GCGTAATACGACTC ACTATAGGTTGACA CGGCCAGGTCGGC CACC SEQ ID NO: 482 TTGACACGGCCAGG TCGGCCACC	SEQ ID NO: 478 CCCTAGACGTCCCTATGAAAAGGCCCGTCTGGATCAGGAATTGAAAATTATCGGC GCCTTTGGTTTACGAAACAAAACGTGAAGTGTGGAGAGTAAAGTACACTTTGGCTA AAATCCGTAAAGCTGCTGGTGAACTGCTCACCGTTGGTGTGCGAATTGGTGTTCTGGATG ATTGTTTGAAGGTAATGCACTTCTACGTCGTTTGGGTGTCTGAAATTGAAGATTTCTTGGAA AGAACAGGATGAAGCTTGATTATGTTTGGGTCTGAAATCTGGTCTGCAAATCATCATG CTAGAGTACTGATTAGGCAGAGAGACACATCCGGGTGCGCAAGCAGGTGGTGAACA TCCCCTCGTTCATCGTGCGGGGTGGCCGACCTGGCCGAGAAGCACATCGACTTCTCCCTGAA GTGCGCCCTTCGGGGGTGGCCGACCTGGCCGTGTCAA

			SEQ ID NO: 483
PC005	SEQ ID NO: 484 ATCCTAATGAAATCA ACGAAATCGCC	SEQ ID NO: 485 GCGTAATACGACTC ACTATAGGTTCCCTA CGTTCCCTGGCCTG CTTC	ATCCTAATGAAATCAACGAAATCGCCAACACCAACTCAAGACAAAACATCCGTAAG CTCATCAAGGATGGTCTTATCATCAAGAGCCAGTGGCAGTACACTCTAGGGCCC GTGTACGGCAAGAACACTGAAGCTAGAAGGAAGGAAGGCATTGTGGATTTGGAAA GAGGAAGGGTACGGCAAATGCCCGTATGCCTCCTCAAAAGGAACTGTGGGTGCAGCG CATGCGGTCCTCAGCGGCCTCCTCACAAAGTACAGGGAGGGCCAAGAAAATCGA CCGCCATCTTTACCACGCCCTGTACATGAAGGTACTGAAAGGTAACGTGTTCAGGAAC AAGAGGGTCCTTATGGAGTACATCACCACAGAAGAAGGCAGAGAAGGCAGGGCC AAGATGCTGTCTGCCAGGCTAACGCCAGGACTGAAGGTGAAGCAGGCCAGG GAACGTAGGGAA
	SEQ ID NO: 486 GCGTAATACGACTC ACTATAGGATCCTAA TGAAATCAACGAAAT CGCC	SEQ ID NO: 487 TTCCCTACGTTCCCT GGCCTGCTTC	
PC010	SEQ ID NO: 489 GCTCAGCCTATTAC CGCCCAACGC	SEQ ID NO: 490 GCGTAATACGACTC ACTATAGGATGGAA AATGAGTATCTGGA AGAAAG	SEQ ID NO: 488 GCTCAGCCTATTACCGCCCAACGCGTTGATTGATCACGTTCGGAAAAATG GTGCAAGTCCACGAACTGGGTACCGAAGGCTGCAGCAAGTCGTACGTGTTCTGT GGAACGAAAGATCTCACCGCCAAGCAAGTCCAGGAGAGTGTTGGGCATTGGAAAA GGGTCACCAAATCCCCAACACAGCCAGGCAACCTGGGCGGCCAGCCCGTGTCAAAA CCCCAAGCTGCCCCTGTACCACCGGGGAGCAGATTCTTGCAGCCCGTGTCAAAA TGCGGACATGAACTTGACAGATCTGACCGGGGAGTTGCGAGCCCGTGTCAAAA GTACATCAGGGCAAAAGACCTCTTAGATCCGAATACGGTGGCAGCCAGGCGCTG TCGGCCCTCTTAGAATGCACCTATCCGAATCATCATGATATTCTTA GGAGGACCATGTCTCTCAGGTCCCGGCCAGGTGTTGAACGACGATTTGAAGCAG CCCATCAAACATTACGATCCACTTGGCAATGCAGACGAGCTGCCACCAACAGCCATTGCAT CTATCAAACATTTACTCCTGCGCCCTGGATCAGTGGCACATGTGTCAAGTCGTTCTCTA CTGCAATTCCACCGGAGGGCACATGGTCATGGCGATTCTCAAAAGAACGACCTCAAGA TTCAAACAAACCTTCCAGCGAGTGTTCTCAAAAGAGTGTTCCAAAGGGAGTTAAAAGTCCAAG TGGGCATCGGCTCGTCGTGCGTGTCCTTGAGGTGAAGCGTTAAAAGCCCTGTGGTTCCGATAC GGAACTAGGCATGGGAATACTGTCAGTGGAAACTTGCAGGTGGAAACTTGCACGTTGGCGCCGAG CTCTACTGTCGGCGCTGTTCTTCGAGGTGCAGTGGAAACGTTAACCAGCATTCGGCGCCCATACCA CAGGGAGGCAGGGGCTGACGAGTGACCACGATTCATCAGCTATCAGCACGCGAGCGG GCAAAGGAGGAGGATCAGAGTGACCACCATTAGCGCTGGCTTCGACCAAGAAGCGGCGGCCAGTTGTGAT CAACAATCCACCACCATTAGCGCTGGCTTCGACCAAGAAGCGGCGGCCAGTTGTGAT GGCCCGAATGCCGGTTACAAGGCGGAATCGGACGAGACTCCCGACGTGCTCA GATGGGTGGACAGGATGTTGATCAGGTTGGGGGAGAACTTCAGTCTGTATCCGCAGTT CATGTACCATTTGAGACGGTCGCAGTTTCTGCAGGTGTTCAATAATTCTCCTGATG AAACGTCGTTTTATAGGCACATGCTGATGCGTGAGGGATTTGACTCAGTCTTTGATC
	SEQ ID NO: 491 GCGTAATACGACTC ACTATAGGGCTCAG CCTATTACCGCCCCA ACGC	SEQ ID NO: 492 ATGGAAAATGAGTAT CTGGAAGAAAG	

			ATGATCCAGCCGGATTTTGTACAGTTACAGCTTCAAGGGCGGCCCGAGCCTGTGTTGTTGGACACAAGCTCTATTCAGCCGGATAGAATCCTCATGGACACTTCTTCCAGATACTCATTTTCCAT
PC014	SEQ ID NO: 494 CTGATGTTCAAAAAC AAATCAAACACATG SEQ ID NO: 496 GCGTAATACGACTC ACTATAGGCTGATG TTCAAAAACAAATCA AACACATG	SEQ ID NO: 495 GCGTAATACGACTC ACTATAGGTGAGCG ATCAGATCCAACCTA GCCTCC SEQ ID NO: 497 TGAGCGATCAGATC CAACCTAGCCTCC	SEQ ID NO: 493 CTGATGTTCAAAAACAAATCAAACACATGATGGCTTTCATTGAACAAGAAGCCAATGAGAAAGGCAGAAGAAAATTGATGCCAAGGCAGAGGAGGAATTCAACATTGAAAAAGGGCGTTTGGTCCAGCAACAGACTCAAGATCATCATGGAGTACTACGAGAAAAAGGAGAAGCAAGTCGAACTTCAAAAGAAAATTCAGTCCTCTAATATGTTGAATCAGGCTCGTTTGAAGGTGCTGAAGTGAGAGGACCATGTCAGAGCAGTCCTGGAGGATGCTCGTAAAGTCTTGGTGAAGTAACCAAGACCAAGAAAATACTCCCAAATTTGGAGAGCCTATCTACAAGGACTGTTCCAGCTGTTCGAGAAGGTGACGGTCCGCGTGAGACCGCGAACAGAGGACCTGTCAGGTCCATCCTGCCCAACCTGCTGCCAAATACAAGGAGCGCCACCGGCAAAGACATCCTACTCAAGGTGGACGATGAGTCGCACCTGTCTCAGAGGATCAGCAACACGATGGAGGCTAGGTTGCTCGCTCGATCGGATCTGATCGCTCA
PC016	SEQ ID NO: 499 ACTGGTCATTCTTGA GGATGTCAAGT SEQ ID NO: 501 GCGTAATACGACTC ACTATAGGACTGGT CATTCTTGAGGATGT CAAGT	SEQ ID NO: 500 GCGTAATACGACTC ACTATAGGTTGGGC ATAGTCAAGATGGG GATCTGC SEQ ID NO: 502 TTGGGCATAGTCAA GATGGGGATCTGC	SEQ ID NO: 498 ACTGGTCATTCTTGAGGATGTCAAGTTTCCAAAATTCAATGAAATTGTCCAGCTCAAATTGGAAGCAGAAGAATTCAATGAAAAGTTTGGAAGTCAGTGGATCAAAGGCAGTTGTTCAGGTATTTGAAGGCACATCAGGTATTGATGCTAAGAACACGGTGTGTGAGTTCACTGGAGATATTCTAAGAACTCCAGTATCAGAAGATATGCTGGGACGTGTCTTCAATGGATCAGGAAAACCATTGATAAAGGTCCCCGATCCTGGCTGCGGACTACCTCGACATCCAAGGACAGCCGGATCACGGCCATCGACCTGGATCAGCGCAGAAATGATCCAGACTGGGATCTCTCCGCCGCTGGTCAAGTACCTGGCAAGTCTGTGCTCAGCCCAGATTGTAGGCAGGACAACTTTGCTATTGTGTTGCTGAAGAGAACGGCTCGATGGAGAACGGATGACCATGAAGACTGCCAGTTCTTCAAGCAGGACTTCGAACTTCTTGGCCTACCGCGCCAACGATCCGAATTCTTGGCGTCGTTTGGCTCGTGCTCTGACGGCGCCGGAATTCTTGACGGAAGAAGTGCCCCGGCCGCCATCGGCCATGGCGAGAAGCACGCGCGGTTTGGTCATCTTGACGGAAGAAGTGCCCCGGCCGCCATCGGCCATGGCGAGAAGCACGTGCTGGTCATCTTGACCGACGGCGTTGCGGAGGGTTCCCCGGTTCTGACTGTAACCGATCTCGAGAAGAAGTGCCCCGGCCGCCATCGGCCATGGCGAGAAGCACGTGCTGGTCATCTTGACCGACGGCGTTGCGGAGGGTTCCCCGGTTCTGACTGTAACCGATCTCACGCAGACGATCCCCATCTTGACTATGCCCAA
PC027	SEQ ID NO: 504 CAAGCTAACTTGAAA GTACTACCAGAAGG	SEQ ID NO: 505 GCGTAATACGACTC ACTATAGGTTTGGA	SEQ ID NO: 503 CAAGCTAACTTGAAAGTACTACCAGAAGGAGCTGAAATCAGAGATGGAGAACGTTTGCCAGTCACAGTAAAGGACATGGGAGCATGGACGATTACCCACAAAAATCCATGCCAGATTACCCACAAAAATCCA

Primers Forward 5' → 3'	Primers Reverse 5' → 3'	dsRNA DNA Sequence
SEQ ID NO: 506 GCGTAATACGACTC ACTATAGGCAAGCT AACTTGAAAGTACTA CCAGAAGG	ATTGAAGGCAATACT CGATCAG SEQ ID NO: 507 TTTTGGAATTGAAGG CAATACTCGATCAG	ACACAACCCCAATGGGCGGTTTGTGTAGTGGTTTGTGGTGATGGAGAGAATACATAATA TACACGGCTATGGCCCTTCGTAACAAAGCATTTGGTAGCGGCTCAAGAATTTGTATG GGCACAGGACTCCAGTGAATATGCCGCGAATCCGGAATCCGACTTTGGTGCCGAAGGAAT TTCAAGAATTTCAAAGAAAAAAGAATTTCAAGTCCGACTTTCTGGCTTAGCTTTCTATGACT CTATGGTGGTTTTCTCTTGGGTGTGAAATCAGTTTCTGGCTTAGCTTTCTATGACT GGGAAACGCTTGAGTTAGTAAGGCGCATTGAAATACAGCCTAGAGCTATCTACTG GTCAGATAGTGGCAAGTTGGTATGCCTTGCTACCGAAGATAGCTATTTCATATTGT CCTATGACTCTGACCAAGTCCAGAAAGCTAGAGATAACAACCAAGTTGCTGAAGA TGGAGTGGAGGCTGCCTTGATGTCCTAGGTGAAATAATGAATCCGTAAGAACA GGTCTTTGGGTGGTGGTAGGAGACTGCTTCATTACACAACGCAGTCAACCGTATCAACTA CTTGTGGGTGGTGTACCTAGAGATGACAGGTTATACTTGGTGATAAAGAGTTAGGAGTA TGGGCTATGTACCTATCNAATTGCTATTATCTGTACTGAAATATCAGACTGCAGTCATGGGAC GTCAGCTATCNAATTGCTATTATCTGTACTGAAATATCAGACTGCAGTCATGGGAC GAGACTTCCCAACGGCTGATCGAGTATTGCCTTCAATTCCAAAA

Table 8-EV

Target ID	Primers Forward 5' → 3'	Primers Reverse 5' → 3'	dsRNA DNA Sequence (sense strand) 5' → 3'
EV005	SEQ ID NO: 577 GACAAAACATCCGC AAACTG SEQ ID NO: 579 GCGTAATACGACTC ACTATAGGGACAAA ACATCCGCAAACTG	SEQ ID NO: 578 GCGTAATACGACTC ACTATAGGCTCCTT GCATCAGCTTGATC SEQ ID NO: 580 CTCCTTGCATCAGC TTGATC	SEQ ID NO: 576 GACAAAACATCCGCAAACTGATTAAAGATGGTCTTATTATTAAAAGCCTGTCGCG GTGCATTCTCGTGCACGTGTACGCAAAAATACTGAGCCCGCAGGAAGGTCGTC ATTGTGGATTTGGTAAAGGAAAGGAACTGCAAATGCTAGGATGCCCAGAAAGGA ATTATGGATTCAACGTATGGAGCATTATACCATGCTTTATATATGAAGCTAAGGGAAAT GTATTCAAGAATAAGAGAGTAATGATGGACTATATCCATAAAAAGAAGGCGGAGAA AGCACGTACAAAGATGCTCAATGATCAAGCTGATGCAAGGAG
EV009	SEQ ID NO: 582 CAGGACTGAAGAAT CTATAATAGG SEQ ID NO: 584 GCGTAATACGACTC ACTATAGGCAGGAC ACTATAGGCAGGAC	SEQ ID NO: 583 GCGTAATACGACTC ACTATAGGCTGGAA AGATGGGTAATACTT C SEQ ID NO: 585	SEQ ID NO: 581 CAGGACTGAAGAATCTATAATAGGAACAAACCCAGGAATGGGTTTTAGGCCAATG CCCGACAACAACGAGAAAGTACCGTGATTTGGTTACAGGGTTCTAATAAAACAA CTACGAAAAATGAAAATGAATCTCCTCTCATATTAGACAAGTATTACACTCCCG GAAAAATAGAAAAGGGAAATATTCCAGTAAAGCGCTGTTCATACGGAGAAAAATTG ATTAGGGGGACAAGTATGTGATGTAGATGTGGAGGAAATGGGAGCCGTGCACCCCG GAAAATCATTTTGATTACCTCAGAAAATGCGCCCTTGTATATTTCTGAAGCTGAACAG

	TGAAGAATCTATAAT AGG	CTGGAAAGATGGGT AATACTTC	GATATATGGATGGGAACCGGAGTACTACAACGATCCAAATGATCTTCCAGATGAT ATGCCGCCAGCAGTTGAAGGACCATATACGTTATAATATCACCAATCAGTGGAGA GAAATACCGTCTGGGTAACATGGCGCAGGTGAAAATCCGGCGACGTGGAGTACTT GGGCCCTGTGAAGTATTACCCATCTTCCAG
EV010	SEQ ID NO: 587 CCAATGGAGACTTG AAGATGTC	SEQ ID NO: 588 GCGTAATACGACTC ACTATAGGCTTCCCT CATCAACATGTGC	SEQ ID NO: 586 CCAATGGAGACTTGAAGATGTCCTTCAACGCCATATTAGAAGTGAAGTGTTCTAGA GAACTTAAAGTACAAGGAGGTATAGGTCCTTGTGTCTCTCTAAATGTCAAAATCC TCTTGTTTCTGATTTAGAAATAGGCATGGTAACACAGTTCAGTGGAAACTGTGTA GCTTAAGTCCAAGCACTACGGTTGCCTTATTTTCGAAGTTGTTAATCAGCATGCA GCACCCATTCCTCAAGGGGGACGTGGATGCATTCAGTTTATTACTCAATATCAGC ATTCAAGTGGTCAGAAAATATTCACCATATTAAGGGTAACTACAATAGCAAGAAATTGGGCGGA TGCCACTGCAAATATTCACCATATTAGCGCTGGCTTTGACGAACAAACTGCGGCT GTTTAATGGCGAGGATCGCTGTATATAGACAGAAATGTGTCAGAAATTTGGAGAATAT TTCTCAGATGGGTTGACAGAATGTTGATACGATTGTGTCAGAAACTTCAGCTTATCCACA GTTTATGTATCATCTACGTCGTTCCCAATTTCTACAAGTGTTCAATAATTCACCAGA TGAAACTTCATTCTATAGGCACACATGTTGATGAGGGAAG
	SEQ ID NO: 589 GCGTAATACGACTC ACTATAGGCCAATG GAGACTTGAAGATG TC	SEQ ID NO: 590 CTTCCCTCATCAACA TGTGC	
EV015	SEQ ID NO: 592 GTTAAGCCTCCAAG GGTATTC	SEQ ID NO: 593 GCGTAATACGACTC ACTATAGGGAGCAC AAAGAAGCCAAGTC AG	SEQ ID NO: 591 GTTAAGCCTCCAAGGGGTATTCTCCTTTACGGGCCTCCCGGCACGGGGAAAACG CTGATCGCCAGGGCCGTTGCCAACGAAACTGGTGCGTTCCTTCCTCATCAATG GGCCCGAGATTATGAGCAAGCTGGCGGGAGATCCGGAGAATCCGAGAGCAATCTTAGAAAGG CTTTGAAGAGGCTGATAAAAACTCTCCTGCAATCATCTTATCGACGAATTAGAC GCAATCGCTCCCAAGCGCGAGAAGACTCATGGTGAGAAGAAAAGTTCCCATGTGATCGTGA TCCCAACTGTTGACTTTGATGGGACGGCCATGAGAACTGCCACTCAGACGTTTCGGCC GATTCGACAGAGAGAATCGGTATCCCCGAGCGTACTGACGATGTAGATTTGGAACAGA ACTCAGAATACACACAAAAACATGAAATTGGCTGACGATGTAGATTTGGAACAGA TTGCCGCAGAGACTCACGGTCATGTAGGTGCTTGACTTGGCTTCTTTGTGCTC
	SEQ ID NO: 594 GCGTAATACGACTC ACTATAGGGTTAAG CCTCCAAGGGGTAT TC	SEQ ID NO: 595 GAGCACAAAGAAGC CAAGTCAG	
EV016	SEQ ID NO: 597 GGTGATCCTTGATA GTGTTAAG	SEQ ID NO: 598 GCGTAATACGACTC ACTATAGGCCTCAG CATAAGATGACATG	SEQ ID NO: 596 GGTGATCCTTGATAGTGTTAAGTTCCAAAATTTAACGAAATTGTACAGCTTCAAGTT ATCAGATGGAACAGTTAGGTCTGGACAAGTTTTGGAAGTCAGTGGACAGAAGGCG GTTGTCCAAGTTTTTGAAGGCACCTCCGGAATTGATGCTAAAAACACTTTATGTGA ATTTACAGGAGATATCTTAAGAAACTCCAGTGTCTGAAGATATGTTGGGTCGTGTGT TTAATGGATCTGGAAAGCCTATCGATAAAGGCCGCCAATCTTAGCTGAAGATTTT CTTGACATTCAAGGTCAACCTATAAATCCTTGGTCTGTCTATCTATCCAGAAGAAAT GATCCAGACTGTATTTCTGCGATTGATGAATTCCATTGCCAGAGGACAA
	SEQ ID NO: 599 GCGTAATACGACTC ACTATAGGGGTGAT CCTTGATAGTAGTGT	SEQ ID NO: 600 CCTCAGCATAAGAT GACATG	

G
AGATTCCAATTTCTCTGCAGCTGGTTTACCCCACAATGAAATGCTGCTCAAATC TGTAGACAAGCTGGTCTTGTCAAAATCCCAGGGAAATCTGTCTTAGATGATCATGA AGACAACTTTGCTATCGTTTCGCCGCTATGGTGTCAATATGGAAACAGCCAGAT TCTTCAAGCAAGATTTTGAAGAGAATGGCTCTATGGAAAATGTGTGCCTATTTTTG AACTTGGCCAATGATCCTACCATTGAAAGAATTATAACACCCGGTTTGACTTTAAC AGCGGCTGAATTTATGGCATATCAATGTGAGAAGCATGTGTTAGTGTCATATTGACTG ACATGTCATCTTATGCTGAGG

Table 8-AG

Target ID	Primers Forward 5'→3'	Primers Reverse 5'→3'	dsRNA DNA Sequence (sense strand) 5'→3'
AG001	SEQ ID NO: 769 GCGTAATACGACTC ACTATAGGGCATGG ATGTTGGACAAATTG G SEQ ID NO: 771 GCATGGATGTTGGA CAAATTGG	SEQ ID NO: 770 GATTCCCAGTTGGAT GGTGTCG SEQ ID NO: 772 GCGTAATACGACTC ACTATAGGGATTTCC AGTTGGATGGTGTC G	SEQ ID NO: 768 GCATGGATGTTGGACAAATTGGGGGGGTGTGTTCGCCCCCAGGCCCTCCACCGGG CCACACAAGCTCAGGGAGTCCCTTCCATTAGTGATTTTCTTGCGTAACAGGTTGAA GTACGCCCTGACAAACTGTGAGGTGACCAAGATCGTTATGCAGAGACTTATTAAG GTCGACGGCAAGTCAGGACTGATCCTAACTATCCTGCTGATTCATGGATGTGA TCACCATTGAAAAAACTGTGACTCACTGCTGAAGAAGCAAAATACAAATTGTGCAAGTCCG TTCACTATTCACAGGATCACTACTGCTGAGAAGCAAAATACAAATTGTCAAGTCCG CAAGGTGCAAACCGGACCAAAAGGTATTCCATTCTTGGTCACCACGATGGTTAGG ACCATTAGGTACCCTGACCCAATGATCAAGGTAAACGACACCAACTCCAACTGGAAA TC
AG005	SEQ ID NO: 774 GCGTAATACGACTC ACTATAGGGCAACAC CAACTCGAGGCAAA AC SEQ ID NO: 776 CAACACCAACTCGA GGCAAAAC	SEQ ID NO: 775 CCTTTTGCCCTTCTGG CGTTAG SEQ ID NO: 777 GCGTAATACGACTC ACTATAGGGCCTTTTG CCTTCTGGCGTTAG	SEQ ID NO: 773 CAACACCAACTCGAGGCAAAACATCCGTAAATTGATCAAGGATGGTTTGATCATTA AGAAACCGGTGGCAGTGCACTGGCGGTTTCGGTAAAAACACAGAAGCTC GCAGGAAGGGAAGGCAACTGCACTGCGGTTTCGGTAAGAGGAAGGTACAGGAAGCGCTC GTATGCCTCAAAAGGAACTATGGATCCAAAAGGATGCGTGTCTTGAGGCGTCTCCT GAAAAAATACAGGGAAGCCAAAAGATCGACAGGCCAAAAGAGAGTGTTGATGGGGAGA ATGAGGGCCAAGGGTAACGTGTTCAAGAACAAGAGAGTGTTGATGAATACATCC ACAAGAGAGGCTGAGAAGGCCCGTGCCAAGAGTGTTGGCCGACCAAGCTAACG CCAGAAGGCAAAAGG
AG010	SEQ ID NO: 779 GCGTAATACGACTC ACTATAGGGCAAACTT TCCAAAGGGGTGTTC	SEQ ID NO: 780 GAAGGATGCCTGGT CATCTTTG	SEQ ID NO: 778 CAAACTTTCCAAAGGGGTGTTCGCGAAGGACCAGAATGGACATTTGAAGATGGCTT TCAACGGTACTTTGGAGGTGAAGTGCTCTCAGGGAATTAAAAGTTCAAGGCGGTAT TGGCTCATGCGGTGTCGGCTAAAATGTAAAAAGTCCTTTGGTAGCGGACACGGAAATA

	G	SEQ ID NO: 782 GCGTAATACGACTC ACTATAGGGAAGGA TGCCTGGTCATCTTT G	GGCATGGGAAACACCGTGCAATGGAAGATGTGCACCTTCAACCCTAGCACGACG ATGGCGCTGTTTTCGGAGGTGGTCAATCAGCATTCGGCCCCCATTCCTCCAAGGTG GTAGAGGATGTATACAGTTTATTACACAATATCAGCACTCGAGTGGCCAAGGAG GATAAGGGTGACGACGATAGCGAGAAATTGGGCGACGCATCGGGCGAATATTCA CCACATCAGCGCGGGTTTCGATCAGGAACGTGCGCGGGTGATTATGGCCCGGAT GGCTGTTTTATAGACGGGAGACCGATGAGAGTCCGATGTTTAAGATGGGTCGAT CGGATGCTGATTCGTTTGTGTCAAAAGTTTGGAGAATATAACAAAGATGACCAGG CATCCTTC
	SEQ ID NO: 781 CAAACTTTCCAAAG GGTGTTCG		SEQ ID NO: 783
AG014	SEQ ID NO: 784 GCGTAATACGACTC ACTATAGGGAAAAG GCCGAGGAAATTGA TG	SEQ ID NO: 785 CAACTGTTGCGAAA TCAGGTCC	GAAAAGGCCGAGGAAATTGATGCCAAGGCGGAAGAAGAATTTAACATTGAAAAGG GCCGGCCTTGTGCAACAACAAAGATTGAAGATCATGGAATACTATGGAAGAAGGA GAAGCAAGTCGAACTACAAAGAGAAATTCAATCCTCCAACATGCTGAACCAAGCC CGTCTTAAGGTTCTGAAAGTCCGCGAAGATCATCGTTTAGAGCTGTATTGGATGAGG CTCGCAAGAAGCTTGGTGAAGTCACCAGGGATCAAGGCAAATATGCCCAGATTCT GGAATCTTTGATCCTTCAGGGACTCTACCAGCTTTCGAGGCAAACGTGACCGTA CGCGTCCGCCCCACAAGACAGAACCTTAGTCCAATCAGTGCTGCCAACCATCGCAA CCAAATACCGTGACGTCACCGGCCGGAGAATGTACACCTGTGCCATCGATGACGAAAC TCAACTGTCCGAATCCGTAACCGCGGCACGTTTGGACCTGATTTCGCAACAGTTG ATTAAGGTCTGCAACACCCTGGAGGCACGTTTGGACCTGATTTCGCAACAGTTG
	SEQ ID NO: 786 GAAAAGGCCGAGGA AATTGATG	SEQ ID NO: 787 GCGTAATACGACTC ACTATAGGCCAACTG TTGCGAAATCAGGT CC	
AG016	SEQ ID NO: 789 GCGTAATACGACTC ACTATAGGGGTGTTC AACGGATCAGGAAA ACC	SEQ ID NO: 790 CGACCGGCCTCTTTC GTAAATG	SEQ ID NO: 788
	SEQ ID NO: 791 GTGTTCAACGGATC AGGAAACC	SEQ ID NO: 792 GCGTAATACGACTC ACTATAGGCGACCG GCTCTTTCGTAAATG	GTGTTCAACGGATCAGGAAAACCCATTGACAAGGTCCTCCAATCTTAGCCGAAG ATTTCTTTGGACATCCAAGGTCAACCCATCAACCCATGGTCGCGTATCTACCCGGA AGAAATGATCCAGACCGGTATCTCCGCGCTGCCGGCCGGGTATGACTCCATCGCGCCGT GGGCAAAAATCCCCATTTTCTCCGCGGGCCGGTTTAGTCAAACTGCGCGGGCAAATCGGCTAATCGA CCCAAATCTGTAGAGACAGGACAATTTCGCCATCGTGTTCGCCGCCATGGGTGTCAACATGGAA CGATCACGAGGACAATTTCGCCATCGTGTTCGCCGCCATGGGTGTCAACATGGAA ACGCCCGGTTTCTTGAATTGGCCAACGATCCCACCATCGAGAGAATCATCACGCCCCCG TTTGGCTCTTCTTGAATTGCCGCCGAATTTTGGCTTATCAATGCGAGAAACACGTGCTG GTTATCTTAACTGATATGTCTTCTTACGCCGGACGTCTGCGGTTCCCCGGTTACACCGATTTG CAGAGAGAAGTAGCTACCCGGACGTCGTGGGGTTCCCCGGTTACACCGATTTG GCCACCATTTTTACGAAAGAGCCGGTCG

Table 8-TC

Target ID	Primers Forward 5' → 3'	Primers Reverse 5' → 3'	dsRNA DNA Sequence (sense strand) 5' → 3'
TC001	SEQ ID NO: 864 GCGTAATACGACTCACTATAGGCGAAACAGGCTGAAGTATGC SEQ ID NO: 866 CTGCGAAACAGGCTGAAGTATGC	SEQ ID NO: 865 GGTGTGCCCATTTGCATCCT SEQ ID NO: 867 GCGTAATACGACTCACTATAGGGGTGTGCCCATTTGCATCCT	SEQ ID NO: 863 CTGCGAAACAGGCTGAAGTATGCCCTTGACCAACTCAGAAGTGACGAAGATTGTTATGCAAAGATTGATTAAAGTTGACGGAAAAGTTAGGACAGACCCAACTACCCGCGGGTTTCATGGATGTTGTGACTATTGAGAAAACTGGGAAATTCTTCCGCTTGATTTATGATGTTAAGGGAAGGTTCACAATCCATCGCATTACTGGAGAAGAGGCCAAATATAAATTGTGCAAAGTGAAGAAGTACAGACAGGCCCCAAGGGCATTCCCTTCTTGGTGACACCGCCGCGACGGACGACTATCAGATACCCAGACCCCATGATCAAGTGAATGACACCATTCAATTGAGAGATTGCCACTTCGAAAATTCTTGATTTTATCAAATTTGAGTCCGGGTAATTTGTGTGTATGATTACTGGAGGTCGTAACTTGGGGCGTGTCGGTACAGTGGTGAGGCCGAGAACGTCACCCAGGTTCCTTCGAACATCGTTCATATTAAGGATGCAAATGGGCACACC
TC002	SEQ ID NO: 869 GCGTAATACGACTCACTATAGGCATCCATGTTGAGGTGGGCA SEQ ID NO: 871 CATCCATGTTGAGGTGGGCA	SEQ ID NO: 870 CTTTGTGAACAGCGGCCATC SEQ ID NO: 872 GCGTAATACGACTCACTATAGGCTTTGTGAACAGCGGCCATC	SEQ ID NO: 868 CATCCATGTTGAGGTGGGCATTTTTGAGGGCGTCCGGCTGCGTTTTCATCGTTTTGAGTACGGCCTGTGTGTTGGTGTTGGCCCCCTGCGAGGGCCTCCCGGCTGCATCTGATGGTGCTGAGGGTGCCATCGATCTGCTGGAGCTGCTTTTCGGTAGCGTTTCTTCCTCTTGATGGCCTGAGGTGCCTGGATGCCGCCGGCTGCTGTTCACAAAG
TC010	SEQ ID NO: 874 GCGTAATACGACTCACTATAGGTACCATTTGCGCCGCTC SEQ ID NO: 876 ATGTACCATTTGCGCCGCTC	SEQ ID NO: 875 ATGTCCTGGTACTTGAGGTTCCTCC SEQ ID NO: 877 GCGTAATACGACTCACTATAGGATGTCCTGGTACTTGAGGTTCCTCC	SEQ ID NO: 873 ATGTCCTGGTACTTGAGGTTCCTCCATTGGGCGATTGTCTCACCGTGGAAATCAAAATTTGGAAAAATGTGTCCATGAGAAGGATCCGATCGGGTTGAATGGAACTAGTGTCGAGGAGGACGCGGGTTCAGGGGGCCGTTGAAACTATAACTGTACAAAATCGGCTGGATCATAATGAAGACTTTGGGGTGGAGGTCCTCCCGCATCAGCATGTGGGGGTAGAACGAGGTCTCGTCTCGGGGGAGTTGTTGAAAACTTGGAGGAATTGGGAGGCGGGGCAAATGGTACAT
TC014	SEQ ID NO: 879 GCGTAATACGACTC	SEQ ID NO: 880 ACAAGGCCGTACGA	SEQ ID NO: 878 CAACAGCGCCTTGAAGATCATGGAATATTACGAGAGAAGGAGGAGAAACCGGTGGAAT

	Primers Forward	Primers Reverse	dsRNA DNA Sequence
	ACTATAGGCAACAG CGCTTGAAGATCAT GG SEQ ID NO: 881 CAACAGCGCTTGAA GATCATGG	ATTTCTGG SEQ ID NO: 882 GCGTAATACGACTC ACTATAGGACAAGG CCGTACGAATTTCT GG	TGCAGAAGAAAATTCAGTCGTCAAACATGCTGAACCAGCCCGTTTGAAAGTATTA AAAGTGCGTGAAGACCACGTCCACAATGTGCTGGATGAGCGCCCGCAAACGTCTG GGCGAAATCACCAATGACCAGCCGAGATATTCACAACTTTTGGAGTCTCTTATCCT CCAGAGTCTCTACCAGTACTTGGGAATCAGTGATGAGTTGTTTGAGAACAATATAG TGGTGAGAGTCAGGCAACAGGACACAGGAGTATAATCCCAGTTGT TGCGACGAAATACAGGGACGCCACTGGTAAGACGTTCATCTTAAAATCGACGAT GAGAGCCACTTGCCATCCGAAACCACCGGAGGACGTT GGTAAAATCAAGATTGACAACACCTTGGAGGCTCGTTTGGATTTAATTGCACAGCA ACTTGTGCCAGAAATTCGTACGGCCTTGT
TC015	SEQ ID NO: 884 GCGTAATACGACTC ACTATAGGCGATAC AGTGTTGCTGAAAG GGAAG SEQ ID NO: 886 CGATACAGTGTTGC TGAAAGGGAAG	SEQ ID NO: 885 TCGGATTCGCCGGC TAATTTAC SEQ ID NO: 887 GCGTAATACGACTC ACTATAGGTCGGAT TCGCCGGCTAATTT AC	SEQ ID NO: 883 CGATACAGTGTTGCTGAAGAGGAAGCGGCGGAAAGAGACCGTCTGCATTGTGCT GGCCGGACGAAAACTGCCCCGATGAGAGATCCGGATGAACAGGATCGTCAGGAA TAATCTACGGGTTAGGCTCTCTGAGCGTCGTCTGGATCCAGCCCTGTCCGACGTC AAATACGGGAAGAGGATCCACGTTTGCCCATCGATGACACGGTCGAAGGGCTC GTCGGAAATCTCTTCGAGGTGTACTTAAAACCATACTTCCTGGAGCGTTATCGACC AATCCACAAGGCGACGTTTTCATCGTCCGTGGTGGCATGCGAGCCGTTGAATTC AAGTGGTGAAACGGAACCGTCACCGATCAAACGGAGAGAGGAGAGGCCTTGAACG TCCATTGTGACGGCTACGACGATATCGGCGGTTGTCGCAAACAACTCGCACAAATCAAAGA CCGTCGGCTAGGACGGTATCCTCTTGTACGGACCTCTCAGGTACCGGTAAAACTTTAATCG CACGTGCAGTGGCCAACGAACCGGTGCTTTCTTTCTTCTTAATCAACGGTCCCGA AATTATGAGTAAATTAGCCGGCGAATCCGA

Table 8-MP

Target ID	Primers Forward 5'→3'	Primers Reverse 5'→3'	dsRNA DNA Sequence (sense strand) 5'→3'
MP001	SEQ ID NO: 1042 GCGTAATACGACTC ACTATAGGGTTTAAA CGCACCCAAAGCAT GG SEQ ID NO: 1044	SEQ ID NO: 1043 CAATACCAACACGC CCTAAATTGC SEQ ID NO: 1045 GCGTAATACGACTC ACTATAGGCAATAC	SEQ ID NO: 1041 GTTTAAACGCACCCAAAGCATGGATGTTGGACAAATCGGGGGGTGTCTTCGCTCC ACGTCCAAGCACCGGTCCACAACAACTTCGTGAATCACTACCGGTTATTGATCTTCT TGCGTAATCGTTTGAAGTATGCCACTTACTGGTGCCGAAGTCACCAAGAGTTGTCATG CAAAGATTAATCAAGGTTGATATCTATCCAACCATCCAAAAAGACCAGTCAATTTCATCCTATG GTTTTATGGGATGTTATATCTGTTTCACCCATCCACAGAATTACTCCTGAAGAAGCAAAATACAAAG ATGTGAAAGGTCGTTTCACCATCGACCCAAAGGTGTGCCCATTTTGCCATTTTAACTAC

	GTTTAAACGCACCC AAAGCATGG	CAACACGCCCTAAA TTGC	TCATGATGGCCGTACTATTCGCTACCCTGACCCTAACATCAAGGTTAATGACACTA TTAGATACGATATTGCATCATCTAAAATTTGGATCATCATCCGTTTGAAACTGGAA ACTTGTCGCATGATAACTGGAGGTCGCAATTTAGGCGTGTTGGTATTG
MP002	SEQ ID NO: 1047 GCGTAATACGACTC ACTATAGGGGTGGC AAAAGGAAGAGAA GG SEQ ID NO: 1049 GGTGGCAAAAAGGA AGAGAAGC	SEQ ID NO: 1048 GCTGATTTAAGTGC ATCTGCTGC SEQ ID NO: 1050 GCGTAATACGACTC ACTATAGGGCTGAT TTAAGTGCATCTGCT GC	SEQ ID NO: 1046 GGTGGCAAAAAGGAAGAGAAGGGACCATCAACCGAAGATGCGATACAAAAGCTT CGATCCACTGAAGACGTGATAAAGAAACAAGAAATTTTAGAAAAAAAATTGA ACAAGAAGTAGCGATAGCCAAAAAAACGGTACAACTAATAAACGAGCTGCATTG CAAGCATTGAAGCGTAAGAAACGGTACGAACACAATTAGCCCAATTGATGGTA CCATGTTAACTATTGAACAACAGCGGGAGCATTAGAAGGTGCCAACACAAATAC AGCAGTATTGACTACCATGAAAACTGCAGACGATGCACTAAATCAGC
MP010	SEQ ID NO: 1052 GCGTAATACGACTC ACTATAGGCAGACC CTGTTCAGAAATATG SEQ ID NO: 1054 CAGACCCTGTTCAG AATATG	SEQ ID NO: 1053 GCATTGGGAATCGA GTTTTGAG SEQ ID NO: 1055 GCGTAATACGACTC ACTATAGGGCATTG GGAATCGAGTTTTTG AG	SEQ ID NO: 1051 CAGACCCTGTTCAGAATATGATGCATGTTAGTGCTGCATTGATCAAGAAGCATCT GCCGTTTAATGGCTCGTATGGTAGTGAACCGTGCTGAAACTGAGGATAGTCCAG ATGTGATGCGTTGGGCTGATCGTACGCTTATACGCTTGTGTCAAAAATTGGTGAT TATCAAAAGATGATCCAAATAGTTCCGATTGCCAGAAAACTTCAGTTTATATCCA CAGTTCATGTATCATCATTAAGAAGGTCTCAATTCTACAAGTTTTAATAATAGTCCT GATGAAACATCATATTATAGGCACACATGTTGATGCGTGAAGATGTTACCCAAAGTTT AATCATGATACAGCCAATTCTGTATAGCTAGTTTAATGGTAGGCCAGAACCTG TACTTTTGGATACCAGTAGTATTCAACCTGATAAAATATTATTGATGGACACATTT TCCATATTTGATATTCCATGGAGAACTATTGCTCAATGGACAATGGATTAT CAAAATAGACCAGAGTAGTAGTAACCTCAAGCAGTTGCTTCAAGCCCCGTTGATG ATGCTCAGGAAATTCTCAAAACTCGATTCCCAATGC
MP016	SEQ ID NO: 1057 GCGTAATACGACTC ACTATAGGGCTGGT ATGGCAGTGGAAAG C SEQ ID NO: 1059 GTTTTCAATGGCAGT GGAAAGC	SEQ ID NO: 1058 CGTGGTGTAATGAT ACGCTC SEQ ID NO: 1060 GCGTAATACGACTC ACTATAGGGCGTGGT GTAATGATACGCTC	SEQ ID NO: 1056 GTTTTCAATGGCAGTGGGAAAGCCGATAGATAAAGGACCTCCTATTTTGGCTGAAG ATTATTTGGATATTGAAGGCCAACCTATTAATCCATACTCCAGAACATATCCTCAAG AAATGATTCAACCTGGTATTCAGCTGCCATTGAAATCATGATCTATTGCTCGTGGAC AAAAAATTCCAATATTTCAGCTGCGTCGTCGTTAAAAAACCTGGTAATCAGTTCTCAA TTTGTAGACAAGCTGCGTCGTCGTTAAAAAACCTGGTAATCAGTTCTTGACGATCAT GAGACAATTTTGCTATGATTTGCTATATTGTCTATGGTGTTAATATGGAAAACAGCCAG ATTCTTTAAACAAGATTTTGAGGAAAATGGTTCAATGGAAATGTTTAAATGGAGAATTGTTTCTT GAATTTAGCTAATGATCCTACTATTGAGCGTATCATTACCACG
MP027	SEQ ID NO: 1062 GCGTAATACGACTC	SEQ ID NO: 1063 CCAAAAATACCATCT	SEQ ID NO: 1061

	Primers Forward	Primers Reverse	dsRNA DNA Sequence
	ACTATAGGGCTCGT TGTTTCCATCCAGA AC SEQ ID NO: 1064 GCTCGTTTGTTTCCA TCCAGAAC	GCTCCACC SEQ ID NO: 1065 GCGTAATACGGACTC ACTATAGGCCAAAA ATACCATCTGCTCCA CC	GCTCGTTTGTTTCCATCCAGAACTTCCCATCGTCGTTAACTGGCTCAGATGGTA CCGTCAGAATTGGCATTCGGTACTTATCTGTTGCTTACGGGGATCTAATAATGTAGCTCTAGG TTATGATGAAGGAAGTATAATGTTAAAGTTGGTCGTGAAGAGCCAGCAATGTCAA TGGATGTTCATGGGGGTAAAATTGTTTGGGCACGTCATAGTGAAATTCAACAAGCT AACCTTAAAGCGATGCTTCAAGCAGAGGAGCCGAAATCAAGATGGTGAACGTT TACCAATACAAGTTAAAGACATGGGTAGCTGTGAAATTATCCACCAGTCAATATCT CATAATCAATGGCTTTGCGTAATAAAGCATTTGGCTGTAATAAAAGCATTTGTATGGTC TTCTGATTCTGAGTATGCCATTAGAGAAATTCTTCTACAATCAAAGTTTTTAAAAA TTTTAAAGAAAAAAAGTCTTTTAAACCAGAAGGTGGAGCAGATGGTATTTTTGG

Table 8-NL

Target ID	Primers Forward 5' → 3'	Primers Reverse 5' → 3'	dsRNA DNA Sequence 5' → 3'
NL001	SEQ ID NO: 1573 GCGTAATACGGACTCA CTATAGGGAAATCAT GGATGTTGGACAAAT TGG SEQ ID NO: 1575 GAAATCATGGATGTT GGACAAATTGG	SEQ ID NO: 1574 ACTGAGCTTCACA CCCCTTGCCC SEQ ID NO: 1576 GCGTAATACGGACT CACTATAGGACTG AGCTTCACACCCCT TGCCC	SEQ ID NO: 1572 GAAATCATGGATGTTGGACAAATTGGGTGTGTATGCACCCGACCCAGCACA GGTCCACACAAGCTGCGAGAATCTCTCCCACTTGTCATATTTTGCGTAATCGGCT CAAGTACGCTTTAACTAACTGTGAAGTGAAGAAATTGTGATGCAGCGTCTCATCA AGGTTGACGGCGAAAGTGAGGACTGACCCCAACTATCCTGCAGTTTTATGACGT TGTTCAAATCGAAAAGACAAACGAGTTCTTCCGTTTGATCTTATGATGTTAAGGGAC GTTTCACCATCCACAGGATCACAGCTGAAGAAGCTAAGTACAACGCTGTGCAAGT GAAGAGGGTTCAGACAGGACCCAAGGGCATTCCATTTTGACCACTCACGATGGA CGCACCATCAGGTATCCAAAATCATGGACTTGGGTCGTGGGCACTGTGT ACATTGCCACATCCAAAATCATGGACTTGGGTCGTGGGCACTGTGT ATGATCACTGGAGGTCGTAACTTGGGTCGTGGGCACTGTGTGGGGACACACTT CGACACCCGGGGTCTCTTCGAACAACGTTTCATCATCGGCACATCGGGGACACACTT TTGCCCACTAGTTGAACAACGTTTCATCATCGGCACATCGGGGACACACTT GTCTCTGCCCAAGGGCCAAGGGTGTGAAGCTCAGT
NL002	SEQ ID NO: 1578 GCGTAATACGGACTCA CTATAGGGATGAAAA GGGCCCTACAACTGG C SEQ ID NO: 1581	SEQ ID NO: 1579 CTGATCCACATCC ATGTGTTGATGAG SEQ ID NO: 1581	SEQ ID NO: 1577 GATGAAAAGGGCCCTACAACTGGCGGAAGCCATTCAGAAACTACGCGAAACAGAG GAAATGCTGATAAAGAACAAGACTTTTAGAAAAGAAAATTGAAGTTGAAATTGG AGTTGCCAGGAAGAATGGAACAAAAACAAAAGAGCCGCGATCCAGGCACTCAAA AGGAAGAAGAGGTATGAAAAGCAATTGCAGCAGATCGATGGAACGTTATCAACAA TTGAGATGCAGAGAGAGAGGCCCCTCGAAGGAGCCAACGACGAATACGGCCGTACTGC

	SEQ ID NO: 1580 GATGAAAAGGGGCCCTACAACTGGC	SEQ ID NO: 1580 GCGTAATACGACTCACTATAGGCTGATCCACATCCATGTGTTGATGAG	AAACTATGAAGAACGCAGCAGCAGATGCTCTCAAAGCGGCTCATCAACACACATGGATGT GGATCAG
NL003	SEQ ID NO: 1583 GCGTAATACGACTCACTATAGGGCGCAAACAGTCCTTACGAGAAGGC	SEQ ID NO: 1584 TTGACGCGACCAGGTCGGCCAC	SEQ ID NO: 1582 TCCGCGTCGTCCTTACGAGAAGGCACGTCTCGAACAGGAGTTGAAGATCATCGGAGAGTATGGACTCCGTAACAAGCGTGAGGTGTGGACTGCTGAACATACGCCCTCGGCCAAGAATTCGTAAGGCCGCTCGTGAGCTGTTGACTCTGGAAGAAGGACCAGAAACGTTTGTTTGAAGGTAAGGTAACGCCCTGCTGCGTCGCCCTGTGTGCGTATTGGAGTGTTGGACGAAGGAAGAAGTGAAGCTCGATTACGTCTGGGTTTAAAAATTGAAGATTTCCTTGAACGTCGTCTACAGACTCAGGTGTACAAACTCGGTTTGCCCAAGTCCATCCATCACGCCCGTGTACTCATCAGACAAGACATATCGGACTCGCGCAGAAGACAACAAGTAGTGAACATTCCGAGCTTTGGTGCGCCGTGGCCGACCTGGTCGCGCTGAAGTCGCCGTTGCGGCGGTGGCCGACCTGGTCGCGCT
	SEQ ID NO: 1585 TCCGCGTCGTCCTTACGAGAAGGC	SEQ ID NO: 1586 GCGTAATACGACTCACTATAGGTTGACGGACCAGGTCGGCCAC	
NL004	SEQ ID NO: 1588 GCGTAATACGACTCACTATAGGGGAGTTGGCTGTGCTGTAAGAACTG	SEQ ID NO: 1589 CTGTTGTTGACTGTTGGATGAGG	SEQ ID NO: 1587 GGAGTTGGCTGCTGTGTAAGAACTGTCTGCTCTCACATCGAAAACATGCTGAAGGGAGTCACAAAGGGATTCCTGTACAAGATGCTCGTGTGTACGCCCATCAACTGTGTGACGACCGAGAACAACTCTGTGAGGTGCGTAACTTCCTGGGCGAGAAGTACACATCCGACGGTGAGGATGGCGCCCGGCCGTCACTGTTACCAACTCGAAGAAGCAGAAGGACGAGCTCATCGTCGAAGGAGCAACAGCAGTCAACAGATCAGCTGCGCCCTCATCCAACAGTCAACAACAG
	SEQ ID NO: 1590 GGAGTTGGCTGCTGTAAGAACTG	SEQ ID NO: 1591 GCGTAATACGACTCACTATAGGCTGTTGTTGACTGTTGGATGAGG	
NL005	SEQ ID NO: 1593 GCGTAATACGACTCACTATAGGCGCAAACACAAATTCACGTCAAAGC	SEQ ID NO: 1594 CCTTCGCTTCTTGGCCTCCTTGAC	SEQ ID NO: 1592 CGCAAACACAAATTCACGTCAAAGCATCAGGAAGCTGATCAAAGACGGTCTTATCATCAAGAAACCGGTTGCAGTACTTCACGTGCTCGCGTTCGTAAAAACACTGAAGCCAGGAGGAAAGGCAGACATTGTGGCTTTGGTAGAGGAAGGTACAGCCAACGCCCGTATGCCCACAAAGGTTCTATGGGTGAATCGTATGCGTGTCTTGAGAGAGACTGTTGAAAAATACAGACAGGTGTAACAGATAAGAAAATCGACAGGCATCGTACCATCACCTTTACATGAAGGCTAGGTGTAACGTATTCAAGAACAAGAGCGTGTATTGATGGAGTTCATTCATAAGAGGAGAGAGAAGGAGGCCGAGAATGAAGATGTTGAACGACCAGGCTGAAGCTCGCGACACAAAGGTCAAGGAGGCCAAGAGCGAAGG
	SEQ ID NO: 1595 CGCAAACACAAATTCACGTCAAAGC	SEQ ID NO: 1596 GCGTAATACGACTCACTATAGGCCTTCTTGGCCTCTTGAC	
NL006	SEQ ID NO: 1598 CGCAAACACAAATTCACGTCAAAGC	SEQ ID NO: 1599	SEQ ID NO: 1597

	GCGTAATACGACTCACTATAGGGTGCTTGTGTCAAGTGGTGTGG SEQ ID NO: 1600 GCGTAATACGACTCACTATAGGGTGCTTGTGTCAAGTGGTGTGG	CGAGATGGGGATAGCGTGAGG SEQ ID NO: 1601 GCGTAATACGACTCACTATAGGCGAGATGGGGATAGCGTGAGG	GTGCTTGTGTCAAGTGGTGTGTGGAGTACATTGACACCCTGGAGGAGGAGACG ACCATGATAGCGATGTGCCGGATGACCTGCGTCAGGACAAGGAGTATGCCTAC TGTACCACCTACACGACTGCCGAGATCCACCAACCAAAGTCCAGGAACACCTATCAGA GCCTCTATTATTCCCCTCCCGATCACAACCAAGTCCAGGAACACCTATCAGA GCGCTATGGGGAAACACGTGGCTGCTGTTCTCAGGGGAGCTTCCTGCGGCATCAACTC GCTCCATGGAGTACTGCTACACTGGATACAACCAGGAGACAGTGTCATTCTCAACGC TCGCCATCGCTGTCGAGCGCGGATTCTTCGAGTTTCTTCCGATCTTACAAAGAT GCAGAATCGAAGCGTATTGGCGACCAAGAGGAGCAATTCGAGAAGCCCACCAGA CAGACGTGTCAGGGAATGAGGAGTGTCTGTGGTGACGATGTGGTTATTGGCAAAACCAT TCATTGCTCCCGGTCTGAGAGTCTGGTGACGATGTGGTATTGGCAAAACCAT AACACTGCCCGATAATGATGACAGAGCTGGAAGTACAACAAGAGGTTCACGAAG AGAGATGCCAGTACTTTCCTGCGTAACAGTGAGACGGGAATCGTCGACCAAGTCA TGTTAACCTTGAACTCTGAAGGTTACAAGTTCGCTTCCCGACGTCAGTCTGTG CGTATCCCGCAGATTGGCGATAAGTTCGCTTCCCGACATGGCCAAAAAGGAACGT GTGGAATACAGTATCGTCAAGAGGACGACGCCCTTTACAAGGCGGAATCGGCACC GGATATTATTATCAATCCTCACGCTATCCCATCTCG SEQ ID NO: 1602
NL007	GCGTAATACGACTCACTATAGGTGAGAGCAATCCTTGACTGTGG SEQ ID NO: 1603 GCGTAATACGACTCACTATAGGTGAGAGCAATCCTTGACTGTGG	CCACGGTGAATAGCCACTGC SEQ ID NO: 1604 GCGTAATACGACTCACTATAGGCCACGGTGAATAGCCACTGC	TGAGAGCAATCCTTGACTGTGGTTTGAACATCCATCTGAAGTACAACATGAATGC ATTCCTCAAGCTGTACTTGGAATGGACACATATTGTGTCAAGCGAAATCCGGTATGG GAAAAACTGCTGTATTTGTTGGCGACATTACAGCAAATTGAACCAACTGACAAC CAAGTCAGTTATTGTCATGTGTCATACCAGAGAGCTTGCATTCCAAATCAGCAA AGAGTATGAAACGATTTTCGAAATGTATGCCAAATATCAAGGTTGGAGTTTTCTTCG GCGGACTGCCGATTCAGAGAGGGATGAGGACGACGTTGAAATTGAACTGTCCTCACAT CGTGGTTGGAACACCGGACGAGCAATTTTGACGAATGTTACGGCAACAGAAGCTGGA CCTCAAGCATCTCAAGCACTTTGTCCTTGACGAAATATTCCGAACAGCTTGGAACTGT TAGATATGCAAGATCCGATGGAGCACTACTGTGCAACTGTCAAGAAAATGTTGAACTGT AGTCATGATGTTCAGTGCAACTCGGAAGTGTCAACTCTCCAGTGTCTGCAAGAAAT TCATGCAAGATCCGCAGCAGCACTATGTCAACTCAAAGAAACGCACGCAAACA CGGCCTGCAGCAGCACTATGTCAACTCAAAGAAACGCACGCAAACA TTTGAATTACTTGACATATCTTGAATTCAACCAGGTTGTTATATTGTGAAGTCAGTG CAGCGGCTGCATGCCCTATCGCCAACTCCTAACAGACGACTTCCTGCGAGTG GCTATTCACCGTGG SEQ ID NO: 1607
	GCGTAATACGACTCACTATAGGTGAGAGCAATCCTTGACTGTGG SEQ ID NO: 1605 GCGTAATACGACTCACTATAGGTGAGAGCAATCCTTGACTGTGG	GCGTAATACGACTCACTATAGGTGAATAGCCACTGC SEQ ID NO: 1606 GCGTAATACGACTCACTATAGGTGAATAGCCACTGC	
NL008	GCGTAATACGACTCA SEQ ID NO: 1608 GCGTAATACGACTCA	GAGCGAGTCTACA SEQ ID NO: 1609 GAGCGAGTCTACA	GATGCTCGGAGAGACCTGGAGGTGTATTAGATGTTTCAAACAGTTTCCATTT

	CTATAGGGATGCTGG AGACCTGGAGGTG SEQ ID NO: 1610 GATGCTGGAGACCTG GAGGTG	AAATTGCCG SEQ ID NO: 1611 GCGTAATACGACT CACTATAGGGAGC GAGTCTACAAAATT GCCG	GATGAGGACGACAAGAAAAGAATGTTTGGTTCTTAGACCATGATTACTTGGAAAA CATGTTCGGGATGTTCAAGAAGTTAATGCTAGAGAAAAGGTTGTGGGTTGGTAC CATACTGACCCAAACTCCACCAAACGATGTTGCAATCAATGAGTTGATTCGTCG TTACTGTCCAAACTGTCTTAGTCATAATGACCTTGAAGAAATCCATGAGGATCGGGTC TACCTACAGAGGCATACAGAGTCGTTGAAGAAATCCATGATGGATCGCCAAC ATCAAAAACATTTGAACATCTGTTGAGAGACATCAAAGATACAACAGTCGGGTCACTGT ATTGGCGTTGAACATCTGTTGAGAGACATCAAAGATACAACAGTCGGGTCACTGT CACAGCGGCGTCACAAATCAGCTGATGGGCTTGAAGGGCTTGCAATTACA GGATATGCGAGACTATTTGAATCAGGTTGTCGAAGGAAAGTTGCCAATGAACCAT CAAATCGTTTACCAACTGCAAGACATCTTCAACCTTCTACCCGATATCGGCCCACGG CAATTTTGTAGACTCGCTC SEQ ID NO: 1612
NL009	SEQ ID NO: 1613 GCGTAATACGACTCA CTATAGGGCGACTAT GATCGACCGCC SEQ ID NO: 1615 GCGACTATGATCGAC CGCC	SEQ ID NO: 1614 GTGTAAGGGGTAGA AGTAGCCCGG SEQ ID NO: 1616 GCGTAATACGACT CACTAGGGTGT AAGGGTAGAAGTA GCCCGG	SEQ ID NO: 1617 GCGACTATGATCGACCGCGGACGCGGTCAGGTGTGCGACGTCAAG AACTGGTTTCCCTGCACCTCTGAGAACAATTTCAACTACCATCAATCGAGCCCTTG TGTTTTTCTCAAACTGAACAAGATAATTGGTTGGCAACCTCAGTACTACAATGAGA CTGAAGGCTTTCCAGATATCAAGTGTGACCTCAAGCGACACATTGCCCAACA GAAGAGTATCAACAAGCTGTTTATGCAAACAATCTGGATAACTCTGGAAGGAGAG GGTCCTCTAGACAAGGAGAATGCAGGGGAGATCCAGTACCAGTACATCCCTAGACAGGGA TTTCCGGGCTACTTCTACCCTTACAC
NL010	SEQ ID NO: 1618 GCGTAATACGACTCA CTATAGGGCTTGTTGT TCCCGTTGGATGTC SEQ ID NO: 1620 GCTTGTTGTTCCCGTT GGATGTC	SEQ ID NO: 1619 GCAACTCCAGTAG ATCGGAGAGGTC SEQ ID NO: 1621 GCGTAATACGACT CACTATAGGGCAA CTCCAGTAGATCG GAGAGGTC	SEQ ID NO: 1622 GCTTGTTGTTCCCGTTGGATGTCTGTATCAACCTTTGAAGGAGAGACCTGATCTAC CGCCTGTACAGTACGATCCAGTTCTTTGTACTAGGAATACTTGTCGTGCAATTCTG AATCCATTGTGCCAAGTCGACTATCGAGCCCAAGCTATGGGTCTGCAACTTTTGTTT CCAGAGGAATCCTTTCCCCCTCAATATGCAGCTATTTCGGAGCAGCAGCATCAACCA GCAGAACTGATACCTTCATTTTCCACCATCGAATACATCATTACCAGAGCGCCAAAC GATGCCGCCGATGTTCGTGGTGGTGGGACACATGTCTGGACGACGAGGAGGCT GGGAGCTTTGAAGGACTCACTGCAGAAGTCGCTGCCGTCGCTGCCGCCGCCCAATGC ACTCATCGGTCTGCATCACGTTCGGCAAGAAGATGGCGCGCCGCTCCACAGCCCATG CAGATCCAGAGCGCCATTGGGCGCGCCTCCCTCGCAAGATGGCGCCGCCGCTCCCACAGCCCATG CAACAGCGCATTCCCGGCGCGCCTCCCTCGCAAGATGGCGCCGCCGCTCCCACAGCCCATG CTGTCGGAAAGTGCGATATGAGTTAACTGATCTGCTTGGGAATTGCAAAGAGA TCCATGGAATGTGGCTCAGGGCAAGAGACCTCTCCGATCTACTGGAGTTGC
NL011	SEQ ID NO: 1623	SEQ ID NO: 1624	

	CCCACTTTCAAGTGY GTRYTRGTCGG SEQ ID NO: 1625 GTTGCCACCCTTGGA GTTGAAG	GTCCATTGTGACC TCGGGAGG SEQ ID NO: 1626 GCGTAATACGACT CACTATAGGGTCC ATTGTGACCTCGG GAGG	GTTGCCACCCTTGGAGTTGAAGTTCACCCCCTTGTATTCACACAAACAGAGGTG TGATTAGGTTCAATGTGTGGGACACAGCTGGCCAGGAAAAGTTCGGTGGACTTCG TGATGGATATTACATTCAGGGAACAATGCGCCATCATTATGTTTGACGTAACGTCAA GAGTCACCTACAAGAACGTTCCCAACTGGCACAGAGATTTAGTGAGGGTTGCGA AAACATTCCCATTGTACTATGCGGCAACAAAGTAGACATCAAGGACAGAGAAGTC AAGGCCAAGAGCAATAGTAGTCTTCCATAGAAGAAGAACCTTCAGTACTACGACATCA GTGCGAAAAGCAACTCAACCTGGACCCAACCTGAGTTGCTCGTGCCGCCGTCCTCGTGGTTGGCAAAGAAGCT GATCGGTGACCCCAACCTGGAGTTCGTGCTGCCGCCATGCCGCCCCTCCTCCCCACCCGA GGTCACAATGGAC SEQ ID NO: 1627
NL012	SEQ ID NO: 1628 GCGTAATACGACTCA CTATAGGGCGCAGCA CGCAGGCACAGGTAG SEQ ID NO: 1630 GCAGCAGACGCAGGC ACAGGTAG	SEQ ID NO: 1629 GAATTTCCTCTTGA GTTTGCCAGCTTG SEQ ID NO: 1631 GCGTAATACGACT CACTATAGGGGAAT TTCCTCTTGAGTTT GCCAGCTTG	GCAGCAGACGCAGGCACAGGTAGACGAGGTTGTCGATATAATGAAAACAAACGTT GAGAAAGTATTGGAGAGGATCAAAAACTATCAGAATTGGATGATCGAGCAGATG CTCTACAGCAAGGCGCTTCACAGTTTGAACAGCAAGCTGGCAAACTCAAGAGGAA ATTC SEQ ID NO: 1632
NL013	SEQ ID NO: 1633 GCGTAATACGACTCA CTATAGGGCGCAGAGC AAGTCTCACATCTCTTC	SEQ ID NO: 1634 GGCAACGGCTCTC TTGGATAG SEQ ID NO: 1636 GCGTAATACGACT CACTATAGGGGCA ACGGCTCTCTTGG ATAG	CGCAGAGCAAGTCTACATCTCTTCACTGGCCTTATTGAAAATGCTTAAGCACGGTC GCGCCGGTGTTCCCATGGAAGTTATGGCCTAATGCTGGGCGAATTGTAGACG ACTACACTGTGCGTGTCATTGATGTATTCGCTATGCCACAGAGTGGAACGGGAGT GAGTGTGGAGGCTGTAGACCCGAGATGTTGGCTGGGGTCTGTGTACCACTCGCACCCGGGCT TCGGCTGCTGAGTCGGGGTGTGCGACATCAACACGCAGGAGCTTCGAGCAAC TATCCAAGAGAGACGGTTGCC
	SEQ ID NO: 1635 CGCAGAGCAAGTCTA CATCTCTTC		
NL014	SEQ ID NO: 1638 GCGTAATACGACTCA CTATAGGCATTGAGC AAGAAGCCAATGAG	SEQ ID NO: 1639 GAGCGGCGACTCTA ATCTCGG SEQ ID NO: 1641 GCGTAATACGACT	CATTGAGCAAGAAGCCAATGAGAAAGCCGAAGAGATCGATGCCAAGGCCGAGGA AGAATTCAACATTGAAAAGGAAGGCTCGTACAGCACGCCTTAAAATCATG GAGTACTATGACACAGAGAAGAGAAGCAGGTTGAGCTCCAGAAAAATCCAATCGT CAACATGCTGAACCAAGGCGCTCTGAAGGACCACTGAACGCGCGAAGATCACG TGAGAAGTGTGCTCAAGAATCCAGAAAACGTCTTGGAGAAGAACGTAACCAGAAACCC AGCCAAGTACAAGAGAAGTCCTCCAGTATCTAATTGTCCAAGGACTCCTGCAGCTG
	SEQ ID NO: 1640 GCGTAATACGACT		SEQ ID NO: 1637

	CATTGAGCAAGAAGCCAATGAG	CACTATAGGGGAGCGCGACTCTAATCTCGG	CTAGAATCAAACGTAGTACTGCGCGTGCGGCCGGAGGCTGAGCGTGAGTCTGATCGAGGGCATTGGCTCATGCGCAGCAGTAGCCGGAAGATGACCGGCAAAGAGGTGGTGGTGAAGCTGAGCGCTGACAACTTCCTGCCCGAGACGGTGTGGAGGCGTCGAGTTGTTCGCCCGCAACGGCCGCATCAAGATCCCCAACACCCTCGAGTCCAGGCTCGACCTCATCTCCCAGGAACTTGTGCCCGAGAATTAGAGTCGCGGCTC **SEQ ID NO: 1642**
NL015	SEQ ID NO: 1643 GCGTAATACGACTCACTATAGGGGACGGCCAGTGCGCTTGTCCG SEQ ID NO: 1645 CTGCGGAGTGCGCTTGTCCG	SEQ ID NO: 1644 GGCCCAAAGCCGCCTAAGCGC SEQ ID NO: 1646 GCGTAATACGACTCACTATAGGGGGCCAAAGCGCCTAAGCGC	SEQ ID NO: 1647 CTGCGGAGTGCGCTTGTCTCCGACATTGTCTCGATCCAGCCTTGCCCAGACGTCAAGTATGGAAAGCGTATCCATGTGCTGCCCATTGATGATACCGTTGAGGGTCTTACAGGAAATCTGTTCGAAGTGCATTCATTGTTGAAGCCATACTTCCTGGAAGCATACAGGCCAATTCACAAGGATGATGCAGATCCATCGCCCTACTGCATTGTCTGCCGACACCGTCATCCATGGTTGAAACAGATCCATCGCCCATCAAACGTGAGGATGAAGAAGACGCAACGCAGTCTGTGAGGGAGACCCCATCAAACGTGAGGATGAAGAAGACGCAACGCAGTCGGCTACGACGACATTGGAGGGCTGCAGAAAGCAGCTGGCGCAGATCAAAGAGATGGTGGAGTTGCGCTGAGGACATCCGTACGGACCACCGGAAAGACGTTGATAGCCGCCACGAGGCATCCTGCTACGGACCACCGGAAAGACGTTGATAGCCGCGCGCCGTCGCGCCAACGAAACGGGGGCCTTCTTCTTCCTCATCAACGACCCGAGATTATGAGCAAATTGGCCGGCGAGTCGGCCATCATCTTCATGATGAGCTGGACGCAATCGAAGCGGACAAAACGCGAGAAGACGCACGGCGAGGTGGAGCGACGCATCGTGTCGCAGCTGCTGACGCTGATGGACGGTCTCAAGCAGAGACTCGCACGTGATTGTCATGGCCCGCCACCAACTCGGCCCCAACTCGATGCCCGGCTTAGGCGCTTTGGCC
NL016	SEQ ID NO: 1648 GCGTAATACGACTCACTATAGGGACCGCCAGTATCAGAAGACATGC SEQ ID NO: 1650 GACGCCAGTATCAGAAGACATGC	SEQ ID NO: 1649 GATGGAGCCGGTTGCGACC SEQ ID NO: 1651 GCGTAATACGACTCACTATAGGGGATGGAGCCGGTTGCGACC	SEQ ID NO: 1652 GACGCCAGTATCAGAAGACATGCTTGGTCGTGTATTCAACGGAAGTGGTAAGCCCATCGACAAAAGGACCTCCCATTCTTGCTGAGGATTATCTCGACATTCAAGGTCAACCCATCAATCCTTGGTCGCGTATCTATCCCGAGGAAATGATCCAGACTGGAATTTCAGCCATCGACGTCATGAACTCGATTGCTGCTCGTGGCTCTCGATGACTCTGTTGGTCTCTGTCAAACTGCCAGGAAGTCAGTTCTCGATGACTCTGAGGACAACTTTGCTATTGTATTCGGAGGAGAACGGCTCTATGGAGGAGCAACATGGAACGTGTCCGTGTTCTTGAACCTGGGCAACGACCCGACGATCGAGCGTCTATCATCACCACCACGACGTGTCCGCGCCCGCCGAGTTCCTGGCCTACCAGTGGCGCTGCGAGAAGCACGCTGTCCGCGGTTCGAGAGTTCCTACGCCGAGGGCGCTGCGAGAAGCACGCTGTGCCGCGGTTCGAGAGTTCCGTCGTGGTTTCCCGGTTACATGTACACCGGTGCCACCATCTGCGAGCGCGGCCGGACGAGTCGAGGGTCGCAAGGGTCCCATC
NL018	SEQ ID NO: 1653	SEQ ID NO: 1654	

	GCGTAATACGACTCA CTATAGGGCAAATGC CTGTGCCACGC SEQ ID NO: 1655 GCAAATGCCTGTGCC ACGGC	GCAATACAGCCGA CCACTCCG SEQ ID NO: 1656 GCGTAATACGACT CACTATAGGGCAA TACAGCCGACCAC TCCG	GCAAATGCCTGTGCCACGCGCCCACAAATAGAAAGCACAACACAGTTTATTCGATCC GAGAAAACAACATACTCGAATGCATCGCGAGGATTCACCACCATTGAGGAGGACTTCAAAGTAG ACACTTTCGAATACCGTCTTCTGCGGAGGTGTCGTTCCGCGAATCTCGATCAG AAACTACTTGCACAGAGGCGGACATGCAACATCCAGCAGAAGCCCGCGAACAAATCCA GGGTCCCCCCTCGGCGCCGCCACACATCCAGTCTTTTCCATCAAGCTCAGCCCCAAGCCTCG GGAGGGCGGGGGATGCCGTCGTCTTTCAAGAACGGTCAGCGCATCGGTCAGAAACACCAGGC CTCCTACTCCAATCACAGACGCCGTGCTTGCTGAAAATCCGAAGTCAACAAAGTCAGCGCTCAAGAC TCCGGCCACTACACGCTGCTTGTCGAATCAGCTGGCACTCAAGATACAGGATACAGTGAGCAATA CAGCAGACAAGAGGTGGAGACGACAGAGGCGGTGGACAGCAGCGAGGCAAGATGA CGCGGGTTTGACTGCCGCGTGACGGGCCGACCCTACCGGCACACGATCCTCGTCAACGAG ATCAAGCGGCCAACACAGTGGCTGACGACGCCACCGGCCGTCACTCGCTGCTTGGACCACGGAGTG TCTGGCAACCACTCGCTCATGATCACCGGCCGTCACTCGCTTGGACCACGGAGTG GTCGGGCTGTATTGC SEQ ID NO: 1657
NL019	SEQ ID NO: 1658 GCGTAATACGACTCA CTATAGGGGCTTCAGA TTTGGGACACGGC SEQ ID NO: 1660 GCTTCAGATTTGGGA CACGGC	SEQ ID NO: 1659 GAACGCCTGCTCC ACATTGG SEQ ID NO: 1661 GCGTAATACGACT CACTATAGGGGAAC GCCTGCTCCACAT TGG	GCTTCAGATTTGGGACACGGCCGGCCGCCAGGAGCGGTTCCGCACGATCACATCGAG CTACTACCGGGGGCGCGCCCAGGCATCATTGTGGTGTACGACTGCACCGACCAGGA GTCGTTCAACAACCTCAAACAGTGCTCGGCAACAAGTGTGATCAGACCAACAACAAAGGTCG AATGTCAACAAAACTGCTCGTCGGCAACAGGTAAGGAATACGCCGACCAGTCTGGGCATTCCGTTCCTGGA TCGACTATACACACAGGCTAAGGAATACGCCGACCAGTCTGGGCATTCCGTTCCTGGA GACGTCGGCGGGGAAGAAGCGCGACCAATGTGGAGCAGGCGTTC SEQ ID NO: 1662
NL021	SEQ ID NO: 1663 GCGTAATACGACTCA CTATAGGGCTCAGTC TCAATTCTGTCACCG SEQ ID NO: 1665 CGTCAGTCTCAATTCT GTCACCG	SEQ ID NO: 1664 CTTCTAGTTCATCC AGGTCGCG SEQ ID NO: 1666 GCGTAATACGACT CACTATAGGCTTCT AGTTCATCCAGGT CGCG	CGTCAGTCTCAATTCTGTCACCGATATCAGCACCACGTTCATTCTCAAGCCACAAG AGAACGTGAAGATAACGCTTGAGGGCGCACAGCCTGTTTCATTTCACACGAACG ACTTGTGATCTCACTGAAGGAGGAGAACTCTATGTTCTAACTCTCTATTCCGATA GTATGCGCAGTGTGAGGAGTTTTCATCTGGAGGAAAGCTGCTGCCAGTGTCTTGAC TACTTGTATCTGTTGCTCAGGTTTACTGGAGGAATTGAACCTGATTGAGCCGAGGGC CATCGAAAGCTCACAGTCCCAGAATCCGGCCAAGAAGAAGAAAAGCTGGATACTTTG GGAGATTGGATGGCATCTGACGTCACTGAAATACGCGACCTGAAGAACTAGAAG

NL022	SEQ ID NO: 1668 GCGTAATACGACTCA CTATAGGCTCACGAG AGGACGGTTGCACAC SEQ ID NO: 1670 CTCACGAGAGGACGGT TGCACAC	SEQ ID NO: 1669 CAGACGGAAGCAC TTGCCG SEQ ID NO: 1671 GCGTAATACGACT CACTATAGGCAGA CGGAAGCACTTGC CG	SEQ ID NO: 1667 CTCACGAGAGGACGGTTGCACACTGATATACTGTTCGGTTTGGTGAAAGATGTCGC CCGATTCAGACCTGACTTGAAGCTGCTCATATCAAGGCCACACTGATGCTCAG AAATTCTCCGAGTTTTCGACGATGCACCCATCTTCAGGATTCCGGCCGTAGATT TCCGGTGGACATCTACTACACAAAGGCGCCGAGGCTGACTACGTGGACGCATG TGTCGTTTCGATCCTGCAGATCCAGATCCACGCCACTCAGCCGCTGGAGACATCCTGGTC TTCCTCACCGATCCTCAGGAGGAGATCGAAACCTGCCAGGAGCTGCTGCAGGACAGA GTGCGCAGGCTTGGGTCTCGTATCAAGGAGCTGCTCATATTGCCGTCTATTCCA ACCTACCCAGTGATATGCGAGGCAAAGATTTCCTGCCCACTCCACCAAATGCTAG AAAGGTAGTATTGGCCACAAATATTGCAGAAACCTACCATCGACAATATAA TCTACGTGATTGATCCTGGTTTTTGTAGTGCCTGTCTGTTTCAAAGGCATCGACCTGGA ATGGAATCGCTTGTTGTAGTGCCTGTCTGTTTCAAAGGCATCGGCCAATCAGCGAGCAG GGCGGGCGGGGACGGGTGGGCGGCCAAGTGCTTCCGTCTG
NL023	SEQ ID NO: 1673 GCGTAATACGACTCA CTATAGGTCCTCGG ACGGGAGGTCC SEQ ID NO: 1675 GTCCTCGGACGGGGAG GTCC	SEQ ID NO: 1674 GCAATGTTGTCCTT GAGCCAGC SEQ ID NO: 1676 GCGTAATACGACT CACTATAGGGCAA TGTTGTCCTTGAG CCAGC	SEQ ID NO: 1672 GTCCTCGGACGGGAGGTCCACGTGTTTACCGGGATTCCGTTTGCGAAACCTCCC ATCGGTCCGTTGCGATTCGGTAAACCGGTTCCCGTGCGACCCGTGGCACGGCGTT CTGGATGCGACCGGCGCTTCCCAACAGCTGCTACCAGGAACGGTACGAGTATTTC CCGGGCTTCGAGGGAGGAGGAAATGTGCCGCACCGGTTGAGAATCCGAATACGAATTTGTCCGAAGATT GTCTGTATTTGAACATATGGGTCGCGCACCGGTTGAGAATCCGGATCTCACGG CAGCGAGGAGAATAAACCAAGAGCGAAGGTGCCGGTGTCGGATCTCTACGG CGGGGGTTACATGAGCGGCACAGCTACACTGACGTGTACGATGCTGACATGGT GGCCGCCACGAGTGACGTCATCGTCGCCTCGAGGACTTGCCTCGAGGACTACGG CGGCTTCCTCTACCTGCCTGGGGACTCTCGGGGACCAGCAGCCCCTGCCTCAAGGACAACA GCAACATGGGGCTCTGGGGACCAGCAGCCCCTGGCTCAAGGACAACA TTGC
NL027	SEQ ID NO: 1678 GCGTAATACGACTCA CTATAGGAGAAGACG GCACGGTGCG SEQ ID NO: 1680 AGAAGACGGCACGGT GCG	SEQ ID NO: 1679 CAATCCAGTTTTTA CAGTTTCGTGC SEQ ID NO: 1681 GCGTAATACGACT CACTATAGGCAAT CCAGTTTTTACAGT TTCGTGC	SEQ ID NO: 1677 AGAAGACGGCACGGTGCGTATTTGGCACTCGGGCACCTACAGGCTGGAGTCCTC GCTGAATTATGGCCTCGAAAGAGTGTGGACCATTTGCTGCATGCGAGGATCCAAC AATGTGGCTCTTGGCTACGACGAAGGCAGCAGCATAATGGTGAAGGTGGGTCGGGAG GAGCCGGCCATCTCGATGGATGTGAACGGTGGAAGAAGATTGTGTGGGCGGCCCAC TCGGAGATACAAACAGGTCAACCTCAAGGCCATGCCGGAGGGCGTCGAAATCAAA GATGGCGAACGAACGACTGCCGGTGTCGCCGTTAAGGATATGGGCAGCTGTGAAATATAT CCGCAGACCACCATCGCTCATAATCCCAACGGCAGATTCCTAAGAAATAAGGCGTTTGGCTCGGC GAGAGTACATAATTCACACATCAATGGTGCTAAGAAATAAGGCGTATCGTTTGTGGAGATG CCAAGAGTTCATTTGGGGACGACTCGTCCGAGTATGCTATCAGAGGAAGGAACA TCCACTGTCAAAGTATTCAAAGAAATCAAAGAAAAGAAATCATTCAAGCCAGAATTT

GGTGCTGAGAGCATATTCGGCGGCTACCTGCTGCTGGGAGTTTGTTCGTTGTCTGGAC
TGGCGGCTGTACGACTGGGAGACCCTGAGCTGGTGCTCGCATCGAGATCCAAC
CGAAACACGTGTACTGGTCGGAGAGTGGGGAGCTGGTGCTGCTGGCCACTGAT
GACTCCTACTTTGTGCTGCCGCTACGACGACCACAGCCGGTGCTGCTGCACGGCGAC
GCCGGTGACGACGCTGTCACGCCGGACGGCGGTCGAGGATGCATTCGAGGTGCCTT
GGTGAAGTGCACGAAACTGTAAAAACTGGATTG

Table 8-CS

Target ID	Primers Forward 5'→3'	Primers Reverse 5'→3'	dsRNA DNA Sequence (sense strand) 5'→3'
CS001	SEQ ID NO: 2041 TAAAGCATGGATGTT GGACAAACTGGG SEQ ID NO: 2043 GCGTAATACGACTC ACTATAGGTAAAGC ATGGATGTTGGACA AACTGGG	SEQ ID NO: 2042 GCGTAATACGACTC ACTATAGGGGTGAG TCGCACGCCCCTTGC C SEQ ID NO: 2044 GGTGAGTCGCACGC CCTTGCC	SEQ ID NO: 2040 TAAAGCATGGATGTGTTGGACAAACTGGGTGGCGTGTACGCGCCGGCCGGTCGAC CGGCCCCCACAAGTTGCGCGAGTGCCTGCCGCTGGTGATCTTCCTCAGGAACCG GCTCAAGTACGCGCTCACCGGAAATGAAGTGCTTAAGATTGTAAAGCAGCGACTT ATCAAAGTTGACGGCAAAGTCAGGACAGACCCCACATATCCCGCTGGATTTATGG ATGTTGTTTCCATTGAAAAGACAAATGAGCTGTTCCGTCTTATATATGTCAAAG GCAGATTTACTATTCACCGTATTACTCCTGAGGAGGCTAAATACAAGCTGTGCAAG GTGCGGCGCGTGGCGACGGGCGTGCCCAAGAACGTCCTTACCTGGTGACCCACGA CGGACGCACCGTGCGCCACCTGCGCGATACCCGACCCACTCATCAAGATCATCCA GCTCGACATCGCCACCTCCAAGATCATGGACTTCATCAAGTTTGAATCTGGTAAC CTATGTATGATCACGGGAGGCCGTAACTTGGGGCGCGTGGGCACCATCGTGTCC CGCGAGCGACATCCCGGGTCCTTGACATCGTGCATATAACGGGACTCCACCGGA CATACCTTCGCTACCAGATTGAACAACGTGTTCATAATCGGCAAGGGCACGAAGG CGTACATCTCGCTGCGCGGGCAAGGGCGTGCGACTCACC
CS002	SEQ ID NO: 2046 CAAGAAGGAGGAGA AGGGTCCATCAAC SEQ ID NO: 2048 GCGTAATACGACTC ACTATAGGCAAGAA GGAGGAGAAGGGTC CATCAAC	SEQ ID NO: 2047 GCGTAATACGACTC ACTATAGGCTTGTCT ACATCGATATCCTTG TGGGC SEQ ID NO: 2049 CTTGTCTACATCGAT ATCCTTGTGGGC	SEQ ID NO: 2045 CAAGAAGGAGGAGAAGGGTCCATCAACACACGAGCTATACAGAAATTACGCGAA ACGGAAGAGAGTTATTGCAGAAGAAACAAGAGTTTCTAGAGGAAGATCGACACTG AATTACAAACGCGGAGAAAACATGGCACAAGAATAAGAGAGTGCCATTGCGGC ACTGAAGCGCAAGAAGCGTTATGAAAGGAAGCGTTACCAGTGATGGCCACGCTT ACCCAAATTGAGGCCCAAAGGGAAGCGCTAGAAGGAGCTAACACCAATACACAG GTGCTTAACACTATGCGAGATGCTGCTACCGCTATGAGACTCGCCCCACAAGGATA TCGATGTAGACAAG

CS003	SEQ ID NO: 2051 TGGTCTCCGCAACA AGCGTGAGG SEQ ID NO: 2053 GCGTAATACGACTC ACTATAGGTGGTGTCT CCGCAACAAGCGTG AGG	SEQ ID NO: 2052 GCGTAATACGACTC ACTATAGGCGAACG GAGACTTCAGCGGAG AAGTCA SEQ ID NO: 2054 CGAACGGAGACTTC AGCGGAGAAGTCA	SEQ ID NO: 2050 TGGTCTCCGCAACAAGCGTGAGGTGTGGAGGGTGAAGTACACGCTGGCCAGGAT CCGTAAGGCTGCCCGTGAGCTGCTCACACTGCAGGCGAGGAGAAAGACCCTAAGAGGTT ATTCGAAGGTAATGCTCCTTCGTCGGTCGTTGGTCTCGGTCTGAAGATCGGTGTGTTGGATGAG AAGCAGATGAAGCTCGATTATGTACTCGGTCTGAAGAGCTTGAGGACTTCTTGGAAC GTCGTCTCCAGACTCAGGTGTTCAAGGCTGGTCTCGTCTAAGTCTATCCATCATGC CCGTATTCTTATCAGACAGAGACACATCCGTGTCCGCAGCAAGTTGTGAACATC CCTTCGTTCATCGTGCGGGCTGGGACTCTCTGGCCAGCACATTGACTTCTGCTGAAGT CTCCGTTCG
CS006	SEQ ID NO: 2056 GGATGATGATGGTA TAATTGCACCAGGG SEQ ID NO: 2058 GCGTAATACGACTC ACTATAGGGGATGA TGATGGTATAATTGC ACCAGGG	SEQ ID NO: 2057 GCGTAATACGACTC ACTATAGGGCGTTAAA TGGTGTAGCATCAC CTATTTCACC SEQ ID NO: 2059 CGTTAAATGGTGTA GCATCACCTATTTCA CC	SEQ ID NO: 2055 GGATGATGATGGTATAATTGCACCAGGGATTCGTTGTGTATCTGGTGACGATGTAGTC ATTGGAAAAACTATAACTTTGCCAGAAAAACGATGAGCTGGAAGGAACATCAA GACGATACAGTAAGAGATGCCTCTACATTCTTGCGAAACAGTGAAACTGGTATT GTTGACCAAGTTATGCTTACACTTAACAGCGAAGGATACAAATTTGTAAAATACG TGTGAGATCTGTGAGAATCCCACAAATTGGAGACAAATTTGCTTCTCGTCGTCATGGTC AAAAGGGACTTGTGTATTCAATATAGGCAAGAAGATATGCCTTTCACTTGTGAA GGATTGACACCAGATATTATCATCAATCCACATGCTATCCCCTCGTATGACAAT TGGTCACTTGATTGAATGTATTCAAGGTAAGGTCTCCTCAAATAAAGGTGAAATAG GTGATGCTACACCATTTAACG
CS007	SEQ ID NO: 2061 CTTGTTGAAACCAG AGATTTTGAGGGC SEQ ID NO: 2063 GCGTAATACGACTC ACTATAGGGCTTGTTG AAACCAGAGATTTTG AGGGC	SEQ ID NO: 2062 GCGTAATACGACTC ACTATAGGGCGGCAT GTCATAATTGAAGAC TATGTTGACTC SEQ ID NO: 2064 CGGCATGTCATAATT GAAGACTATGTTGA CTC	SEQ ID NO: 2060 CTTGTTGAAACCAGAGATTTTGAGGGCTATCGTCGATTGCGGTTTCGAGCACCCT TCAGAAGTTCAACATGAATGTATTCCCCAAGCTGTTTTGGGAATGGATATTCTTTG TCAAAGCTAAATCCGGAATGGAAAAACCGCGTATTTGTTTTAGCAACACTGCAA CAGCTAGAACCTTCAGAAATAAGCAAGGAATATGAGAGGTTCTCTAAATATATGGCTGGTG ACTCGCTTTCCAAATAAGCAAGGAATATGAGAGGTTCTCTAAATATATGGCTGGTG TTAGAGTATCTGTATTCTTTGGTGGATGCCAATTCAGAAGATGAAGAAGTATTG AAGACAGCCTGCCCGCACATCGTTGTTGGTACTCCTGGCAGAATATTAGCATTGG TTAACAACAGAAGAGTGCTTGAATCTCTAGACATGAGACGTGATGTTTTCTGCAACACCTATG GACAAAATGCTTGAAATCGTGAAGATCCTATGCAGCAACATTATGTTATGTCTGGATGATG ACACCCCTCACGTCTGTAAGAAATTTATGCAGGTTTGCAGCAACAGCTTTGGAAGCTGGTTATGTTGATGATG AAAAGAATAAGAAGTTATTTGAACTTGTTGGATGTACTGCGAGTTCAACCAAGTTGT CATATTTGTAAAGTGCAGTGCGCGCTGCATAGTCTCGCCACAGCTGCTGCTGACAGAC

CS009	SEQ ID NO: 2066 ACGTTTCTGCAGCG GCTGGACTC SEQ ID NO: 2068 GCGTAATACGACTC ACTATAGGCGGTTTC TGCAGCGGCTGGAC TC	SEQ ID NO: 2067 GCGTAATACGACTC ACTATAGGGATAATT CTTATCGTACGCTGT CATATTCCTG SEQ ID NO: 2069 GATAATTCTTATCGT ACGCTGTCATATTCC TG	CAAAACTTCCCAGCTATTGGTATACACCGAAATATGACTCAAGATGAGCGTCTCTC CGCTATCAGCAGTTCAAAGATTTCAGAAGAGGATCCTTGTTGCCACAAATCTTT TTGGACGGGGTATGGACATTGAAAGAGTCAACATAGT CTTCAATTAT GACATGCCG SEQ ID NO: 2065 ACGTTTCTGCAGCGGCTGGACTCACGGGGAGCCCATGTGGCAGCTGGACGAGAGC ATCATCGGCACCAACCCGGGCTCGGCTTCCGGCCCACGCGCCAGAGGTCGC CAGCAGCGGTCATCTGGTATAAAGGCAACGACCCCAACAGCCAACAATTCTGGGTG CAAGAAACCTCAACTTTCTAACCGGCTACAAACGAGACGGTAAGAAAGCAGGAG CAGGCCAGAACAACCACAACTGCCTACAACTGCCTCTGTGTAGAGGCACGTAAGGT GTGCGACGGTGGACATCAGCGCCCTGCCATCTTCCTCAAACTCAACAGATCTTCGGCTGG ATACCACAAGTCCACGCCCCTACAACAGCTCCGACAGCCTGCCCACTGACGCCCGACGAC AGGCCGCACTTCTACAACAGCGGAATATGACAGCGGTACGATAAGAATTATC TTGAAGGAGCACATCAGGAATATCAGGAATATGACAGCGGTACGATAAGAATTATC
CS011	SEQ ID NO 2071 CGACACTTGACTGG AGAGTTCGAGA SEQ ID NO: 2073 GCGTAATACGACTC ACTATAGGCGACAC TTGACTGGAGAGT CGAGA	SEQ ID NO: 2072 GCGTAATACGACTC ACTATAGGCTCTAG GTTACCATCACCGA TCAACT SEQ ID NO: 2074 CTCTAGGTTACCATC ACCGATCAACT	SEQ ID NO: 2070 CGACACTTGACTGGAGAGTTCGAGAAAAGATATGTCGCCACATTAGGTGTCGAGG TGCATCCCTTAGTATTCCACACAAATAGAGGCCCTATAAGGTTAATGTATGGGAT ACTGCTGGCCAAGAAAGTTTGGTGGTCTCCGAGATGGTTACTACTATCCAAGGTC AATGTGCCATCATCATCATGTTCGATGTAACGTCTCGTGTCACCTACAAAAATGTACCC AACTGGCCACAGAGATTTAGTGCGAGTCTGTGTGAAGGCATTCCAATTGTTCTTTGTG GCAACAAAGTAGATATCAAGGACAGAAAGTCAAAGCAAAAACTATTGTTTTCCAC AGAAAAAGAAACCTTCAGTATTATGACATCTCTGCCAAGTCAAACTACAATTTCGA GAAACCCTTCCTCTGGTTAGCCGAGAAAGTTGATCGGTGATGGTAACCTAGAG
CS013	SEQ ID NO: 2076 TGCCGAACAGGTAT ACATCTCGTCTTTGG SEQ ID NO: 2078 GCGTAATACGACTC ACTATAGGTGCCGA ACAGGTATACATCTC GTCTTTGG	SEQ ID NO: 2077 GCGTAATACGACTC ACTATAGGCCACTA CAGCTACAGCACGT TCAGAC SEQ ID NO: 2079 CCACTACAGCTACA GCACGTTCAGAC	SEQ ID NO: 2075 TGCCGAACAGGTATACATCTCGTCTTTGGCCCTGTTGAAGATGTTAAAACACGGG CGCGCCGGTGTTCCAATGGAAGTTATGGGACTTATGTTAGGTGAATTTGTTGATG ATTACACGGTGCGTGTCATAGACGTATTTGCCATGCCTCAAACTGGCACAGGAGT GTCGGTTGAAGCTGTAGCTGTAGATCCTGTCTTCCAAGCAAAGATGTTGGATATGTTGAAG CAAACTGGACGACGACCTGAGATGCTAGTGGGATGGTCGACATTAATACTCAGCAGTCTTCGAAGCTTTGTCT GATGTTGGTTATCTGGAGTCGACATTAATACTCAGCAGTCTCTTCGAAGCTTTGTCT GAACGTGCTGTAGCTGTGTAGTGG
CS014	SEQ ID NO: 2081 CAGATCAAGCATAT GATGGCCTTCATCG	SEQ ID NO: 2082 GCGTAATACGACTC ACTATAGGGAACAA	SEQ ID NO: 2080 AGATCAAGCATATGATGGCCTTCATCGAACAAGAGAGGCTAATGAAAAGGCCGAGGA

	A	TGCGGTACGTATTTCGGGC	
	SEQ ID NO: 2083 GCGTAATACGACTC ACTATAGGCAGATC AAGCATGATGGC CTTCATCGA	SEQ ID NO: 2084 GAACAATGCGGTAC GTATTTCGGGC	AATCGATGCAAAGGCCGAAGAGGAGTTCAACATTGAAAAAGGCCGCCTGGTGCA GCAGCAGCGGCTCAAGATCATGGAATACTACGGAAAAGAAAGAGAAACAAGTGGAA CTCCAGAAAAGATCCAATCTTCGAACATGCTGCAACGTTCTCGACGAGGCTCGCAAGCGCC TCAAAGTGCGTGAGGACCACGTACGCAACGTGAAACTTTACACAGATCTGCTGGTCACGCTCGT CGTACAAGCCCTATTCCAGCTCATGTACACGTCCATATTGGGCAAGCCACCAGTTCGCGGTTAGGCAG GCGGACGTCTCTTAGTACAGTCCATATTGGGCAAGCCACGAGAATCCTGCCCGC CAAAGATCAAGAAGACAGTTCAATTGAAGATCAAGGACAACCTATCAAGCGAGAAGAAGAGCC CGATACTTGTGGCGGAGTGGAACTTATTGCTGCTGAGGCGTATTAAGATCAGC AACACTCTGGAGTCTCGTCGTCTGGAGCTGAGCCCAACAACTGTTGCCCGAAATAC GTACCGCATTGTTC
CS015	SEQ ID NO: 2086 ATCGTGCTTTCAGA CGATAACTGCCCCC	SEQ ID NO: 2087 GCGTAATACGACTC ACTATAGGCCATTAC GATCACGTGCGATG ACTTC	SEQ ID NO: 2085 ATCGTGCTTTCAGACGATAACTGCCCCGATGAGAAGATCCGCATGAACCGCGTCG TGGCGAAACAACTTGCGTGTACGCCCTGTCAGACATAGTCTCCATAGCGCCTTGTCC ATCGGTCAAATATGGAAACGGGTACATATATTGCCCATTGATGATTCTGTCGAG GGTTTGACTGGAAATTTATTCGAAGTCTACTTGAAACCATACTTCATGGAAGCTTA TCGGCCTATCCATCGCGATGACACATTCATGGTTCGCGGGGCATGAGGGCTGT TGAATTCAAGTGGTGGAGACTGATCCGTCGCCGTATTGCATCGTCGCTCCCGAC ACAGTGATACACTGCGAAGGAGACCCTATCAAACGAGAGAAGAAGAGCC CTAAACGCCGTAGGGTACGACGACATCGGTGGCTGTGTAAACAGCTCGCTCAG ATCAAAGAGATGTCGAGTTGCTCCTCTAAGGCATCTCATGTATGGCCGCCGCAAATTG GTGTGAAGCCGCCACGTGGCAGTGCTAATGAAACTGGTGCATTCTCTTTCTGATCAAC CTCTCATTGCTGCTGGGCGCAGTGCTAATGAAACTGGTGCATTCTCTTTCTGATCAAC GGGCCGGAGATCATGTCCAAACTCGCGGGCGAGTCCGAATCAACCTTCGCAAG GCATTCGAGGAGCGGACAAGAGGGGAGAAGACTCACGGTGAAGTGAAGAACTGG ATGCCATCGCAACTACTTACTCTTATGGATGAAGAAGTCATCGCACGTGATCGTA ATGG
	SEQ ID NO: 2088 GCGTAATACGACTC ACTATAGGATCGTG CTTTCAGACGATAAC TGCCCC	SEQ ID NO: 2089 CCATTACGATCACG TGCGATGACTTC	
CS016	SEQ ID NO: 2091 AGGATGGAAGCGGG GATACGTTTGAG	SEQ ID NO: 2092 GCGTAATACGACTC ACTATAGGGCACCC CTGTCTCCGAAGAC ATGTT	SEQ ID NO: 2090 AGGATGGAAGCGGGGGATACGTTTGAGCATCTCCTTGGGAAGATACGGAGCAGC TGCCAGCCGATGTCCAGCGACTCGAATACTGTGCGGTTCTCGTAGTTGCCCTGTG TGATGAAGTTCTTCTCGAACTTGGTGAGGAACTCAGGAGTAGAGCAGATCGTCGGG TGTCAGGGCTTCCTCACCGACGACACGCCTTCATGGCCTGCACGTCCTTACCGATG GCGTAGCAGCCGGTACAGCTGGTTGGAAACATCAGAGTGGTCCTTGCGGTCATT CCCTCACCGACGGCAGACTTCATGAGCAGGAGGACGAGAGAGGCAGCAGCGTTACA GGCGGGTAGATCGTGTCGTTGTGTGGAGCTGACGGGTCTACGGTGTCCCTCAG TGATGTAGCCGGTTAAATCGGGAATAGGGATGGTGATGTCGTTGCGTTGGGCATAGT
	SEQ ID NO: 2093 GCGTAATACGACTC ACTATAGGAGGGATG GAAGCGGGGATACG	SEQ ID NO: 2094 GCACCCCTGTCTCC	

| | TTTGAG | GAAGACATGTT | CAAGATGGGGATCTGCGTGATGGATCCGTTTCTACCCTCTACACGGCCCGGCTCTC
TCGTAGATGTGGCCAAATCGGTGTACATGTAACCTGGGAAACCACGTCGTCCG
GGCACCTCCTCACGGGCCGGCGACACTTCACGCAGAGCCTCCGGTACGAAGA
CATGTCAGTCAAGATTACCAGCACGCACGTGTTTCTCACACTGGTAGGCCAAGAACTCA
GCAGCAGTCAAGGCCAAAACGTGGTGTGATGATTCTCTCAATAGTGGGATCGTTGG
CCAGATTCAAGAACAGGCACACGTTCTCCATGGAGCCGTTCTCCTGGAAGTCCTG
CTTGAAGAACCGGGCCGTCTCCGTGTCGTCTCCATGTTCACACCCATGGCGGCGAACACGATGGC
AAAGTTGTCCTACAGATCTGGGCGGCAATTTGCCGGGGATCTTTACAAGACCG
GCTTGCCTACAGATCTGGGCGGCAATTTCGTTGTGTGCGAGACCGGCAGCCGAG
AAAATGGGGATCTTTTGCCCCGCGAGCAATGGAGTTCATCACGTCGATAGCGGGAGA
TACCAGTCTGGATCATTTCCTCAGGGTAGATACGGGACCAGGGGTTGATGGGCT
GTCCCTGGATGTCCAAAAAGTCTTCAGCAAGGATTGGGGGACCTTTGTCAATGGGG
TTTTCCAGAGCCGTTGAATACGCGACCCAACATGTCTTCGGGAGACAGGGGTGC |
| CS018 | SEQ ID NO: 2096
CGTCCCTGTACCTG
CTCAGCAATCCCA

SEQ ID NO: 2098
GCGTAATACGGACTC
ACTATAGGCCGTCCC
TGTACCTGCTCAGC
AATCCCA | SEQ ID NO: 2097
GCGTAATACGGACTC
ACTATAGGCAGCGT
CGAGGCCCCCACCTT

SEQ ID NO: 2099
CAGGCGTCGAGGCCC
CACCTT | SEQ ID NO: 2095
CGTCCCTGTACCTGCTCAGCAATCCCAACAGCAGCAGAGTTACCGCCACGTCAG
CGAGAGCGTCGAACACAAATCCTACGGCACGCAAGGGTACACCACTTCGGAACA
GACCAAGCAGACAGCAGAAGGTGGCTACACCAACGGTTCCGACTACTCTTCCAC
AGGGAATCCATCACGAAGCGGGTACATTGGCGGTACATTGGCGACAGACATTCAGATCAGCACG
GAGGTCGACAAGTCTCTCGGTGTGGTGACCCCTCCTAAGATAGCACAAAAGCCTA
GGAATTCCAAGCTGCAGGAGGGAGCCGACGCTCAGTTTCAAGTGCAGCTGTCGG
GTAACCCGGCCGCGGGTGTCATGGTTCAAGAACGGGCAGAGGATAGTCAACT
CGAACAAACACGAAATCGTGATACTGGCATACCTGGCGCGTGGAGTCGCCCTCAGAAACCATAATCAACCATCAAACAATACTTAGGGTAAGAAAC
GCGTCGTCACATGCAATGGATACTGCGCGTGGAGTGCGCCCTCAGAAAACCTAACGGAT
AAGATCATAAATCACAATCACATAATGGACAATCAGCAAACAGCTGTAGAAGAAAGA
GTAGAGTTAATGAAAAAGCTCTCGCTCCGCAATTCGTAAGAGTCTGCCAAGACC
GCGATGTAACGGAGGGAAAATGACGCGGATTCGATTGCCGCGTCACGGGCAGAC
CTTACCCAGAAGTAGTTAGTAACGAATCGTGTAATCATGCACGCAACAAGCGTCGAT
CATAAAGATATTAGTAACGAATCGTGTAATCATGTATAGCACGCAACAAGACCGGCGAAACTT
CGTTTCAGTGTAGGCTGAACGTGAACGTGAACGGCTCAACGTGGTCGCTCTCCCAAATT
CGTGGAGCGGTTCAGCACGCTCAACGCGTCGCGCAGGGCCGAGCCGTCAGCTGC
ACGCGGCGCGCGGTGGCCGTGGCACGCCTACGCGCACCATCACATGGCAGAAGGACGGGC
GTTCAAGTTATACCCAATCCAGAGCTACGAATAAATACCGAAGGTGGGCCTCGA
CGCTG |

Table 8-PX

Target ID	Primers Forward 5' → 3'	Primers Reverse 5' → 3'	dsRNA DNA Sequence (sense strand) 5' → 3'
PX001	SEQ ID NO: 2340 GCGTAATACGACTC ACTATAGGCGAGGT GCTGAAGATCGTGA AG SEQ ID NO: 2342 CGAGGTGCTGAAGA TCGTGAAG	SEQ ID NO: 2341 CTTGCCGATGATGA ACACGTTG SEQ ID NO: 2343 GCGTAATACGACTC ACTATAGGCTGCC GATGATGAACACGT TG	SEQ ID NO: 2339 CGAGGTGCTGAAGATCGTGAAGCAGCAGGCGCCTCATCAAGGTGGACGGCAAGGTCCG CACCGACCCCACCTACCCGCTGGATTCATGGATGTTGTGTCGATTGAAAAGACC AATGAGCTGTTCCGTCGATCTACGATGTGAAGGGGACGCTTCACCATCCACCGCA TCACTCCCGAGGAGGCCAAGTACAAGCTGTGCAAGGTGAAGCGGCGTGGCGACG GGCCCCAAGAACGTGCCGTCATCATCGTGACGCACAACGGGCCGCACGCGTGCGCTAC CCCGACCCGCTCATCATCAAGGTGACCATCAGTGACTCAGCTAACCTGCCACCTGC AAGATCATGGACATCATCAAGTTCGACTCAGGTAACCTGTCATGATCACGGGAG GGCGTAACTTGGGGCGAGTGGGCGCACCATCAAGGAGCAGCACACCGGACGAGGCAGCGGAG AGCTTCGACATCGTCCACATCAAGGAGACACACCCTTCGCCACCAGGT TGAACAACGTGTTCATCATCGGCAAG
PX009	SEQ ID NO: 2345 GCGTAATACGACTC ACTATAGGCAGCTA CAAGTATTGGGAGA ACCAG SEQ ID NO: 2347 CAGCTACAAGTATT GGGAGAACCAG	SEQ ID NO: 2346 TGTTGATCACTATGC CGGTCCT SEQ ID NO: 2348 GCGTAATACGACTC ACTATAGGTGTTGAT CACTATGCCGGGTCC T	SEQ ID NO: 2344 CAGCTACAAGTATTGGGAGAACCAGCTCATTGACTTTTTGTCAGTATACAAGAAGA AGGGTCAGACAGCGGGTGCTGGTCAGAACATCTTCAACTGTGTACTTCCGCAACC CGCCCCCACACGGCAAGGTGTGCGACGTGGACATCCGGCGGCTGGGAGCCCTGC ATTGATGAGAACCACTTCTCTTTCCACAAGTCTTCGCCATCTTCTTGAAGCT GAATAAGATCTACGGCTGGCGTCCAGAGTTCTACAAGGACACGGCTAACCTGCCT GAAGCCATGCCCGTGGACTTGAGACCCACATTCGTAACATTACTGCCTTCAACA GAGACTATGCGAACATGGTGTGGTGTCGTGCCACGGCGAGACGCGGCGGAC AAGGAGAACATCGGGCGGTGCGCTACCCGAGGGTATCTGAGCCCGGGTAC TTCTACCCGTACGAGAACGCCGAGGGTATCTGAGCCCGCTGTCGCCGTGCAT TTGGAGAGGCCGAGGACCGGCATAGTGATCAACA
PX010	SEQ ID NO: 2350 GCGTAATACGACTC ACTATAGGACCAGC ACTCTAGTGGACAA CGTC SEQ ID NO: 2352 ACCAGCACTCTAGT GGACAACGTC	SEQ ID NO: 2351 CTGTATCAATGTACC GCGGCAC SEQ ID NO: 2353 GCGTAATACGACTC ACTATAGGCTGTATC AATGTACCGCGGCA C	SEQ ID NO: 2349 ACCAGCACTCTAGTGGACAACGTCGCGTTCGGGTCACCACTGTCGCGCGCAATT GGGGGCGACGGCAGCCGCCAACTTACACCACATATCGGGGGCTTCGACCAGGAG GCGGCGGGCGGTGGTGATGGCGGCGGCTGGTGTACGCGGGAGCGAGGAGG ACGGGCGCCCGACGTGCTGCGCGTGGCTCGACCCGAACAGCTTCGTCTGTCGTGCCAGA AGTTCGGCGGAGTACGGCGAAGGACGACCCGAACAGCTTCGTCTGTCGGAGAACT TCAGCCTGTACCCGCAGTTCATGTACCACCTGCGCCGCTCGCAGTTCCTGCGAGGT CTTCAACAACTGCCCGACCAATCCCTCATCATGATCCGCCGGATCCTCTACTGTCGTACAGCTTCG GACCTGACCCATCCCTCATCATCATGATCCGATCCTCTACTCGTACAGCTTCG GAGGCGCGCCCCGACCCGGTCGTGTTAGACACCAGCTCCATCCAGCCCGACCCGCA

			TCCTGCTGCTCATGGACACCTTCTTCCAGATCCTCATCTACCATGGAGAGAGACAATGGC GCAATGGCGCGGCTCTCCGCTACCAAGACATGGCTGAGTACGGAGAAACTTCAAGCA GCTGCTGCCGAGCCCGTGGACGACGCGCAGGAGATCCTGCAGACCAGGTTCC CCGTGCCGCGGTACATTGATACAG
PX015	SEQ ID NO: 2355 GCGTAATACGACTC ACTATAGGGACGAG AAGATCCGCATGAA CC	SEQ ID NO: 2356 GATGATGGCCGGAG AGTTCTTG	SEQ ID NO: 2354 GACGAGAAGATCCGCATGAACCGGTCGTCCGGAACAACCTGCGAGTGCGCCTG TCAGACATTGTGTCCATGGCTCCTTGCCCGTCAGTGAGTACGGCAAGAGAGTTC ATATTCTGCCCATTGATGACTCTGTTGAGGGTTGACTGGAAACCTGTTCGAAGTC TACCTGAAGCCGTACTTCATGGAGGCGTACGGCCCATCCACCGCGACGACACG TTCATGGTGCGCGGCGCCTACTGCATCGTGTGCCCGTCAAGTGGTGGAGACCGA CCCCTCGCCCTACTGCATCGTGTGGCCCCCGACACGGTCATTCATTGTGAGGGAGA GCCGATTAAACGCGAGGAAGAAGAGGAGGCTCTCAACGCCGTCGCGGCTACGACGA CATCGGCGGCGGTGCCGCGAAGCAGCTGGCGCAGATCAAGGAGATGGTGGAGCTGC CGCTGCGCGCCACCCCTCGCTGTTCAAGGCCATCGGGGTCAAGCCGCGCGGGGG ATACTGATGTACGGGCGCCCCGATCCCATTCTTCTTCCTCATCAACGCCCCGAGATCATGTCGA GCTAATGAGACGGGCGCATTCTTCTTCCTCATCAACGCCCCGAGATCATGTCGA AACTCGCCGGTGAATCCGAGTCGAACCTGCGCGCAAGGCGTTCGAGGAGGGGGACA AGAACTCTCCGGCCATCATC
	SEQ ID NO: 2357 GACGAGAAGATCCG CATGAACC	SEQ ID NO: 2358 GCGTAATACGACTC ACTATAGGGATGAT GGCCGGAGAGTTCT TG	
PX016	SEQ ID NO: 2360 GCGTAATACGACTC ACTATAGGGTGGGT CGTATTTTCAACGG CTC	SEQ ID NO: 2361 AGTGATGTACCCGG TCAAGTCG	SEQ ID NO: 2359 CTGGGTCGTATTTTCAACGGCTCCGGCAAGCCCATCGACAAGGGGCCCCGATC CTGGCCGAGGAGTACCTGGACATCCAGGGCAGCCCATCAACCCGTGGTCCCGT ATCTACCCGGAGGAGATGATCCAGAGATCCCCATCTTCTCCGCCGGCCGGTCTGATGAACT CCATCGCCCGTGGTCAGAAGATCCCCATCTTGTCTTGTAGGCAGGCTGGTCTTGTCAAGGTCCCCGGAAA ATCCGTGTTGGACGACCACGAAGACAACTTCGCCATCGTGTTCGCGGAGGAACGGTTC AGTCAACATGGAAGACCGGCCAGGTTCTTCAAGCAGGACTTCGAGGAGAACGGTTC CATGGAGAACGTCGTGTCTGTCTTGGTAATCTTGACGACATGTCTTGGCCTACCAGTGC ATTATCACGCCGAGGTTGGCGCTGAATCTTGACGAGGTGGCCAATGGCCATTGAGAGG GAGAAACACGTGTGTTGGTAATCTTGACGAGGTGGCCAATGGCCATTGAGAGG GTGAAGTGTCAGCCGCCGTGAGGAGTGCCCGGACGACGTGGTTTCCCAGGTT ACATGTACACGGCGATTTGGCCACAATCTACGAGCGCGCCATCCTGACCGATCGGAGGGCC GCAACGGCTCCATCACGCAGATCCCCATCCTGACCGACCATGCCCAACGACGACATCA CCCACCCCCATCCCGACTTGACCGGGTACATCACT
	SEQ ID NO: 2362 CTGGGTCGTATTTTC AACGGCTC	SEQ ID NO: 2363 GCGTAATACGACTC ACTATAGGGAGTGAT GTACCCGGTCAAGT CG	

Table 8-AD

Target ID	Primers Forward 5' → 3'	Primers Reverse 5' → 3'	dsRNA DNA Sequence (sense strand) 5' → 3'
AD001	SEQ ID NO: 2462 GCGTAATACGACTCACTATAGGGCTCCT AAAGCATGGATGTTGG SEQ ID NO: 2464 GCTCCTAAAGCATGGATGTTGG	SEQ ID NO: 2463 CAATATCAAACGAGCCTGGGTG SEQ ID NO: 2465 GCGTAATACGACTCACTATAGGCAATATCAAACGAGCCTGGGTG	SEQ ID NO: 2461 GCTCCTAAAGCATGGATGTTGGACAAACTCGGAGGAGGAGTATTCGCTCCTCGCCCCAG TACTGGCCCCCACAAATTGCGTGAACTGTTTACCTTTGGTGATTTTTCTTCGCAATCG GCTCAAGTATGCTCTGACGAACTGTGAAGTAACGAAGATTGTTATGCAGCGACTTAT CAAAGTTGACGGCAAGGTGCGAACCGATCCGAACTTATCCCGCTGGTTTCATGGATG TTGTCACCATTGAGAAGACTGCGAGAGTTCTTCAGCGTGGTGTATGATGTGAAGGC CGTTTCACCAATTCACAGATTAGTCAGAAGAAGCCAAGTACAAGCTCTGCGAAGGTC AGGAGAGTTCAAACTGGGCCAAAAGTATTCCATTCTTGGTGACCCATGATGGCCG TACTATCCGTTATCCTGACCCAGTCATTAAAGTTAATGACTCAATCCAATTGGATATT GCCACTTGTAAAATCATGGACCACACATCAGATTTGAATCTGGCAACCTGTGTATGATT ACTGGTGGACGTAACTTGGGTGCGAGTGTTGTGTGAGTCGAGAACGTCACC CAGGCTCGTTTGATATTG
AD002	SEQ ID NO: 2467 GCGTAATACGACTC ACTATAGGGAAGAA AGATGGAAAGGCTC CGAC SEQ ID NO: 2469 GAAGAAGATGGAA AGGCTCCGAC	SEQ ID NO: 2468 CATCCATGTGCTGA TGAGCTGC SEQ ID NO: 2470 GCGTAATACGACTC ACTATAGGCATCCAT GTGCTGATGAGCTG C	SEQ ID NO: 2466 GAAGAAGATGGAAAGGCTCCGACCACTGGTGAGGCCATTCAGAAACTCAGAGAAA CAGAGAAAATGTTAATCAAAAGCAGGAATTTTAGAGAGAAGAAAATCGAACAAGAAA TCAATGTTGCAAAGAAAATGGAACGAAAAATAAGCGAGCTGCTATTCAGGCTCTGA AAAGGAAAAAGAGGTATGAAAAACAATTGCAGCAAATTGATGGCACCTTATCCACAA TTGAAATGCAAAGAAGCTTTGGAGGGTGCTAATACTATACAGCTGTATTACAAA CAATGAAATCAGCAGCAGAGATGCCCTTAAAGCAGCTCATCAGCACATGGATG
AD009	SEQ ID NO: 2472 GCGTAATACGACTC ACTATAGGGTCTTCT TCCAGACACTGGAT CCTC SEQ ID NO: 2474 GTCTTCTTCCAGACA CTGGATCCTC	SEQ ID NO: 2473 CGTGTTCATCTCCCT CGAGTTG SEQ ID NO: 2475 GCGTAATACGACTC ACTATAGGCGTGTT CATCTCCCTCGAGT TG	SEQ ID NO: 2471 GTCTTCTTCCAGACACTGGATCCTCGTATTCCCACCTGGCAGTTAGATTCTTCTATC ATTGGCACATCACCTGGCCTAGGTTTCCGGCCAATGCAGAAGATAGCAATGTAGA GTCAACTCTCATCTGGTACGGTGGAACAGATCGTGATGACTTCCGTCAGTGGACAG ACACCCTTGATGAATTTCTTGCTGTCTGTACAAGACTCCTGGTCTCTGACCCCTGGTCGAG GTCAGAACATCCACAACTGTGACTATGATAAGCCGCAAAGAAAGGCCAAGTTTGC AATGTGGACATCAAGAATTGGCATCCCTGCCATTCAACAAGATCTACAATTGGATCCCTGAA TACTACAATGAGAGTAGTACGAGATTTGCCTGAGCAGATGCCAGAAGACCTGAAGCAGTA CATCCACAACCTGGAGAGTAACAACTCGAGGGAGATGAACACG
AD015	SEQ ID NO: 2477 GCGTAATACGACTC	SEQ ID NO: 2478 AGAATTTCAAGGCG	SEQ ID NO: 2476

		SEQ ID NO: 2481
ACTATAGGGTTGAA GGACTAACCGGGAA TTTG SEQ ID NO: 2479 GTTGAAGGACTAAC CGGGAATTTG	ACCAGTGG SEQ ID NO: 2480 GCGTAATACGACTC ACTATAGGAGAATT CAAGGCGACCAGTG G	GTTGAAGGACTAACCGGGGAATTTGTTTGGAGGTGTACTTAAAACCGTACTTTCTCGAA GCATACCGACCCATTCACAAAGATGATGCGTTTATTGTTCGTGGTGGTATGCGGAGCA GTAGAATTCAAAGTAGTGGAAACAGATCCTTCACCATATTGTATTGTTGCTCCTGATA CTGTTATTCACTGTGAAGGTGATCCAATAAAACGTGAAGAGAAACAGCATTAA ATGGTGGTTATGATGACATTGGGGGTTGCCGAAAACAGTAGCAGATCAAG GAAATGGTGGAATTGCCATTACGGCGACCCCTGCTCTTTAAGGCTATTGTGTTAAG CCACCGAGGGGAATACTGTCTATGGAACCCCTGCAACCCTCTTTAAGCCCTCATTGC CAGGGCTGTGGCTAATGAAACTGGTGCATTCTTCTTTTAATAAATGGCTGTCTGAAATT ATGAGCAAGCTTGCTGTGGTGAATCTGAAAGCAACTTACGTAAGGCATTTGAAGAAGCT GATAAGAATGTCTCCGGCAATTATATTATTGATGAACTAGATGCCATAGTTTCACAACTTTAA GAGAAAAACTCATGGAGCAAGTTCACAATGTTATTGGTCGCGATTTGATAGGGAAATTGATATTG TGGATGGTCTGAAGCAAAGTTGCCTTGCCCGGCGCTTGGCAGATTTGATAGGGAAATTGATATTG ACTCTATTGATGGTGCCACTGTCGTCGCCTTGCGCCTTGAAATTCT GTATACCCAGATGCCACTGTCGTCGCCTTGCGCCTTGAAATTCT SEQ ID NO: 2481
AD016	SEQ ID NO: 2482 GCGTAATACGACTC ACTATAGGACCCGG AAGAAATGATCCAG AC	SEQ ID NO: 2483 ATGTAGCCTGGGAA GCCTCTTC SEQ ID NO: 2485 GCGTAATACGACTC ACTATAGGATGTAG CCTGGGAAGCCTCT TC	ACCCGGAAGAAATGATCCAGACGGGATCTCGACCATCGACGTGATGACGTCCATC GCGGAGGGGCAGAAGATCCCCATCTTCTCGGGGCGGGGATCTGCCACACAACGAGA TCGCTGCGCAGATCTGCCGACAGGCGGGGCTGGTGCAGCACAAGGAGAACAAGGA CGACTTCGCCATCGTGTTCGCGGCGACGGGGATGGGCGCCGTGCAACATGGAGACGGCGCTTC TTCAAGCGCGGAGTTCGCGCAGACGGGCGCGGTGCAACGTGGTGCTTCCTCAACC TGGCCAACGACCCCACCATCGAGCGCCATCATCACCCCGCGCCGCTCACCGT GGCCGAGTTCCTGCGCGGAGGGGCGCTGCAACAAGCACGTGCTCGTCATCGATGACCGACA TGACCTCCTACGGCGAGGGCTTCGCGCGAGGTGAGCGCGCGGCGGAGGTTC CTGGGGCGAAGAGGCTTCCCAGGCTACAT
	SEQ ID NO: 2484 ACCCGGAAGAAATG ATCCAGAC		

Table 9-LD

Target ID	Hairpin Sequence 5' → 3'
LD002	SEQIDNO: 240 GCCCTTGCAATGTCATCCATCATCATGTCGTGTACATTGTCCACGTCCAAGTTTTTATGGGCGTTTTCTTAAGAGCTTCAGCTGCCATTTTCAT AGATTCCAATACTGTGGTGTTCGTACTAGCTCCCTCCCAGAGCTTCTCGTTGGTGAAGTTCAATAGTAGTTAAAGTGCCATCTATTTGCAACT GATTTTTTTCTAATCGCTTCTTCCGCGCTTCAGCGTCGTCGACCATATGTCGCCGCCACTAGTGATCGTGTATGTTCAGTGTCAAGCTGA ACTAGTGCGGCGCCCTGCAGGTCGACCATATGTCGCCGCCGCCACTAGTGATCGTGTATGTTCAGTGTCAAGCTGA CCTGCAAACACGTTAAATGCTAAGAAGTTAGAATATATGAATATATGAATAAGCTGTAAATAAAACT CATTAACTAATATCACCCTCTAGAGTATAATAATCAAATTCGACATTTGACTTTCAAGAGTAGGCTAATGTAAAATCTTTATATATTTC

	TACAATGTTCAAAGAAACAGTTGCATCTAAACCCCTATGGCCATCAAATTCAATGAACGCTAAGCTGATCCGGCGGAGATTTTCAGGAG CTAAGGAAGCTAAAATGGAGAAAAAATCACTGGATATACCACCGTTGATATATCCCAATGGCATCGTAAAGAACATTTGAGGCATTT CAGTCAGTTGCTCAATGTACCCTATAAACCAGACACGTTCAGCTGGATATTACGGCCCTTTCAGCTGAATGCTCATCCGGAATTCCGTATA TTATCCGGGCCTTTATTCACATTCTTGCCCGCCTGATGAATGCTCATCGCTCTGGAGTGAATACCACGACGATTCC TGGGATAGTGTTCACCCTTGTTACACCGTTTCCATGAGCAAACGTTTCATCGCTCTGGAGTGAAACCTAAGGGTTATTGAGAATATGTT GGCAGTTTCTACACATATTCCTGGGTGAGTTGGCGTGTTCACCAGTTTGATTAAACGTGGCCAATATGGACAACTCTTCGCCCCCGTTTCACCAT TTCGTCTCAGCCAATCCCTGGGTGAGTTTCACCAGTTTGATTAAACGTGGCCAATATGGACAACTCTTCGCCCCCGTTTCACCAT GGGCAAATATTATACGCAAGGCGACAAGGTGCTGATGCCGCTGGCGAGGTGCTGATGCCGCTGGCGAGGGCGTAAACGCTGGATCAGCTTAATATGACTCTCAATA CAGAATGCTTAATGACTACAACAGTACTGCGATAGTAGTGGCGTAAACGCTGGATCAGCTTAATATGACTCTCAATA AAGTCTCATACCAACAAGTGCCACCTTATTCAACCATCAAGAAAAAAGCCAAAATTTATGCTACTCTAAGGAAAACTTCACTAAAGAAG ACGATTTAGAGTGTTTTACCAAGAATTTCTGTCATCTTACTAAACAACTAAAGATCGGTGTGATACAAAAACCTAATCTCATTAAAGTTTA TGCTAAAAATAAGCATAATTTTACCCACTAAGCGTGACCAGATAAACATAACTCAGCCAGACCATATATATTGGTGGCTCAAATCA TAGAAACTTACAGTGAAGACACAGAAAGCCGTAAGAAGAGGCAAGAGTATGAAAACCTTACCTCATCATTTCCATGAGGTTGCTTCTGA TCCCGCGGGATATCCACCACTTTGTACAAGAAAGCTGGGTCAATTCGCCCTTGAGCGGCCATGCAAGCGCTGAGGCGGAAGAAGCG ATTAGAAAAAAATCAGTTGCAAATAGATGGCACTTAACTACTATTGAACTTCAACGAGAAGCTCTGGAGGGAGCTAGTACGAACACC ACAGTATTGGAATCTATGAAAAATGCAGCTGAAGCTCTTAAGAAAGCCCATAAAAACTTGGACGTGGACAATGTACGACGACATGATGG ATGACATTGCAAGGGC
LD006	SEQIDNO: 241 GCCCTTGGAGCGGAGACTACAACAACTATGGCTGGCAGGTGTTGGTGCTTCTCGGTGGTGGAATACATCGACACTCTTGAAGAAGA AACTGTCATGATTGCGATGAATCCTGAGGATCTTCGGCAGGACAAAGAAATAGTGCTTATTGTACGACCTACACCACTGCGAAATCCAC CCGGCCATGATCTTGGGCGGTTCGGCGGTCTACATTACGAATTTCCCGATCTATAACCTTCCCGATCTAACCAGAGCAACACCTACCAGAGCGCTATG GGTAAGCAAGCTATGGGGTCTACATTACGAATTTCCACGTGGACACCGCCACCGCTACTACCGCCACAAACCT CTGGTCACTACCAGGTCTATTCTGTATTCTGAACGCGTCTGTGTGGAAGAGGATTTTTCCGATCCGTGTTTTATCGTTGTTCCTATAAAGAT GTTATAATCAAGAGAGATTCTGTATTCTGAACGCGTCTGTGTGGAAGAGGATTTTTCCGATCCGTGTTTTATCGTTGTTCCTATAAAGAT GCCGAATCGAAGCGAATTGGCGATCAAGAAAGCAGTTCGACTTCCTTCTTTATGTGTGTTAATAAGTGGTATATCACTA GTGCGGCCGCCTGCAGGTCTAAGATGCTAAAAGTTGAAATATATGAGACACGTTAAATGGTAATGAAGTGTAATAAACCGAGTATAAACTCATT CAAACACGTTAAATGCTAAGAAGTTAGAATATATGAGACACGTTAAATGGTAATGAAGTGTAATAAACCGAGTATAAACTCATT AACTAATATCACCTCTAGAGTATAATAAACCCCTATGGCCATCAAATTGACTTCAAGAACGTGATATCCCAATGGCATCGTAAAGAACATCTTATATTTCTACA ATGTTCAAAGAAACAGTTGCATCTAAACCCCTATGGCCATCAAATTGACTTCAAGAACGTGATATCCCAATGGCATCGTAAAGAACATCTTATATTTCTACA GGAAGCTAAAATGGAGAAAAAATCACTGACTACCTATAAACCAGAACCTTTTAAAGACCGTAAAGAAAATAAGCACAAGTTTTAT CAGTTGCTCAATGTACCTTAATAAACCAGAACCTTTTAAAGACCGTAAAGAAAATAAGCACAAGTTTTAT CCGGCCTTTATTCACATTCTTGCCCGCCTGATGAATGCTCATCGCTCTGGAGTGAAACGTTTCATCGCTCTGGTGATATGG GATAGTGTTCACCCTTGTTACACCGTTTCCATGAGCAAACGTTTCATCGCTCTGGTGATATGG AGTTTCTACACATATTCCTGGGTGAGTTTACGGTGTTCACCAGTTTGATTTAAACGTGGCCAATATGGGTTTATTGAGAATATGTTTTTC GTCTCAGCCAATCCCTGGGTGAGTTTACGGTGTTCACCAGTTTGATTTAAACGTGGCCAATATGGACAACTCTTCGCCCCCGTTTCCACCATGG GCAAATATTATACGCAAGGCGACAAGGTGCTGATGCCGCTGGCGAGGTGCTGATGCCGCTGGCA GAATGCTTAATGACTACAACAGTACTGCGATAGTGGCGATTCAGCTTAATATGACTCTCAATAAA

GTCTCATACCAACAAGTGCCACCTTATTCAACCATCAAGAAAAAGCCAAAATTTATGCTACTCTAAGGAAAACTTCACTAAGAAGAC
GATTAGAGTGTTTTACCAAGAATTTCTGTCATCTTACTAACGTGTGATACAAAACCTAATCTCATTAAGGTTTATG
CTAAAAATAAGCATAATTTACCCACTAAGCGTGACCAGATAAACATAAACTCAGCACCAGCATATATATTGGTCGTCAAATCATA
GAAACTTACAGTGAAGACACAGAAAGCCGTAAGAAAGGCAAGAGTATGAAAACTTACCTACTCATTTCCATGAGGTTGCTTCTGATC
CCGCGGGATATCACCACTTTGTACAAGAAACACGGATCGGGAAAAATCCTCTTTCCACAGCAGAGACGGTTCAGAAATAAACAGAAT
ATCTTTATAGGAACGATAAAACGGATAGCAACTATACTGTTGATCCCGGCTGGGTAATTCTCTGAACCGCAGATACTCCATAGACCA
CAGTATAACAAGCAATAGCAACTATACTGTTGATCCCGGCTGGTAATTCTCTGAACCGCAGATACTCCATAGACCCCCATAGCTTGC
AGGTTTGTGCGGGTAGTATAGCACGTGGGCTGGGCTCTGGTTCCTTGGGCTCTGGTAGTTCGTCACAATAAGCATATTCTTTGTCCT
CATAGCGCTCTGGTAGGTGTTCCTTGGGCTCTGGTAGGTCGTACAATAAGCATATTCTTTGTCCTGCCGAAGATCCTCAGGATTCAT
GGTGGATTTCGCAGTGTCGATGTATTCCACCACACCAGAAGCAACCAACACCTGCCAGCCATAGTTGTTGTAGTCTCGCTCCAAGGGC
TTCTTCTTCAAGAGTGTCGATGTATTCCACCACACCAGAAGCAACCAACACCTGCCAGCCATAGTTGTTGTAGTCTCGCTCCAAGGGC

SEQIDNO: 242

GCCCTTCCGAAGAAGGATGTGAAGGGTACTTACGTATCCATACACAGTTCAGGCTTCAGAGATTTTTTATTGAAACCAGAAATTCTAA
GAGCTATAGTTGACTGCGGTTTTGAACACCCTTCAGAAGTTCAGCAATGTATTCCTCAAGCTGTCATTGGCATGGACATTTTATGT
CAAGCCAAATCTGGTATGGGCAAAACGGCAGTGTTGTTCTGGCAACAATTGGAACCAGCGGACAATGTTGTTTACGTTT
TGGTGATGTGTCACACTCGTGAACTGGCTTCCAAATCAGCAAGAGTACGAGAGGTTCAGTAAATATATGCCCAGTGTCAAGGTGG
GCGTCTTTTCGGAGGAATGCCTATTGCTAGGAAGCTAGTCCTCAAGAACCTCACACCAGCAAGTGATGATGTTCAGTGCCACTCAGCAAA
GTATTTGGCGCTTGTCAAGTCTAGGAAGCGTCCAGGAAATCTACAGAAACACCCCTCACACCAAGTGATGATGTTCAGTGCCACTCAGCAAA
TTGGATATGAGGAGGAGACGTCCAGGAAATCATGCAAGTCCAATGGAGGTGTATGTAGACGATGAAGCCAAATTGAGGTTGCACGGATTA
GAAATCAGGGCCGGTGTGCAAGAAACTCAAAGGAAATGAAAAGAATAAAAATTATTTGAGTTGCTGTCGATGTTCTCGAATTTAATCAGGTGGTCATT
CAACAGCATTACGTTAAACTCAAAGAAAATGAAAAGAATAAAAATTATTTGAGTTGCTGACTGAACAGAATTCCCAGCCATAGGAATTCACAGAGGAATG
TTGTGAAGTCCGTTCAAGAGGTTGTGTCGGTATGAGCAGTTCAAGATTCCAGAAGAGAATATTGGTAGCTACGAATCTCTTTGGGCGTGGC
GACCAGAAGAGAGGTTGTCTCGGTATGAGCAGTTCAACTGTCTTCAACTATGGCCAGAAGGACTCGCACCTACTGCGAAGGCGAATTCACCAG
ATGGACATCAAAGGGTCAACATTGTCTTCAACTATGGCCAGGCCGCCTCAGGTGCATCGAAGGCGCCACTAGTGATGC
CTTTCTTGTACAAAGTGGTATATCACTACTAGTGCGGCGCCGTTAAATGCTCAAGCACGTTAAATGCTAGATATATGGTATGTATATGAATAAG
TGTTATGTTCAGTGTCAAGCTGACCTGCAAACACGTTAAATGCTAGATATATGGTATGTATATGAATAAG
CTGTAAATAACCGAGTATAAACTCATTAACTATGTTCAAAGAAAACAGTTGCATCTAAACCCCTATGGCCATCAAATTCAATGAACGCTAAGCT
TAATGTAAAATCTTTATATATTTCTACAATGTTCAAAGAAAACAGTTGCATCTAAACCCCTATGGCCATCAAATTCAATGAACGCTAAGCT
GATCCGGCGAGATTTCAGGAGCTAAGGAAGCTAAAATGGAGAAAAAATCACTGGATATATCCCAATGGCATC
GTAAAGAACATTTGAGGCATTCAGTCAGTTGCTCAATGTAACCTATAACCAGACCGTTCAGCTGGATATTACGGCCTTTTAAAGACC
GTAAAGAAAAATAAGCACAGTTTATCCGGCGTATGGGATAGTGTTCTACACATATTCCGGCGATTCTCATCCGGAATTCCGTATGGCAAT
GAAAGACGGTGAGCGTGGTGATATGGGCAGTTTCTACACCTGTTCCATGAGCAAACTGAAACGTTTCATCGCTCTCTGG
AGTGAATACCACCGACGATTTCCGGCAGTTTCGTCTCGACCATTATTCGCAAGATGTGGCGTGTTACGGTGAAACCTGGCCAATATGGACAAC
TTCTTCGCCCCCGTTTCCATGTCGGCAGAAATGCTTAATGAATTACAAACAGTGCTTAAACGTGCTGGCCAATATGGACAAC
GTCTGTGATGGCTTCCATGTCGGCAGAAATGCTTAATGAATTACAAACAGTGCTTAAACGTGCTGGCCAATATGGACAAC
ATCAGCTTAATATGACTCTGATAAGTCTCAATACCAAGTGTCTCATTATTCAACCATCAAGAAAAAAGCCAAAATTTATGCTACTC

LD007

	TAAGGAAACTTCACTAAAGAAGAAGACGATTTAGAGTGTGTTTACCAAGAATTTCTGTCATCTTACTAAACAACTAAAGATCGGTGTGATAC AAAACCTAATCTCATTAAAGTTTATGCTAAAATAAGCATATAATTTACCCCACTAAGCGTGACCAGATAAACATAACTCAGCACACCAGAG CATATATATTGGTGGCTCAAATCATCATAGAAACTTACAGTGAAGACACAGAAACCGTAAGAAAGCCGTAGAGAGTATGAAACCTTACCTCA TCATTCCATGAGGTTGCTTCTGCCATATCATAGTTGAAGACAATGTTGACCCTTTCAATGTCCATGCCAAAGAGATTCGTAGCTACC GGTGTCGGAGTCCTCTGGAAATCTTTGAAGACAATGTTGAAGACAATGTTGACCCTTTCAATGTCCATGCCAAAGAGATTCCTATGGCTGGGAA AATATTCTCTTCTGGAAATCTTTGAACTGCTCATACCGAGACAACCACACTTTGAACGGACTTCACAAAATGACCACCTGATTAAATTCGAGAACATCG AGCAACTCAAATAATTTTTATTCTTTATTCTTTGAGTTAACGTAATGCTGTTGTAATCCGTGCAACGTCAATTGGCTTCATCGT CTACATACACCTCCATTGGATCTTGCATGAATTTCTTGCACACGGCTGATTTCTTGCTGAGTGTGGCACTCAACATCATCACTTGC TTGGTGTGAGGGGTGTTTCTGTAGATTCCTGGACGTCTCTCCTCATATCCAACAGTTCTAACATTTATCGCACTCATCAAGAATGAA GTGTTTCAGGTTCTTGAGGACTAGCTTCATCGTTAGCAATAGGCATTCACGAGTGTGACACTGGGCATATATTTACTGTGGACATTT GTTTTTCAAATACTTCTTGATTTGCTAGTCTTGTGTAGTCCCATACCGAGACTTGGCTGGTTCCAATTGTTG CGTACTCTTTGCTGAGGACTCGTTAGCAATAGGCATTCACGAGTGTGACACTGGGCATATATTTACTGTGGAATA CAGTGTCGCCAGAACAAACACTGCCGTTTGCCCATACCAGTTGCTTGACATAAATGTCCATGCCAATGACAGCTTGAGGAATA CATTCGTGCTGCTGAACTTCTGAAGGGTGTTCAAAACCGAGTCAACTATAGCTCTTAGAATTTCTGGTTTCAATAAAAATCTCTGAAGCC TGAACTGTGTATGGGATACGTAAGTACCCTTCACATCCTTTCTTCGGAAGGGC
LD010	SEQIDNO: 243 GCCCTTCGCCATGGGCCATTGGGCGATGGTTTCGCCATGGAATATCAGAATTCTGGAAGAAACGTGTCCATGAGCAGAATTCTATCGGGTTGGATG GAACTCGTATCCAAAAGCACAGGTTCTCGGTGGTCCATTGAAACTGTAGAGCTGTGAGTATCGGCTGGATCATGATCAGCGACTGCCGTG AGGTCTTCGCGCATAAGCATGTGCCTGTAGAAGGACGTTTCGTCGGGGAGAATTGTTAAACACCTGCAGGAACTGTGACCTTCTCAAA TGGTACATGAACTGCGGGTAGAGGCTGAAGTTTCGCCCAAGCGAACGAATTCGGGTCGTCCTTGTTATATTCGCCGAATTTCTGG CACAGAACGTATCAACATCCTATCGACCCATCTCAAAACATCAGGGCTATCGTCGATTCCGCTCTGTAAACTGCCATCCTCGCCATTA TCACTGCGGCTGCCTCTGTCGATCCAGTAGCATGCTGATATTGCCATGGTACTTGGAGTTACCGTTACACAATTCAACTGTCGTTA CTCGGATCCTCTTCTGCCCACTAGCATGCTGATATTGCCATGGTACTTGGAGTTACCGTTACACCATTTCCCCCTTGAGGTATGGGAGCGGAAT GTTGGTTGACGACCTCGAAGAACAAAGGATTCTTCACATTCAACGAAACAAGATCCAAATACCAAGTTTGCTTGAACAGTTTG TTCGGTGTCGGGAAACCAAGTACCATTAAAATGCCATCTACGACCATATGTCCCCGTGAATTACAACACTGTTTCATCTCCATCAATCCTGTCTGATCCCAAAGCGC ACCCTCCAGAGTACCATTAAAATGCCATCTACGACCATATGTCCCCGTGAATTACAACACTGTTTCATCTCCATCAATCCTGTCTGATCCCAAAGCGC GAATTGAACGAGTCGCCCATGGCCATTGGTGGTGAGATCTGAGATCTGGCGTATGGCTGTTGCTTCTTCATGTATTTGGCAT TGTCTTTTGGATGTCGTGGTGAGATCTGATAGGTTGCTTCAGATCATCATTGCTTCAGATCATCATTCCAACAACCCAATGGCTTCCCGTCGATCT AACGAATAGCATGACCCTGGCACCAGTATTGGCGTATGGCCATGGTCTCTTGCAACTCTCCAATAAGATCAGTGAGGTTCATGTCGCATTTCGAGAT AAGGGCGCCATTGCCTTGGTGGACAGGCCATGGGTCGTAGGAGCTTGCTCAGGCCTCAGCGTTGTCCTGGTCTTGTGGAAAACGTAAGA GGGTTGAAGGAACCTGCTTCCTGGGCGTAGGAGCTTAGCTTGCTAGGTCTTTCGTCCTGTGAGGTCTTTGTCCTCGGAAAACGTAAGA TTTGCTGCAGCCCTCGGTACCCTAGTTCGTGCACTTGGACCATCTTCCCAAAGGTAATCAACCCTATCAAGGCATTCGGGGGCAACAA GCTCAAAGACAACATCTGCAACGAATCCTTGAGAGAAGGGCGAATTCAACCAGCTTTCTTGTACAAAGTGGTATATCACTAGTGCGGCCGC CTGCAGGTCGACCATAGTGTCGACCTAGTTCGATGGTGTTGTTTATGTTCAGTTGTTCAGTTGCTTCAAGTGTCAAGCTGCAAACACGTTA

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SEQIDNO: 244

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LD011

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LD016	SEQIDNO: 246
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Table 9-PC

Target ID	Hairpin Sequence 5' → 3'
PC001	SEQ ID NO: 508 AGATTCAAAATTTGATGTAGTCAAGAATTTAGATGTAGCAATTTCCATTTGAATTGTGTCATTCATTCACTTTGATGTGTGGGGTCAGGGTAACGAATGGTTCTGCCATCATGTGTTACCAACAAATGGGATTCCTTTGGGACCAGTTTGGACTCTCCTTACTTTACACAACTTGTATTTTGCCTCTTCAGCTGTAATACGGTGCACAGCAAATCTTCCTTAACATCATAGATCAGACGGAAAATTCACCAGTCTTCTCAATAGTAATGACATCCATGAAACCAGCAGGTAATTAGAATCAGTCCTCACTTACCATCAACTTGATCAACCTTGTGAGGCCCGGACCAATTTAGTGACTTCACTGTTTGTAAGGGCTACTTCAGCCTGTTACGAAGGAAAATCACTCAAGGGCGAATTCGACCCAGCTTTCTTGTACAAAGTGGTGATATCACTAGTGCGGCCGAAGACACCCCCAAATTGTCCAACATCCATGCAGGGCGGCCGCACTAGTGCAGTGCGGCCGCCTGCAGGTCGACCATATGGTGCAGGCGGCCGCACTAGTGCAGTGCGGCCGCCAAACACGTTAAATGCTAAGAAGTTAGAAATATATGAGACACGTTAACTGGTATATGAATAAGCTGTAAATAACGAGTATAAACTCATTAACTAATATCACCTCTAGAGTATATAATCAAATTCGACAATTTGACTTTCAAGAGTAGGCTAATGTAAAATCTTTATATATTCTCAAGAAACAGTTGCATCTCAACCCTATGCCATCAAATTCAATGAACGTAAGCTGATCCGGCGAGATTTCAGGAGCTAAGGAAGCTAAAATGGAGAAAAAATCACTGGATATACCACCGTTGATATTACGGCCTTAAAGAAGAAAATAAGCACAAGTTTTATCCGGCCCTTATTCACACCTATAACCAGACCGTTCAGCTGGATATTACGCCGGCGCAAGCACCGATCGCATCGGAATTCCGTATGGCAATGAAAGACGGTGAGCTGGTGATATGGGATAGTGTTCACCCTTGTTTCTTGCCCGCCTGATGAATGCTCATCCGGAATTCCGTATGGCAATGAAAGACGGTGAGCTGGTGATATGGGATAGTGTTCTCCACCATATTCGTACACCGTTTGGCGTGTTACGGTGAAAACCTGGCCTATTTCCCTAAAGGGTTATTGAGAATATGTTTTCGTCTCAGCCAATCCCTGGGTGAGTTTCACCAGTTTTGATTTAAACGTGGCCAATATGGACAACTTCTTCGCCCCCGTTTTCACCATGGGCAAATATTATACGCAAGGCGACAAGGTGCTGATGCCGCTGGCGATTCAGGTTCATCATGCCGTCTGTGATGGCTTCCATGTCGGCAGAATGCTTAATGAATTACAACAGTACTGCGATGAGTGGCAGGGCGGGGCGTAAACGCGTGGATCAGCTTAATGTTTTATGTGGTGTTTTACCAAGAATTCATTCAACCATCCAGAAAAAGCCAAACTTAGTGTGTATCAATATCTCATTAAAAAGCCAGAATATCAGAATAGTTTATGCTGATAAACCTTATATTATTCTGATACAAATCGGTGATACAAATAAGTTTATGCTGTAAAATCAAGTTTATGATTAAGATATTTAAGTGTTTCTCATTCATCCATGAGTATCAAGTTTTACATCATCATAGAAACAGAAAATGCTCTGACAAGGTCTTTATTGGTCTGATACACAGAGATAAAACCTCATCTCGTCCGCCTTTCTTCGCCCCCTCGTCTCATCCAACAGTGAAGTGAAGTTCATGCATCCCCGGCCTCCACCCTTACAAGAAAGCGGGTCGGAATTCGGCCTTTAGTGATTTCCTTTCGTTAGTGGAGTATCCCTGGTTAGTGAACGGCTGTAATTCTTAATTACCTGTTTCATGATGATCTGTGTCGTTGCATACAGTAGTGTAAAGTAAGGAGGAGTCCAAACTGTCCCAAAGGAATCCCATTTTTGGTGTCTGATGTAGTTTAACTTGAGACTGATTCATTTGCTGTGCACCGTATTACAGCTGAGTGAAATACAAGTTGTGAAGTAAGGAGGAGTCCAAACTGTGTCACGAACATGGCAGCAGAACCATTCGTTACCCTGACCCCACATCCAACATCAAAGTTGAATGACACAATTCAAAATGGAAATTGCTACATCTAAAAATTCTTGACTACATCAAAATTTGAATCT
PC010	SEQ ID NO: 509 CTCTCAAGGATTCTTTGCAGATGTCGCTCAGCCTATTACCGCCCAACGCGGTTGATTGGATCACGTTCGGAAAAATGGTGCAAGTCCACGAACTGGGTACCGAAGGCTGCAGCAAGTCGTGCTAGCAAGTCGTACGTGTTCTGTGGAACGAAGATCTCACCGCCAAGCAAGTCCAGGAGATGTTG

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PC016	SEQ ID NO: 511 TTGGGCATAGTCAAGATGGGGATCTGCGTGATGGAGCCGTTGCGGCCCTCCACACGACCGGCGCGCTCGTAAATGGTGGCCAGATCG GTGTACATGTAACCGGGGAAACCCCTACGGGCCGGGCCACTTCTTCTCGAGCGGCAGACACCTCACGCAGCAAGCCTCCGGTACGACGAC ATGTCCGTCAAGATGACCAGCACGTGCTTCTCGCACTGGTAGGCCAAGAATTCGGCGGCCGTCAGAGCCAAACGCGGGCGTGATGATG CGCTCGATGGTCGGATCGTTGGCCAAGTTCAAGAACAGAACAACAATAGCAAAGTTGTCTTCATCCAGCACAGACTTGCCAGGTACTTTGA GGCAGTTTCCATGTTGACACCCATAGCAGCAGACAAACACAATAGCAAAGTTGTCTTCATGGTCATCCAGCACAGACTTGCCAGGTACTTTGA CCAAGCCAGCCTGCCTACAAATCTGGGCTGCAATCTCATTGTGGGCAGCCCAGCGGGGAAGATCGGAAGATCCGGGATCTTCTGCCCTCTGG CGATAGAGTTCATCACGTCGATGGCCGTGATCCGATCAGGATCGGGCCCTTATCAACACCGTGTTTCCTGATCCAATGGGTTTTCCTGATCAATAACCTGTGTCC TTGGATGTCGAGGTAGTCCTCAGCCAGGATCGGGGGGACCTTATCCAGTCCACACCGTGTTCTTAGCATCAATACCTGATGTGCCTTCAAATACCTGAACAA CTGCCTTTGACTTCCACTGACTTCCAAAACTTGTCCAGATCGTAGAGTTCCATCTGCCAATTTGAGCTGGACAATTTCATTGAATTTTGGAA ACTTGACATCCTCAAGAATGACCAGTAAGGCGCCGCCGCGCCACTAGTCGAATTCGACCCAGCTTCTTGTACAAAGTGGTGATATCACTAGTGCGGCGCCCTGCA GGTCGACCATATGTCGACCTGCAGGCGCCGCCGCCGAATTCGAGCGGCCGCCCACTAGTCGAATTGACCTGCAAACACGTTAAATGCT AAGAAGTTAGAATATATGAGACACGTTAACTGGCCATCAAATTTGACTTTCAAGATAGCTGTATATGAATAAGCTGTAAATAACGAGTATAAACTCATTAACTAATATCACCTCTAGA GTATAATATAATCAAATTGGCCATCAAATTTGACTTTCAAGAGAGCTAAGCTGATCCGGGCGAAGAACATTTTATCCGGCCCTTTATTCAACTTTTATATTTCTACAATGTTCAAGAAAACAGTTGC AATCACTGGATACCACCGTTGGATATTACGGGCCTTTTAAAGACCGTAAAGAAAATAAGCACAAGTTTTATCCGGCCCTTTATTCAACTTTTATATTTCTACAATGTTCAAGAAAACAGTTGC CCAGACCGTTCAGCTGAATGCTCATCCGGAATTCGGATATGGCAATGCAATGAAAGACGGTGAGCTGTGATATGGATAGTGTTCCAATGTACCTATAA GTTTTCCATGAGCAAACTGAAACGTTTCATCGCCTATTTCCCTAAAGGGTTATTGGAGTGAATACCACGACGATTTCCTCACACATATTCGCAAGAT GTGGCGTGTTACGGTGAAAACCTGGCCAATATGGCACAACTTCTTCGCGGCCTTTTCGTCTCAGCCAATCCCTGGGTGAGTTTC ACCAGTTTGATTTAAACGTGGCCAATATGGCCAATATGTTTTTCGTCTGCAAATATTATACGCAAGGGCGACAAGGT GCTGATGCCGCTGGCGATTCAGGTTCATCATGCGCGTGATCAGTCGGCAAATGCTTAATGAATTACAACAGTACTGCG ATCAAGAAAAAAGCCAAAATTTATGCGTAAACGCGTGTAAACGCGTAAATATGTGATCTCTAATATGCGTCGATCAGTCGGATCAGTCGGCAAATGCTTAATGAATTACAACAGTACTGCG TTACTAAACAACTAAAGATCGGTGTGATACAAAACCTAATCTCATTAAAGTTTATGCTAAAATAAGCATAATTTATCCACTAAGCGTGAC CAGATAAACATAACTCAGCACACCAGAGCATATATTGGTGCTCAAATCATAGAAAACTTACAGTGAAGACACAGAAAAGCCGTAAGAA GAGGCAAGAGTATGAAACCTTACCTCATCATTTCCATGAGGTTGCTTCTGATCCCCGGGATATCGACTCAGTTTCCAGCTGAAATTGTCCAGCTCAATGAAAATTGGCGAGATGGAACTCTA TCGAATTCGCCCTTACTGGTCATTCTTGAGGATGTCAAGTTTCCAAAATTCAATGAAATTGCCCCAGGTGTCAATTGTCCAGCTCAATGAAAATTGGCGAGATGGAACTCTA

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Table 9-MP

Target ID	Hairpin Sequence 5′ → 3′
MP001	SEQ ID NO: 1066 GTTTAAACGCACCCAAAGCATGGATGTTGGACAAATCGGGGGGGTGTCTTCGCTCCACGTCCAAGCACCGGTCCAAGCACACAAAACTTCGTG AATCACTACCGTTATTGATCTTCTTGCGTAATCGTTTGAAGTATGCACTTACTGGTGCCGAAGTCACCAAGATTGTCACCAAGATTA ATCAAGGTTGATGGCAAGTCCGTACCGACCCTAATTATCATTTATGGATGTTATATCTCAAAGACCAGTGAGCACT TTAGATTGATCTATGATGTGAAAGGTCGTTCACCATCCACAGAATTACTCCTGAAGAAGCAAAATACAAGTTGTGTAAAGTAAGAGG GTACAAACTGGACCCAAAGGTGTGCATCATCTAAAATTTTGGATCATCATCCGTTTGAAACTGGAAACATCAAGGTTAATG ACACTATTAGATACGATATTGCATCATCTAAAATTTTGGATCATCATCCGTTTGAAACTGGAAACATCAAGGTTAATG AATTTAGGCGGTGTTGTTATTGAAGGGCCGAATTCGACCCAGCTTTCTTGTACAAGTGGTGATATCACTAGTGCGGCCGCCTGCAGG TCGACCCATATGGTCGACCTGTAGGCCGCCCACACTAGTCCGTTAACTGGTATAAGCTGTAAATAACTCATTAACTAATATCACCTCTAGA GTATAATATATCAAATTCGACAATTTGACTTTCAAGAGTTAGGCTAATTGAATAAGTAAAATCTTTATATTGTAAAGAAACAGTTG CATCTAAACCCCTATGGCCATCAAATTCAATGAACGCTAAGTCGATCGGCATCGTAAAGAACATTTCAGGAGCATTGCTCAATGTGCTACCTA AAATCACTAGGATATACCACCGTTGATATTACGGCCCTTTTAAAGACCGTAAAGAAAGACGGTGGATAGTGTTCACCTA TAACCAGACCGTTCAGCTGAATGCTATCCGGAATTCCGGTATGGCAATGAAAGACGGTGGATAGTGTTCACCCTTGTT TTGCCCGCCTTCATGATGAATGCTCATCGGTGAAACGTTTCATCGCTGTGGAGTGAATACCACGACGATTTCCGGCAGTTTCTACACATATTCG CAAGATGTGGCGTGTTACGGTGAAACTGTTTAAACGTGGCCAAATAATGTTTTCGTCTCAGCCAATCCCTGGG TGAGTTTCACCAGTTTGATTTAAACGTGGCCAAATAATGTTTTCGTCTCAGCCAATCCCTGGG GACAAGGTGCTGATGCCGCGGATTCAGGTTCATCATGCCGTCTGTGATGCGTCCATGTGGCAGAATGCTTAATGAATTACAA

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SEQ ID NO: 1067

MP002

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| MP010 | SEQ ID NO: 1068 |

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| MP016 | SEQ ID NO: 1069 |

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SEQ ID NO: 1070

MP027

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Table10-LD

bioassay	bacterial host strain	treatment	no. of survivors	total weight	average weight / larvae
I		diet only	8*	1.0245	0.1281
		pGN29	8*	1.0124	0.1266
	AB309-105	pGBNJ003 clone 1	4	0.0273	0.0068
		pGBNJ003 clone 2	1	0.0091	0.0091
		pGBNJ003 clone 3	25	0.7113	0.0285
		pGBNJ003 clone 4	12	0.1379	0.0115
		pGBNJ003 clone 5	12	0.1808	0.0151
II		diet only	8*	1.0435	0.1304
		pGN29	8*	1.1258	0.1407
	BL21(DE3)	pGBNJ003 clone 1	33	0.5879	0.0178
		pGBNJ003 clone 2	42	0.8034	0.0191
		pGBNJ003 clone 3	33	0.3441	0.0104
		pGBNJ003 clone 4	21	0.1738	0.0083
		pGBNJ003 clone 5	33	0.3628	0.0120

Tables 10-NL (a)

RNAi	Mean % survival (days post start)									Survival analysis[1]
	0	1	2	3	4	5	6	7	8	
gfp	100	98	90	82	68	60	44	32	20	-
diet only	100	98	96	86	74	68	58	54	38	-
NL002	100	98	90	76	68	34	6	0	0	+
NL003	100	98	74	48	36	22	12	2	0	+
NL005	100	100	74	56	40	20	16	6	4	+
NL010	100	96	74	56	48	30	18	12	8	+

[1] = Data were analysed using Kaplan-Meier survival curve analysis

	Chi squared	P value	Sig. Dif. [2]
diet versus:			
NL002	29.06	<0.0001	Yes
NL003	39.59	<0.0001	Yes
NL005	29.55	<0.0001	Yes
NL010	21.04	<0.0001	Yes
gfp dsRNA versus:			
NL002	15.09	0.0001	Yes
NL003	22.87	<0.0001	Yes
NL005	15.12	<0.0001	Yes
NL010	8.838	0.0029	Yes
diet versus gfp dsRNA	4.030	0.0447 (~0.05)	No

[2] alpha < 0.05

Tables 10-NL (b)

RNAi	Mean % survival (days post start)									Survival analysis[1]
	0	1	2	3	4	5	6	7	8	
gfp	100	96	84	82	76	70	54	50	44	-
diet only	100	96	88	82	76	70	54	50	44	-
NL009	100	94	75	63	42	30	24	22	14	+
NL016	100	94	84	78	54	44	36	18	14	+

[1] = Data were analysed using Kaplan-Meier survival curve analysis

	Chi squared	P value	Sig. Dif. [2]
diet versus:			
NL009	11.98	0.0005	Yes
NL016	8.98	0.0027	Yes
gfp dsRNA versus:			
NL009	13.69	0.0002	Yes
NL016	11.37	0.0007	Yes
diet versus gfp dsRNA	0.03317	0.8555	No

[2] alpha < 0.05

Tables 10-NL (c)

RNAi	Mean % survival (days post start)									Survival analysis[1]
	0	1	2	3	4	5	6	7	8	
gfp	100	92	84	78	72	62	58	56	48	-
diet only	100	84	72	68	64	58	52	42	42	-
NL014	100	86	68	60	46	32	24	18	14	+
NL018	100	82	70	54	40	30	18	14	12	+

[1] = Data were analysed using Kaplan-Meier survival curve analysis

	Chi squared	P value	Sig. Dif.[2]
diet versus:			
NL014	8.088	0.0045	Yes
NL018	10.47	0.0012	Yes
gfp dsRNA versus:			
NL014	14.55	0.0001	Yes
NL018	17.64	<0.0001	Yes
diet versus gfp dsRNA	0.6548	0.4184	No

[2] alpha < 0.05

Tables 10-NL (d)

RNAi	Mean % survival (days post start)										Survival analysis[1]
	0	1	2	3	4	5	6	7	8	9	
gfp	100	96	84	84	72	68	68	66	66	62	-
diet only	100	96	86	82	74	72	70	70	66	58	-
NL013	100	94	82	68	50	40	30	28	20	20	+
NL015	100	100	72	30	18	12	8	6	6	6	+
NL021	100	100	84	58	50	44	40	34	34	22	+

[1] = Data were analysed using Kaplan-Meier survival curve analysis

	Chi squared	P value	Sig. Dif.[2]
diet versus:			
NL013	15.73	<0.0001	Yes
NL015	39.44	<0.0001	Yes
NL021	12.75	0,0004	Yes
gfp dsRNA versus:			
NL013	16.42	<0.0001	Yes
NL015	39.15	<0.0001	Yes
NL021	14.1	0,0002	Yes
diet versus gfp dsRNA	0.1031	0,7481	No

[2] alpha < 0.05

Table 11-NL

NL002 RNAi	Mean % survival (days post start)								Survival analysis[1]
	0	1	2	3	4	5	6	7	
diet only	100	100	96	90	86	78	78	78	-
1 µg/µl	100	84	80	44	26	8	6	6	+
0.2 µg/µl	100	84	60	12	8	4	2	2	+
0.08 µg/µl	100	84	62	18	14	6	6	6	+
0.04 µg/µl	100	84	48	24	22	22	22	22	+

[1] = Data were analysed using Kaplan-Meier survival curve analysis

	Chi squared	P value	Sig. Dif.[2]
diet versus:			
NL002 1 µg/µl	57.53	<0.0001	Yes
NL002 0.2 µg/µl	74.54	<0.0001	Yes
NL002 0.08 µg/µl	64	<0.0001	Yes
NL002 0.04 µg/µl	39.49	<0.0001	Yes

[2] alpha < 0.05

Claims

1. An isolated nucleotide sequence comprising a nucleic acid sequence selected from the group comprising:

(i) sequences represented by any of SEQ ID NOs 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 49 to 158, 159, 160-163, 168, 173, 178, 183, 188, 193, 198, 203, 208, 215, 220, 225, 230, 240 to 247, 249, 251, 253, 255, 257, 259, 275 to 472, 473, 478, 483, 488, 493, 498, 503, 508 to 513, 515, 517, 519, 521, 533 to 575, 576, 581, 586, 591, 596, 601, 603, 605, 607, 609, 621 to 767, 768, 773, 778, 783, 788, 793, 795, 797, 799, 801, 813 to 862, 863, 868, 873, 878, 883, 888, 890, 892, 894, 896, 908 to 1040, 1041, 1046, 1051, 1056, 1061, 1066 to 1071, 1073, 1075, 1077, 1079, 1081, 1083, 1085, 1087, 1089, 1091, 1093, 1095, 1097, 1099, 1101, 1103, 1105, 1107, 1109, 1111, 1113, 1161 to 1571, 1572, 1577, 1582, 1587, 1592, 1597, 1602, 1607, 1612, 1617, 1622, 1627, 1632, 1637, 1642, 1647, 1652, 1657, 1662, 1667, 1672, 1677, 1682, 1684, 1686, 1688, 1690, 1692, 1694, 1696, 1698, 1700, 1702, 1704, 1730 to 2039, 2040, 2045, 2050, 2055, 2060, 2065, 2070, 2075, 2080, 2085, 2090, 2095, 2100, 2102, 2104, 2106, 2108, 2120 to 2338, 2339, 2344, 2349, 2354, 2359, 2364, 2366, 2368, 2370, 2372, 2384 to 2460, 2461, 2466, 2471, 2476, 2481 or 2486, or the complement thereof,

(ii) sequences which are at least 70 %, preferably at least 75%, 80%, 85%, 90%, more preferably at least 95%, 96%, 97%, 98% or 99% identical to a sequence represented by any of SEQ ID NOs 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 49 to 158, 159, 160-163, 168, 173, 178, 183, 188, 193, 198, 203, 208, 215, 220, 225, 230, 240 to 247, 249, 251, 253, 255, 257, 259, 275 to 472, 473, 478, 483, 488, 493, 498, 503, 508 to 513, 515, 517, 519, 521, 533 to 575, 576, 581, 586, 591, 596, 601, 603, 605, 607, 609, 621 to 767, 768, 773, 778, 783, 788, 793, 795, 797, 799, 801, 813 to 862, 863, 868, 873, 878, 883, 888, 890, 892, 894, 896, 908 to 1040, 1041, 1046, 1051, 1056, 1061, 1066 to 1071, 1073, 1075, 1077, 1079, 1081, 1083, 1085, 1087, 1089, 1091, 1093, 1095, 1097, 1099, 1101, 1103, 1105, 1107, 1109, 1111, 1113, 1161 to 1571, 1572, 1577, 1582, 1587, 1592, 1597, 1602, 1607, 1612, 1617, 1622, 1627, 1632, 1637, 1642, 1647, 1652, 1657, 1662, 1667, 1672, 1677, 1682, 1684, 1686, 1688, 1690, 1692, 1694, 1696, 1698, 1700, 1702, 1704, 1730 to 2039, 2040, 2045, 2050, 2055, 2060, 2065, 2070, 2075, 2080, 2085, 2090, 2095, 2100, 2102, 2104, 2106, 2108, 2120 to 2338, 2339, 2344, 2349, 2354, 2359, 2364, 2366, 2368, 2370, 2372, 2384 to 2460, 2461, 2466, 2471, 2476, 2481 or 2486, or the complement thereof, and

(iii) sequences comprising at least 17 contiguous nucleotides of any of the sequences represented by SEQ ID NOs 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 49 to 158, 159, 160-163, 168, 173, 178, 183, 188, 193, 198, 203, 208, 215, 220, 225, 230, 240 to 247, 249, 251, 253, 255, 257, 259, 275 to 472, 473, 478, 483, 488, 493, 498, 503, 508 to 513, 515, 517, 519, 521, 533 to 575, 576, 581, 586, 591, 596, 601, 603, 605, 607, 609, 621 to 767, 768, 773, 778, 783, 788, 793, 795, 797, 799, 801, 813 to 862, 863, 868, 873, 878, 883, 888, 890, 892, 894, 896, 908 to 1040, 1041, 1046, 1051, 1056, 1061, 1066 to 1071, 1073, 1075, 1077, 1079, 1081, 1083, 1085, 1087, 1089, 1091, 1093, 1095, 1097, 1099, 1101, 1103, 1105, 1107, 1109, 1111, 1113, 1161 to 1571, 1572, 1577, 1582, 1587, 1592, 1597, 1602, 1607, 1612, 1617, 1622, 1627, 1632, 1637, 1642, 1647,

1652, 1657, 1662, 1667, 1672, 1677, 1682, 1684, 1686, 1688, 1690, 1692, 1694, 1696, 1698, 1700, 1702, 1704, 1730 to 2039, 2040, 2045, 2050, 2055, 2060, 2065, 2070, 2075, 2080, 2085, 2090, 2095, 2100, 2102, 2104, 2106, 2108, 2120 to 2338, 2339, 2344, 2349, 2354, 2359, 2364, 2366, 2368, 2370, 2372, 2384 to 2460, 2461, 2466, 2471, 2476, 2481 or 2486, or the complement thereof,

or wherein said nucleic acid sequence is an orthologue of a gene comprising at least 17 contiguous nucleotides of any of SEQ ID NOs 49 to 158, 275 to 472, 533 to 575, 621 to 767, 813 to 862, 908 to 1040, 1161 to 1571, 1730 to 2039, 2120 to 2338, 2384 to 2460, or a complement thereof.

2.   A double stranded ribonucleotide sequence produced from the expression of a polynucleotide sequence of claims 1, wherein ingestion of said ribonucleotide sequence by a plant insect pest inhibits the growth of said insect pest.

3.   The ribonucleotide sequence of claim 2, wherein ingestion of said sequence inhibits expression of a nucleotide sequence substantially complementary to said sequence.

4.   A composition comprising a ribonucleotide sequence according to claim 2 or 3 and further comprising at least one adjuvant and optionally at least one surfactant.

5.   A composition comprising at least one double-stranded RNA, one strand of which has a nucleotide sequence which is complementary to at least a part of a nucleotide sequence selected from the group of sequences as defined in claim 1, and optionally further comprising at least one suitable carrier, excipient or diluent.

6.   A cell transformed with a polynucleotide comprising a nucleic acid sequence as defined in claim 1, optionally operably linked to a regulatory sequence.

7.   The cell of claim 6 wherein said cell is a prokaryotic cell, such as a gram-positive or gram-negative bacterial cell; or wherein said cell is an eukaryotic cell, such as a yeast cell or an algal cell.

8.   The cell of claim 7 wherein said cell is a bacterial cell.

9.   The cell of claim 7 wherein said cell is a yeast cell.

10.   A composition comprising at least one bacterial cell or yeast cell comprising at least one polynucleotide as defined in claim 1.

11.   The composition of claim 10 wherein said bacterial or yeast cell is inactivated or killed, for instance by heat treatment or mechanical treatment.

12.   A composition comprising at least one bacterial or yeast cell expressing at least one double-stranded RNA, one strand of which has a nucleotide sequence which is complementary to at least a part of a nucleotide sequence selected from the group of sequences as defined in claim 1, and optionally further comprising at least one suitable carrier, excipient or diluent.

13.   The composition of any of claims 5, or 10 to 12, said composition further comprising at least one pesticidal agent selected from the group consisting of a chemical insecticide, a patatin, a *Bacillus thuringiensis* insecticidal protein, a *Xenorhabdus* insecticidal protein, a *Photorhabdus*

insecticidal protein, a *Bacillus laterosporous* insecticidal protein, and a *Bacillus sphearicus* insecticidal protein, said pesticidal agent being active against the same plant insect pest as defined in claim 2, or wherein said pesticidal agent is active against one or more other plant insect pests.

14. The composition of any of claims 10 to 12, wherein said at least one bacterial or yeast cell further comprises or further expresses at least one pesticidal agent selected from the group consisting of a chemical insecticide, a patatin, a *Bacillus thuringiensis* insecticidal protein, a *Xenorhabdus* insecticidal protein, a *Photorhabdus* insecticidal protein, a *Bacillus laterosporous* insecticidal protein, and a *Bacillus sphearicus* insecticidal protein, said pesticidal agent being active against the same plant insect pest as defined in claim 2, or wherein said pesticidal agent is active against one or more other plant insect pests.

15. A composition of any of claims 5, or 10 to 12, further comprising at least one further bacterial or yeast cell comprising or expressing at least one pesticidal agent selected from the group consisting of a chemical insecticide, a patatin, a *Bacillus thuringiensis* insecticidal protein, a *Xenorhabdus* insecticidal protein, a *Photorhabdus* insecticidal protein, a *Bacillus laterosporous* insecticidal protein, and a *Bacillus sphearicus* insecticidal protein, said pesticidal agent being active against the same plant insect pest as defined in claim 2, or wherein said pesticidal agent is active against one or more distinct plant insect pests.

16. The composition of any of claims 13 to 15 wherein said *Bacillus thuringiensis* insecticidal protein is selected from the group consisting of a Cry1, a Cry3, a TIC851, a CryET170, a Cry22, a binary insecticidal protein CryET33 and CryET34, a binary insecticidal protein CryET80 and CryET76, a binary insecticidal protein TIC100 and TIC101, and a binary insecticidal protein PS149B1.

17. The composition of any of claims 13 to 16 as an agent for killing insects.

18. The composition of any of claims 13 to 16 for use as a medicament for preventing or treating a human or animal body from infestation by insects.

19. A spray comprising at least one composition according to any of claims 10 to 18 and optionally further comprising at least one adjuvant and at least one surfactant.

20. A housing or trap or bait for a pest containing a composition as defined in any of claims 10 to 18.

21. Use of a composition of any of claims 10 to 18, a spray of claim 19 or a housing, trap or bait of claim 20 for killing or inhibiting growth of an insect chosen from the group comprising comprising *Leptinotarsa* spp. (e.g. *L. decemlineata* (Colorado potato beetle), *L. juncta* (false potato beetle), and *L. texana* (Texan false potato beetle)), and

      - wherein said nucleic acid in said composition comprises a polynucleotide, or

      - wherein a bacterium or a yeast cell in said composition comprises or expresses a polynucleotide,

      said polynucleotide having a nucleotide sequence selected from the group comprising:

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(i) sequences represented by any of SEQ ID NOs 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 49 to 158, 159, 160 to 163, 168, 173, 178, 183, 188, 193, 198, 203, 208, 215, 220, 225, 230, 240 to 246, or 2486, or the complement thereof,

(ii) sequences which are at least 70 %, preferably at least 75%, 80%, 85%, 90%, more preferably at least 95%, 96%, 97%, 98% or 99% identical to a sequence represented by any of SEQ ID NOs 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 49 to 158, 159, 160 to 163, 168, 173, 178, 183, 188, 193, 198, 203, 208, 215, 220, 225, 230, 240 to 246, or 2486, or the complement thereof, and

(iii) sequences comprising at least 17 contiguous nucleotides of any of the sequences represented by SEQ ID NOs 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 49 to 158, 159, 160 to 163, 168, 173, 178, 183, 188, 193, 198, 203, 208, 215, 220, 225, 230, 240 to 246, or 2486, or the complement thereof,

or wherein said nucleic acid sequence is an orthologue of a gene comprising at least 17 contiguous nucleotides of any of SEQ ID NOs 49 to 158, or the complement thereof.

22.   Use of a composition of any of claims 10 to 18, a spray of claim 19 or a housing, trap or bait of claim 20 for killing or inhibiting growth of an insect chosen from the group comprising *Phaedon* spp. (e.g. *P. cochleariae* (mustard leaf beetle)), and

- wherein said nucleic acid in said composition comprises a polynucleotide, or

- wherein a bacterium or a yeast cell in said composition comprises or expresses a polynucleotide,

said polynucleotide having a nucleotide sequence selected from the group comprising:

(i) sequences represented by any of SEQ ID NOs 247, 249, 251, 253, 255, 257, 259, 275 to 472, 473, 478, 483, 488, 493, 498, 503, 508 to 512, or the complement thereof,

(ii) sequences which are at least 70 %, preferably at least 75%, 80%, 85%, 90%, more preferably at least 95%, 96%, 97%, 98% or 99% identical to a sequence represented by any of SEQ ID NOs 247, 249, 251, 253, 255, 257, 259, 275 to 472, 473, 478, 483, 488, 493, 498, 503, 508 to 512, or the complement thereof, and

(iii) sequences comprising at least 17 contiguous nucleotides of any of the sequences represented by SEQ ID NOs 247, 249, 251, 253, 255, 257, 259, 275 to 472, 473, 478, 483, 488, 493, 498, 503, 508 to 512, or the complement thereof,

or wherein said nucleic acid sequence is an orthologue of a gene comprising at least 17 contiguous nucleotides of any of SEQ ID NOs 275 to 472, or the complement thereof.

23.   Use of a composition of any of claims 10 to 18, a spray of claim 19 or a housing, trap or bait of claim 20 for killing or inhibiting growth of an insect chosen from the group comprising *Epilachna* spp. (e.g. *E. varivetis* (mexican bean beetle)), and

- wherein said nucleic acid in said composition comprises a polynucleotide, or

- wherein a bacterium or a yeast cell in said composition comprises or expresses a polynucleotide.

said polynucleotide having a nucleotide sequence selected from the group comprising:

(i) sequences represented by any of SEQ ID NOs 513, 515, 517, 519, 521, 533 to 575, 576, 581, 586, 591 or 596, or the complement thereof,

(ii) sequences which are at least 70 %, preferably at least 75%, 80%, 85%, 90%, more preferably at least 95%, 96%, 97%, 98% or 99% identical to a sequence represented by any of SEQ ID NOs 513, 515, 517, 519, 521, 533 to 575, 576, 581, 586, 591 or 596, or the complement thereof, and

(iii) sequences comprising at least 17 contiguous nucleotides of any of the sequences represented by SEQ ID NOs 513, 515, 517, 519, 521, 533 to 575, 576, 581, 586, 591 or 596, or the complement thereof,

or wherein said nucleic acid sequence is an orthologue of a gene comprising at least 17 contiguous nucleotides of any of SEQ ID NOs 533 to 575, or the complement thereof.

24.   Use of a composition of any of claims 10 to 18, a spray of claim 19 or a housing, trap or bait of claim 20 for killing or inhibiting growth of an insect chosen from the group comprising *Anthonomus* spp. (e.g. *A. grandis* (boll weevil)), and

- wherein said nucleic acid in said composition comprises a polynucleotide, or

- wherein a bacterium or a yeast cell in said composition comprises or expresses a polynucleotide,

said polynucleotide having a nucleotide sequence selected from the group comprising:

(i) sequences represented by any of SEQ ID NOs 601, 603, 605, 607, 609, 621 to 767, 768, 773, 778, 783 or 788, or the complement thereof,

(ii) sequences which are at least 70 %, preferably at least 75%, 80%, 85%, 90%, more preferably at least 95%, 96%, 97%, 98% or 99% identical to a sequence represented by any of SEQ ID NOs 601, 603, 605, 607, 609, 621 to 767, 768, 773, 778, 783 or 788, or the complement thereof, and

(iii) sequences comprising at least 17 contiguous nucleotides of any of the sequences represented by SEQ ID NOs 601, 603, 605, 607, 609, 621 to 767, 768, 773, 778, 783 or 788, or the complement thereof,

or wherein said nucleic acid sequence is an orthologue of a gene comprising at least 17 contiguous nucleotides of any of SEQ ID NOs 621 to 767, or the complement thereof.

25.   Use of a composition of any of claims 10 to 18, a spray of claim 19 or a housing, trap or bait of claim 20 for killing or inhibiting growth of an insect chosen from the group comprising *Tribolium* spp. (e.g. *T. castaneum* (red floor beetle)), and

- wherein said nucleic acid in said composition comprises a polynucleotide, or

- wherein a bacterium or a yeast cell in said composition comprises or expresses a polynucleotide,

said polynucleotide having a nucleotide sequence selected from the group comprising:

(i) sequences represented by any of SEQ ID NOs 793, 795, 797, 799, 801, 813 to 862, 863, 868, 873, 878 or 883, or the complement thereof,

(ii) sequences which are at least 70 %, preferably at least 75%, 80%, 85%, 90%, more preferably at least 95%, 96%, 97%, 98% or 99% identical to a sequence represented by any of SEQ ID NOs 793, 795, 797, 799, 801, 813 to 862, 863, 868, 873, 878 or 883, or the complement thereof, and

(iii) sequences comprising at least 17 contiguous nucleotides of any of the sequences represented by SEQ ID NOs 793, 795, 797, 799, 801, 813 to 862, 863, 868, 873, 878 or 883, or the complement thereof,

or wherein said nucleic acid sequence is an orthologue of a gene comprising at least 17 contiguous nucleotides of any of SEQ ID NOs 813 to 862, or the complement thereof.

26.   Use of a composition of any of claims 10 to 18, a spray of claim 19 or a housing, trap or bait of claim 20 for killing or inhibiting growth of an insect chosen from the group comprising *Myzus* spp. (e.g. *M. persicae* (green peach aphid)), and

- wherein said nucleic acid in said composition comprises a polynucleotide, or

- wherein a bacterium or a yeast cell in said composition comprises or expresses a polynucleotide,

said polynucleotide having a nucleotide sequence selected from the group comprising:

(i) sequences represented by any of SEQ ID NOs 888, 890, 892, 894, 896, 908 to 1040, 1041, 1046, 1051, 1056, 1061, or 1066 to 1070, or the complement thereof,

(ii) sequences which are at least 70 %, preferably at least 75%, 80%, 85%, 90%, more preferably at least 95%, 96%, 97%, 98% or 99% identical to a sequence represented by any of SEQ ID NOs 888, 890, 892, 894, 896, 908 to 1040, 1041, 1046, 1051, 1056, 1061, or 1066 to 1070, or the complement thereof, and

(iii) sequences comprising at least 17 contiguous nucleotides of any of the sequences represented by SEQ ID NOs 888, 890, 892, 894, 896, 908 to 1040, 1041, 1046, 1051, 1056, 1061, or 1066 to 1070, or the complement thereof,

or wherein said nucleic acid sequence is an orthologue of a gene comprising at least 17 contiguous nucleotides of any of SEQ ID NOs 908 to 1040, or the complement thereof.

27.   Use of a composition of any of claims 10 to 18, a spray of claim 19 or a housing, trap or bait of claim 20 for killing or inhibiting growth of an insect chosen from the group comprising comprising *Nilaparvata* spp. (e.g. *N. lugens (brown planthopper)*), and

- wherein said nucleic acid in said composition comprises a polynucleotide, or

- wherein a bacterium or a yeast cell in said composition comprises or expresses a polynucleotide,

said polynucleotide having a nucleotide sequence selected from the group comprising:

(i) sequences represented by any of SEQ ID NOs 1071, 1073, 1075, 1077, 1079, 1081, 1083, 1085, 1087, 1089, 1091, 1093, 1095, 1097, 1099, 1101, 1103, 1105, 1107, 1109, 1111, 1113, 1161 to 1571, 1572, 1577, 1582, 1587, 1592, 1597, 1602, 1607, 1612, 1617, 1622, 1627, 1632, 1637, 1642, 1647, 1652, 1657, 1662, 1667, 1672 or 1677, or the complement thereof,

(ii) sequences which are at least 70 %, preferably at least 75%, 80%, 85%, 90%, more preferably at least 95%, 96%, 97%, 98% or 99% identical to a sequence represented by any of SEQ ID NOs 1071, 1073, 1075, 1077, 1079, 1081, 1083, 1085, 1087, 1089, 1091, 1093, 1095, 1097, 1099, 1101, 1103, 1105, 1107, 1109, 1111, 1113, 1161 to 1571, 1572, 1577, 1582, 1587, 1592, 1597, 1602, 1607, 1612, 1617, 1622, 1627, 1632, 1637, 1642, 1647, 1652, 1657, 1662, 1667, 1672 or 1677, or the complement thereof, and

(iii) sequences comprising at least 17 contiguous nucleotides of any of the sequences represented by SEQ ID NOs 1071, 1073, 1075, 1077, 1079, 1081, 1083, 1085, 1087, 1089, 1091, 1093, 1095, 1097, 1099, 1101, 1103, 1105, 1107, 1109, 1111, 1113, 1161 to 1571, 1572, 1577, 1582, 1587, 1592, 1597, 1602, 1607, 1612, 1617, 1622, 1627, 1632, 1637, 1642, 1647, 1652, 1657, 1662, 1667, 1672 or 1677, or the complement thereof,

or wherein said nucleic acid sequence is an orthologue of a gene comprising at least 17 contiguous nucleotides of any of SEQ ID NOs 1161 to 1571, or the complement thereof.

28.   Use of a composition of any of claims 10 to 18, a spray of claim 19 or a housing, trap or bait of claim 20 for killing or inhibiting growth of an insect chosen from the group comprising *Chilo* spp. (e.g. *C. suppressalis* (rice striped stem borer), *C. auricilius* (gold-fringed stem borer), or *C. polychrysus* (dark-headed stem borer)), and

- wherein said nucleic acid in said composition comprises a polynucleotide, or
- wherein a bacterium or a yeast cell in said composition comprises or expresses a polynucleotide,

said polynucleotide having a nucleotide sequence selected from the group comprising:

(i) sequences represented by any of SEQ ID NOs 1682, 1684, 1686, 1688, 1690, 1692, 1694, 1696, 1698, 1700, 1702, 1704, 1730 to 2039, 2040, 2045, 2050, 2055, 2060, 2065, 2070, 2075, 2080, 2085, 2090 or 2095, or the complement thereof,

(ii) sequences which are at least 70 %, preferably at least 75%, 80%, 85%, 90%, more preferably at least 95%, 96%, 97%, 98% or 99% identical to a sequence represented by any of SEQ ID NOs 1682, 1684, 1686, 1688, 1690, 1692, 1694, 1696, 1698, 1700, 1702, 1704, 1730 to 2039, 2040, 2045, 2050, 2055, 2060, 2065, 2070, 2075, 2080, 2085, 2090 or 2095, or the complement thereof, and

(iii) sequences comprising at least 17 contiguous nucleotides of any of the sequences represented by SEQ ID NOs 1682, 1684, 1686, 1688, 1690, 1692, 1694, 1696, 1698, 1700, 1702, 1704, 1730 to 2039, 2040, 2045, 2050, 2055, 2060, 2065, 2070, 2075, 2080, 2085, 2090 or 2095, or the complement thereof,

or wherein said nucleic acid sequence is an orthologue of a gene comprising at least 17 contiguous nucleotides of any of SEQ ID NOs 1730 to 2039, or the complement thereof.

29.   Use of a composition of any of claims 10 to 18, a spray of claim 19 or a housing, trap or bait of claim 20 for killing or inhibiting growth of an insect chosen from the group comprising *Plutella* spp. (e.g. *P. xylostella* (diamontback moth)), and

- wherein said nucleic acid in said composition comprises a polynucleotide, or

- wherein a bacterium or a yeast cell in said composition comprises or expresses a polynucleotide,

said polynucleotide having a nucleotide sequence selected from the group comprising:

(i) sequences represented by any of SEQ ID NOs 2100, 2102, 2104, 2106, 2108, 2120 to 2338, 2339, 2344, 2349, 2354 or 2359, or the complement thereof,

(ii) sequences which are at least 70 %, preferably at least 75%, 80%, 85%, 90%, more preferably at least 95%, 96%, 97%, 98% or 99% identical to a sequence represented by any of SEQ ID NOs 2100, 2102, 2104, 2106, 2108, 2120 to 2338, 2339, 2344, 2349, 2354 or 2359, or the complement thereof, and

(iii) sequences comprising at least 17 contiguous nucleotides of any of the sequences represented by SEQ ID NOs 2100, 2102, 2104, 2106, 2108, 2120 to 2338, 2339, 2344, 2349, 2354 or 2359, or the complement thereof,

or wherein said nucleic acid sequence is an orthologue of a gene comprising at least 17 contiguous nucleotides of any of SEQ ID NOs 2120 to 2338, or the complement thereof.

30.   Use of a composition of any of claims 10 to 18, a spray of claim 19 or a housing, trap or bait of claim 20 for killing or inhibiting growth of an insect chosen from the group comprising comprising *Acheta* spp. (e.g. *A. domesticus* (house cricket)), and

- wherein said nucleic acid in said composition comprises a polynucleotide, or

- wherein a bacterium or a yeast cell in said composition comprises or expresses a polynucleotide,

said polynucleotide having a nucleotide sequence selected from the group comprising:

(i) sequences represented by any of SEQ ID NOs 2364, 2366, 2368, 2370, 2372, 2384 to 2460, 2461, 2466, 2471, 2476 or 2481, or the complement thereof,

(ii) sequences which are at least 70 %, preferably at least 75%, 80%, 85%, 90%, more preferably at least 95%, 96%, 97%, 98% or 99% identical to a sequence represented by any of SEQ ID NOs 2364, 2366, 2368, 2370, 2372, 2384 to 2460, 2461, 2466, 2471, 2476 or 2481, or the complement thereof, and

(iii) sequences comprising at least 17 contiguous nucleotides of any of the sequences represented by SEQ ID NOs 2364, 2366, 2368, 2370, 2372, 2384 to 2460, 2461, 2466, 2471, 2476 or 2481, or the complement thereof,

or wherein said nucleic acid sequence is an orthologue of a gene comprising at least 17 contiguous nucleotides of any of SEQ ID NOs 2384 to 2460, or the complement thereof.

31.   Use of a composition of any of claims 10 to 18, a spray of claim 19, or a housing, trap or bait of claim 20 in a pharmaceutical or veterinary application.

32.   A method for preventing insect growth on a plant or for preventing insect infestation of a plant comprising applying a composition of any of claims 10 to 18 or a spray of claim 19 to said plant.

33.   A method for improving yield, comprising applying to a plant an effective amount of a composition of any of claims 10 to 18 or a spray of claim 19.

34.   The method of claim 32 or 33 wherein said plant is chosen from the group comprising alfalfa, apple, apricot, artichoke, asparagus, avocado, banana, barley, beans, beet, blackberry, blueberry, broccoli, brussel sprouts, cabbage, canola, carrot, cassava, cauliflower, a cereal, celery, cherry, citrus, clemintine, coffee, corn, cotton, cucumber, eggplant, endive, eucalyptus, figes, grape, grapefruit, groundnuts, ground cherry, kiwifruit, lettuce, leek, lemon, lime, pine, maize, mango, melon, millet, mushroom, nut aot, okra, onion, orange, an ornamental plant or flower or tree, papaya,, parsley, pea, peach, peanut, peat, pepper, persimmon, pineapple, plantain, plum, pomegranate, potato, pumpkin, radicchio, radish, rapeseed, raspberry, rice, rye, sorghum, soy, soybean, spinach, strawberry, sugarbeet, sugargcane, sunflower, sweet poatao, tangerine, tea, tobacco, tomato, a vine, waetermelon, wheat, yams and zucchini.

34. The method according to any of claims 32 to 34 wherein said insect is selected from the group comprising *Leptinotarsa* spp. (e.g. *L. decemlineata* (Colorado potato beetle), *L. juncta* (false potato beetle), or *L. texana* (Texan false potato beetle)); *Lema* spp. (e.g. *L. trilineata* (three-lined potato beetle)); *Epitrix* spp. (e.g. *E. cucumeris* (potato flea beetle), *E. hirtipennis* (flea beetle), or *E. tuberis* (tuber flea beetle)); *Epicauta* spp. (e.g. *E. vittata* (striped blister beetle)); *Epilachna* spp. (e.g. *E. varivetis* (mexican bean beetle)); *Phaedon* spp. (e.g. *P. cochleariae* (mustard leaf beetle)); *Nilaparvata* spp. (e.g. *N. lugens (brown planthopper))*; *Laodelphax* spp. (e.g. *L. striatellus (*small brown planthopper)); *Nephotettix* spp. (e.g. *N. virescens* or *N. cincticeps* (green leafhopper), or *N.nigropictus* (rice leafhopper)); *Sogatella* spp. (e.g. *S. furcifera* (white-backed planthopper)); *Acheta* spp. (e.g. *A. domesticus* (house cricket)); *Blissus* spp. (e.g. *B. leucopterus leucopterus* (chinch bug)); *Scotinophora* spp. (e.g. *S. vermidulate* (rice blackbug)); *Acrosternum* spp. (e.g. *A. hilare* (green stink bug)); *Parnara* spp. (e.g. *P. guttata* (rice skipper)); *Chilo* spp. (e.g. *C. suppressalis* (rice striped stem borer), *C. auricilius* (gold-fringed stem borer), or *C. polychrysus* (dark-headed stem borer)); *Chilotraea* spp. (e.g. *C. polychrysa* (rice stalk borer)); *Sesamia* spp. (e.g. *S. inferens* (pink rice borer)); *Tryporyza* spp. (e.g. *T. innotata* (white rice borer), or *T. incertulas* (yellow rice borer)); *Cnaphalocrocis* spp. (e.g. *C. medinalis* (rice leafroller)); *Agromyza* spp. (e.g. *A. oryzae* (leafminer), or *A. parvicornis* (corn blot leafminer)); *Diatraea* spp. (e.g. *D. saccharalis* (sugarcane borer), *or D. grandiosella* (southwestern corn borer)); *Narnaga* spp. (e.g. *N. aenescens* (green rice caterpillar)); *Xanthodes* spp. (e.g. *X. transversa* (green caterpillar)); *Spodoptera* spp. (e.g. *S. frugiperda* (fall armyworm), *S. exigua* (beet armyworm), *S. littoralis* (climbing cutworm), or *S. praefica* (western yellowstriped armyworm)); *Mythimna* spp. (e.g. *Mythmna (Pseudaletia) seperata* (armyworm)); *Helicoverpa* spp. (e.g. *H. zea* (corn earworm)); *Colaspis* spp. (e.g. *C. brunnea* (grape colaspis)); *Lissorhoptrus* spp. (e.g. *L. oryzophilus* (rice water weevil)); *Echinocnemus* spp. (e.g. *E. squamos* (rice plant weevil)); *Diclodispa* spp. (e.g. *D. armigera* (rice hispa)); *Oulema* spp. (e.g. *O. oryzae* (leaf beetle); *Sitophilus* spp. (e.g. *S. oryzae* (rice weevil)); *Pachydiplosis* spp. (e.g. *P. oryzae* (rice gall midge)); *Hydrellia* spp. (e.g. *H. griseola* (small rice leafminer), or *H. sasakii* (rice stem maggot)); *Chlorops* spp. (e.g. *C. oryzae* (stem

maggot)); *Diabrotica* spp. (e.g. *D. virgifera virgifera* (western corn rootworm), *D. barberi* (northern corn rootworm), *D. undecimpunctata howardi* (southern corn rootworm), *D. virgifera zeae* (Mexican corn rootworm); *D. balteata* (banded cucumber beetle)); *Ostrinia* spp. (e.g. *O. nubilalis* (European corn borer)); *Agrotis* spp. (e.g. *A.ipsilon* (black cutworm)); *Elasmopalpus* spp. (e.g. *E. lignosellus* (lesser cornstalk borer)); *Melanotus* spp. (wireworms); *Cyclocephala* spp. (e.g. *C. borealis* (northern masked chafer), or *C. immaculata* (southern masked chafer)); *Popillia* spp. (e.g. *P. japonica* (Japanese beetle)); *Chaetocnema* spp. (e.g. *C. pulicaria* (corn flea beetle)); *Sphenophorus* spp. (e.g. *S. maidis* (maize billbug)); *Rhopalosiphum* spp. (e.g. *R. maidis* (corn leaf aphid)); *Anuraphis* spp. (e.g. *A. maidiradicis* (corn root aphid)); *Melanoplus* spp. (e.g. *M. femurrubrum* (redlegged grasshopper) *M. differentialis* (differential grasshopper) or *M. sanguinipes* (migratory grasshopper)); *Hylemya* spp. (e.g. *H. platura* (seedcorn maggot)); *Anaphothrips* spp. (e.g. *A. obscrurus* (grass thrips)); *Solenopsis* spp. (e.g. *S. milesta* (thief ant)); *or* spp. (e.g. *T. urticae* (twospotted spider mite), *T. cinnabarinus* (carmine spider mite); *Helicoverpa* spp. *(e.g. H. zea* (cotton bollworm), or *H. armigera* (American bollworm)); *Pectinophora* spp. (e.g. *P. gossypiella* (pink bollworm)); *Earias* spp. (e.g. *E. vittella* (spotted bollworm)); *Heliothis* spp. (e.g. *H. virescens* (tobacco budworm)); *Anthonomus* spp. (e.g. *A. grandis* (boll weevil)); *Pseudatomoscelis* spp. (e.g. *P. seriatus* (cotton fleahopper)); *Trialeurodes* spp. (e.g. *T. abutiloneus* (banded-winged whitefly) *T. vaporariorum* (greenhouse whitefly)); *Bemisia* spp. (e.g. *B. argentifoli* (silverleaf whitefly)); *Aphis* spp. (e.g. *A. gossypii* (cotton aphid)); *Lygus* spp. (e.g. *L. lineolaris* (tarnished plant bug) or *L. hesperus* (western tarnished plant bug)); *Euschistus* spp. (e.g. *E. conspersus* (consperse stink bug)); *Chlorochroa* spp. (e.g. *C. sayi* (Say stinkbug)); *Nezara* spp. (e.g. *N. viridula* (southern green stinkbug)); *Thrips* spp. (e.g. *T. tabaci* (onion thrips)); *Frankliniella* spp. (e.g. *F. fusca* (tobacco thrips), or *F. occidentalis* (western flower thrips)); *Empoasca* spp. (e.g. *E. fabae* (potato leafhopper)); *Myzus* spp. (e.g. *M. persicae* (green peach aphid)); *Paratrioza* spp. (e.g. *P. cockerelli* (psyllid)); *Conoderus* spp. (e.g. *C. falli* (southern potato wireworm), or *C. vespertinus* (tobacco wireworm)); *Phthorimaea* spp. (e.g. *P. operculella* (potato tuberworm)); *Macrosiphum* spp. *(e.g. M. euphorbiae* (potato aphid)); *Thyanta* spp. *(e.g. T. pallidovirens* (redshouldered stinkbug)); *Phthorimaea* spp. *(e.g. P. operculella* (potato tuberworm)); *Helicoverpa* spp. *(e.g. H. zea* (tomato fruitworm); *Keiferia* spp. *(e.g. K. lycopersicella* (tomato pinworm)); *Limonius* spp. (wireworms); *Manduca* spp. *(e.g. M. sexta* (tobacco hornworm), or *M. quinquemaculata* (tomato hornworm)); *Liriomyza* spp. *(e.g. L. sativae, L. trifolli* or *L. huidobrensis* (leafminer)); *Drosophilla* spp. (e.g. *D. melanogaster, D. yakuba, D. pseudoobscura* or *D. simulans*); *Carabus* spp. (e.g. *C. granulatus*); *Chironomus* spp. (e.g. *C. tentanus*); *Ctenocephalides* spp. (e.g. *C. felis* (cat flea)); *Diaprepes* spp. (e.g. *D. abbreviatus* (root weevil)); *Ips* spp. (e.g. *I. pini* (pine engraver)); *Tribolium* spp. (e.g. *T. castaneum* (red floor beetle)); *Glossina* spp. (e.g. *G. morsitans* (tsetse fly)); *Anopheles* spp. (e.g. *A. gambiae* (malaria mosquito)); *Helicoverpa* spp. (e.g. *H. armigera* (African Bollworm)); *Acyrthosiphon* spp. (e.g. *A. pisum* (pea aphid)); *Apis* spp. (e.g. *A. melifera* (honey bee)); *Homalodisca* spp. (e.g. *H. coagulate* (glassy-winged sharpshooter)); Aedes spp. (e.g. Ae. aegypti *(yellow fever mosquito)); Bombyx spp. (e.g. B. mori (silkworm)); Locusta spp. (e.g. L. migratoria* (migratory locust)); *Boophilus* spp. (e.g. *B. microplus* (cattle tick)); *Acanthoscurria* spp. (e.g. *A.*

gomesiana (red-haired chololate bird eater)); *Diploptera* spp. (e.g. *D. punctata* (pacific beetle cockroach)); *Heliconius* spp. (e.g. *H. erato* (red passion flower butterfly) or *H. melpomene* (postman butterfly)); *Curculio* spp. (e.g. *C. glandium* (acorn weevil)); *Plutella* spp. (e.g. *P. xylostella* (diamontback moth)); *Amblyomma* spp. (e.g. *A. variegatum* (cattle tick)); *Anteraea* spp. (e.g. *A. yamamai* (silkmoth)); and *Armigeres* spp. (e.g. *A. subalbatus*).

34.   A method for preventing insect growth on a substrate comprising applying a composition of any of claims 10 to 18 or a spray of claim 19 to said substrate.

35.   A method for treating and/or preventing a disease or a condition caused by a target organism, comprising administering to a subject in need of such treatment and/or prevention, a composition of any of claims 10 to 18 or a spray of claim 19.
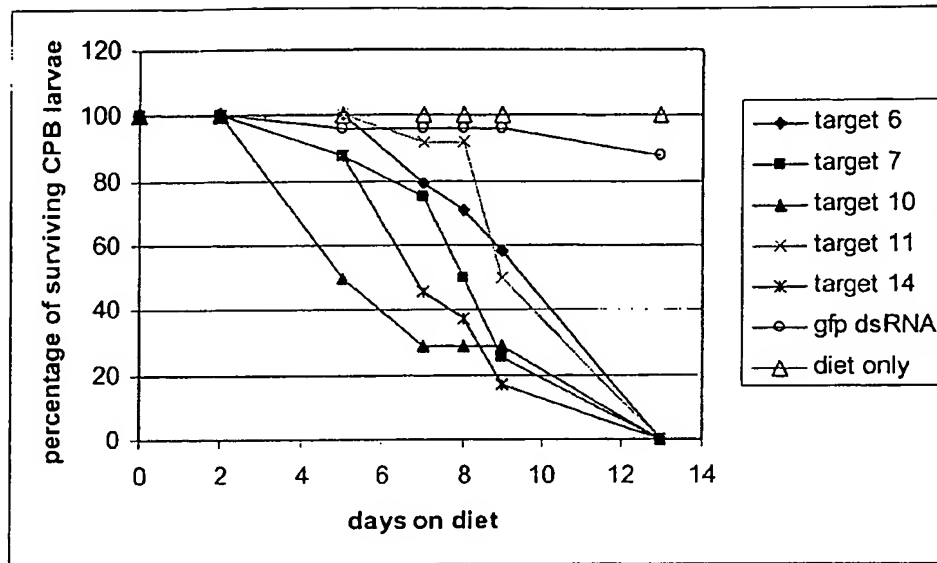
FIGURE 1-LD
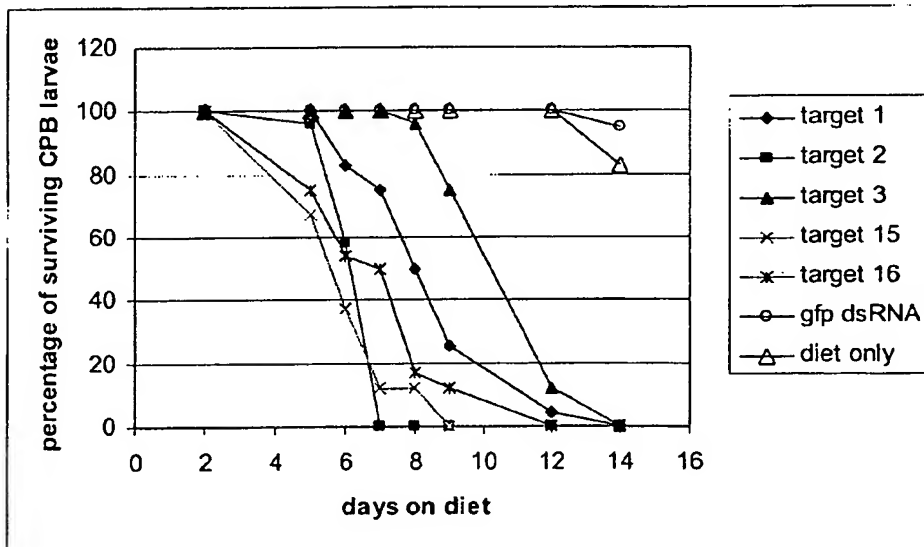
FIGURE 2-LD
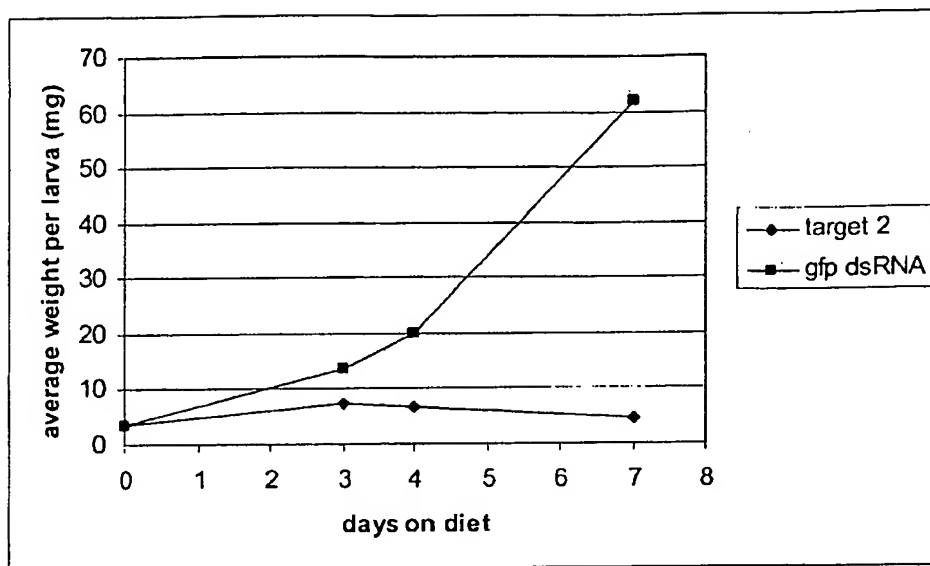
FIGURE 3-LD
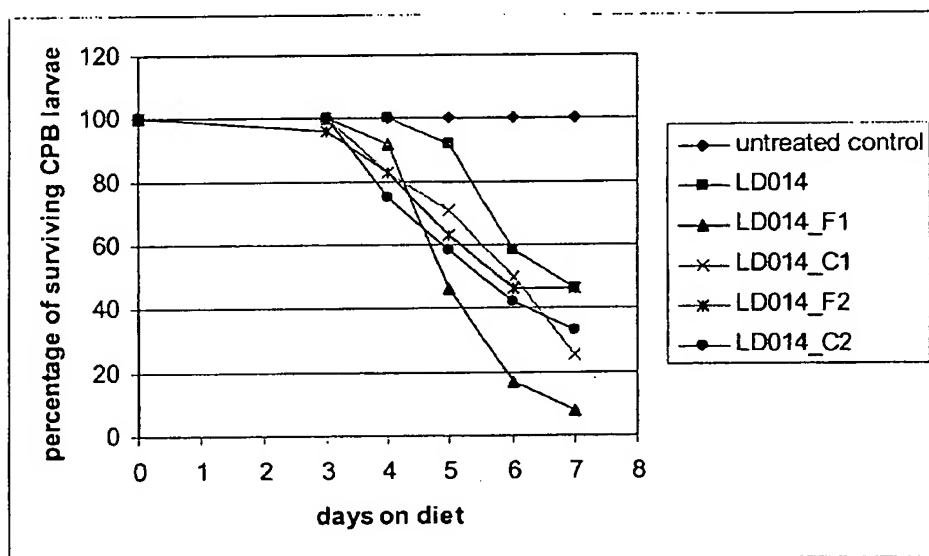
FIGURE 4-LD
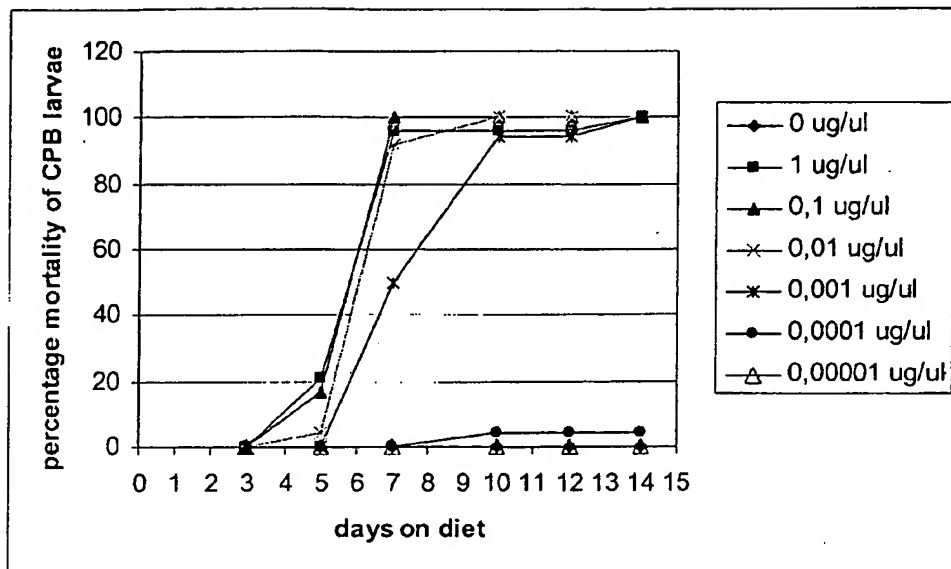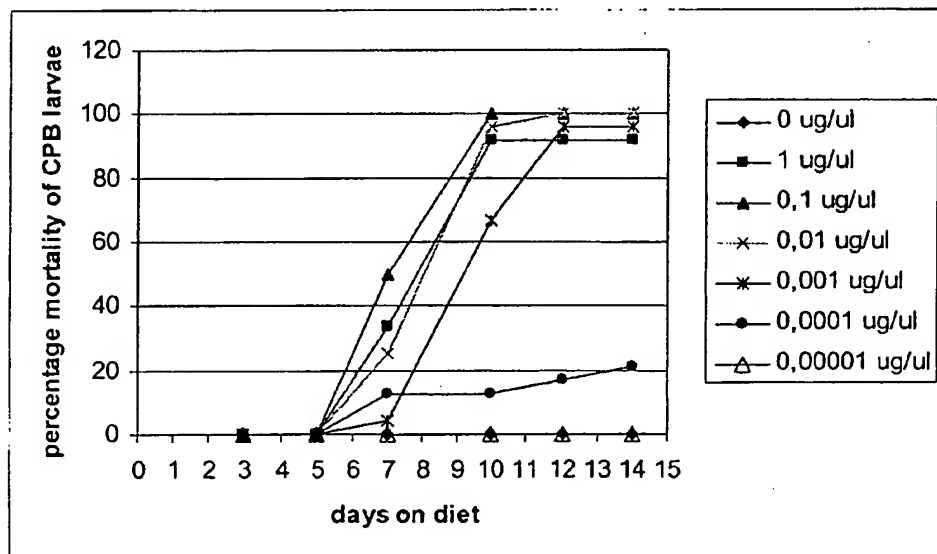
FIGURE 5-LD (a)

FIGURE 5-LD (b)
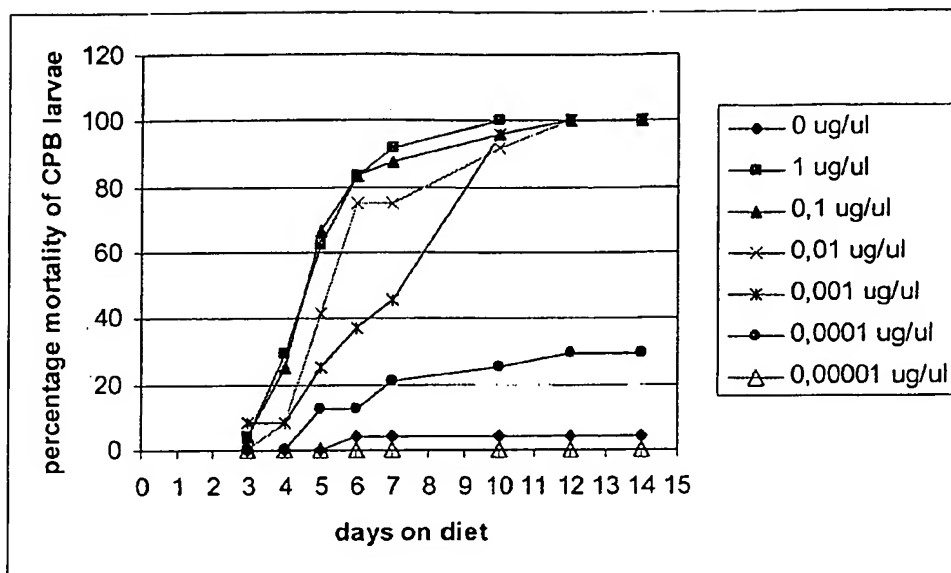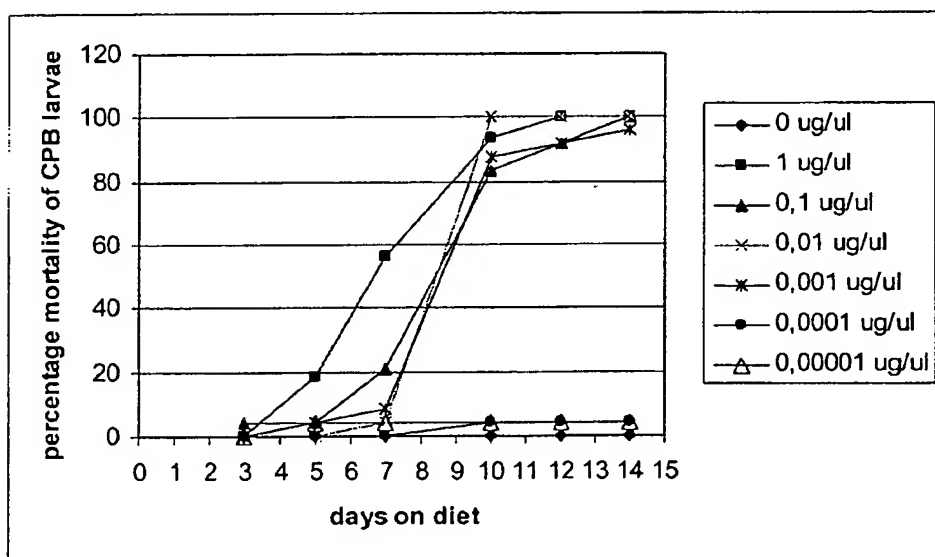
FIGURE 5-LD (c)

FIGURE 5-LD (d)
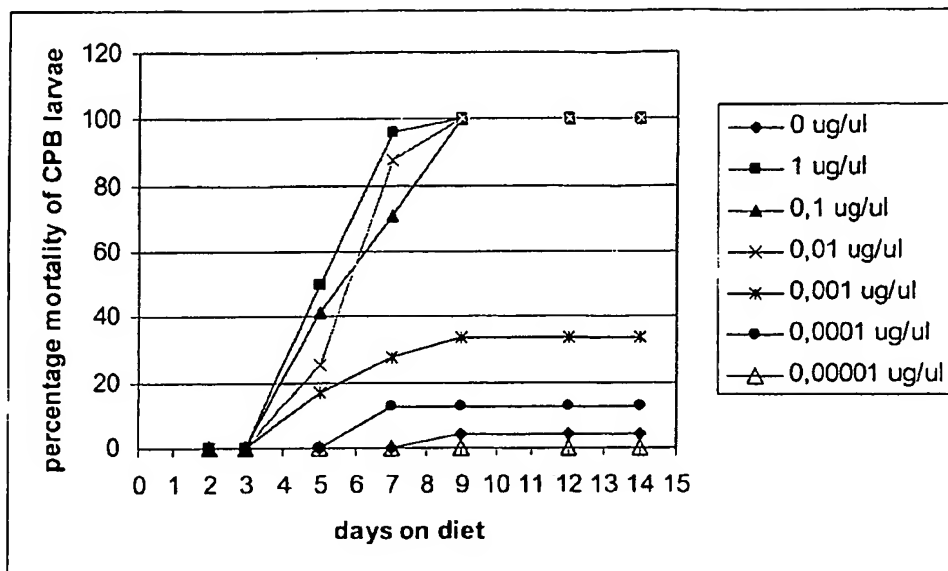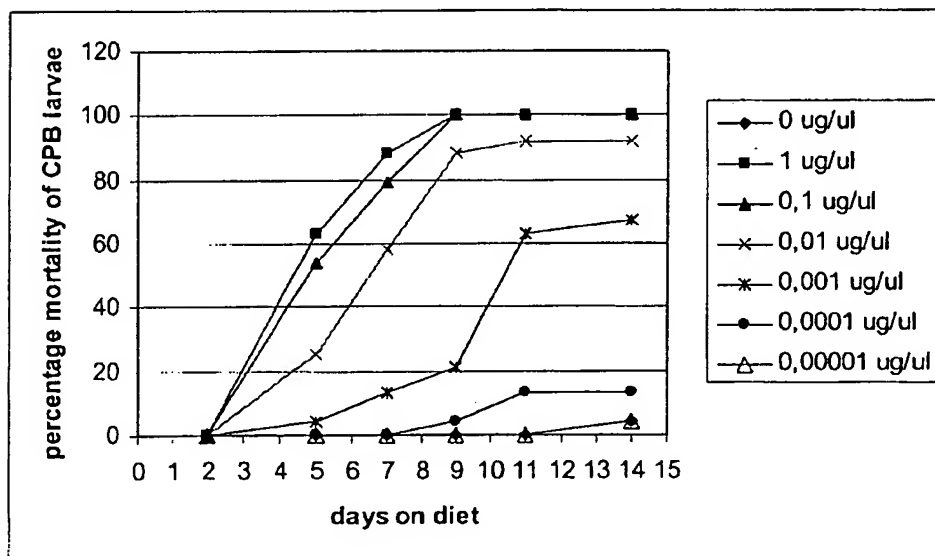
FIGURE 5-LD (e)

FIGURE 5-LD (f)
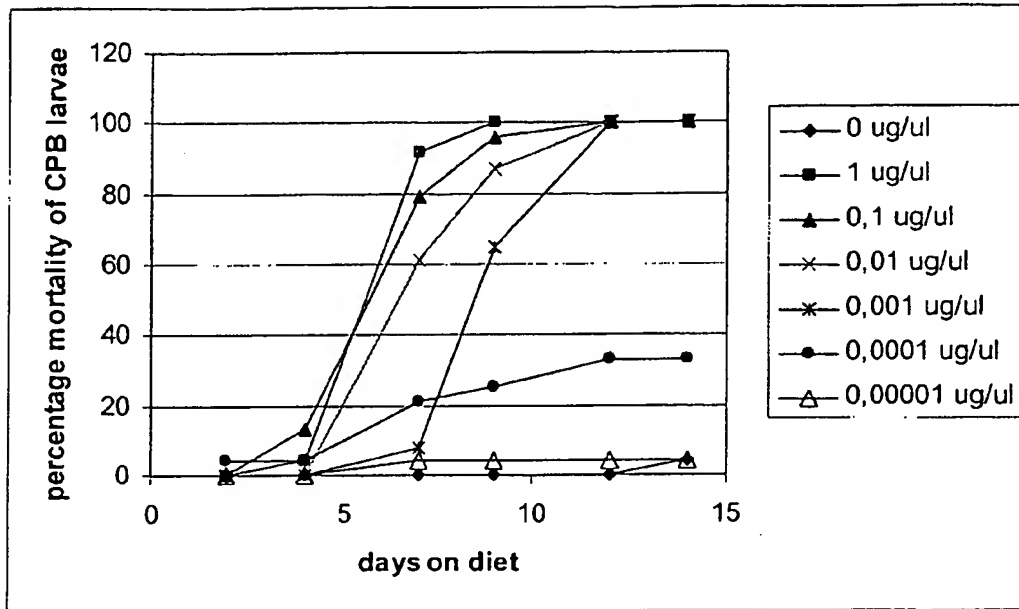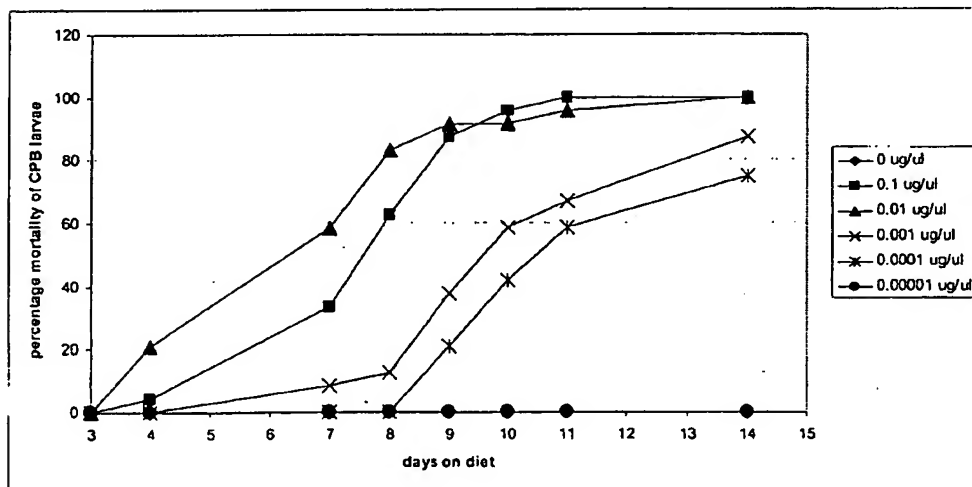
FIGURE 5-LD (g)

FIGURE 5-LD (h)
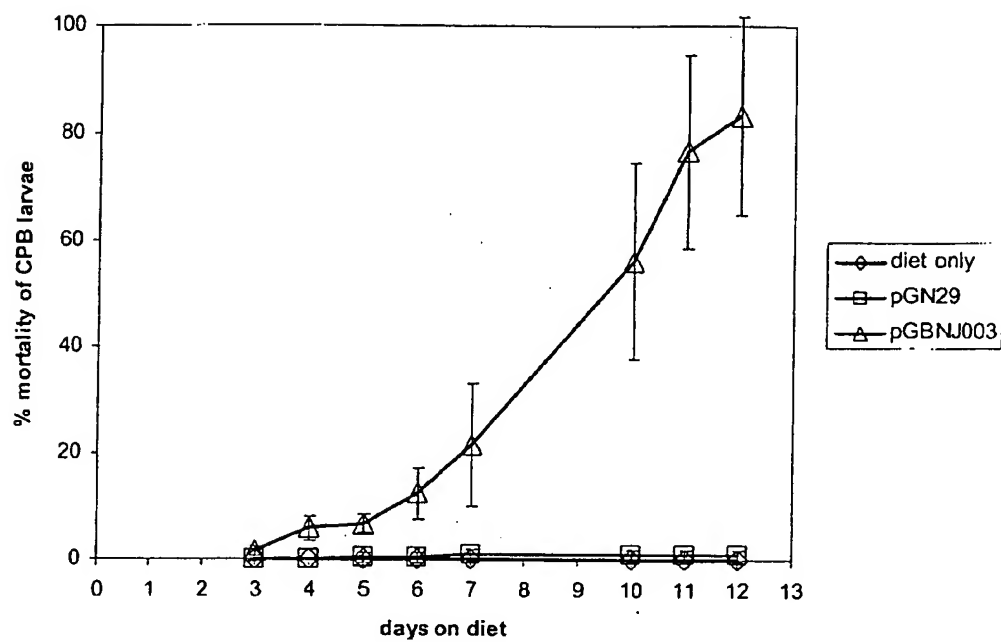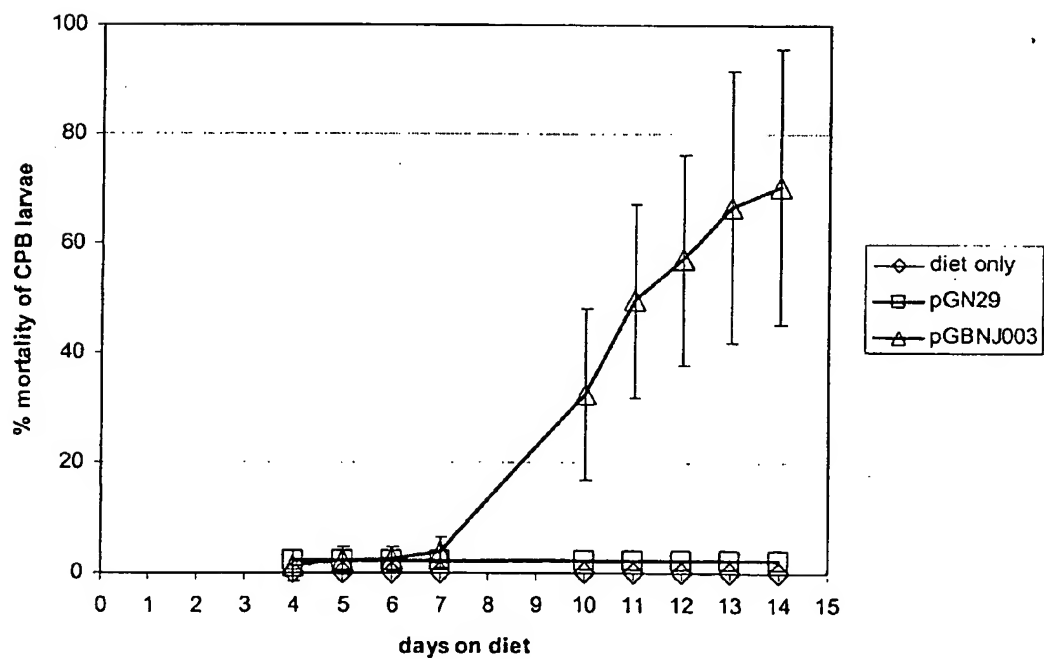
FIGURE 6-LD (a)

FIGURE 6-LD (b)
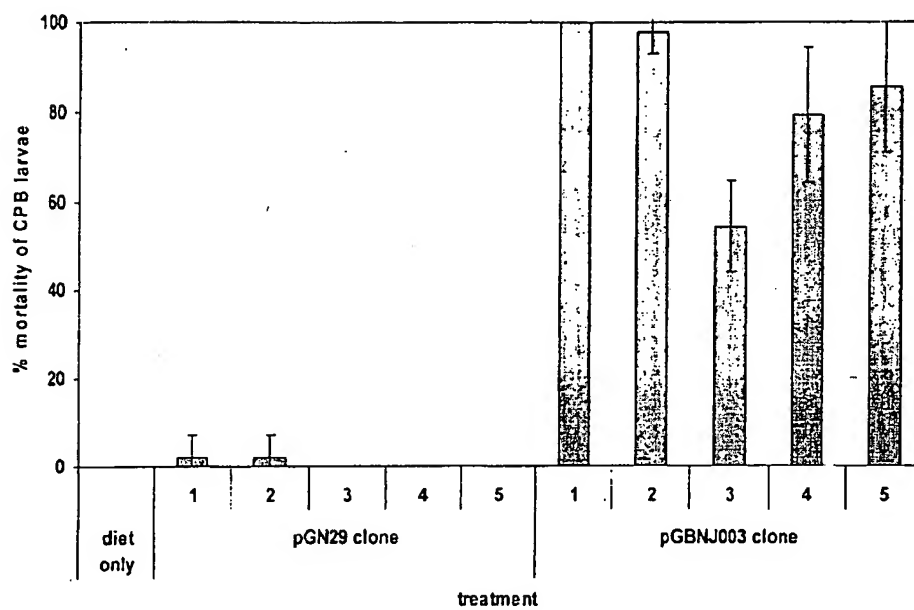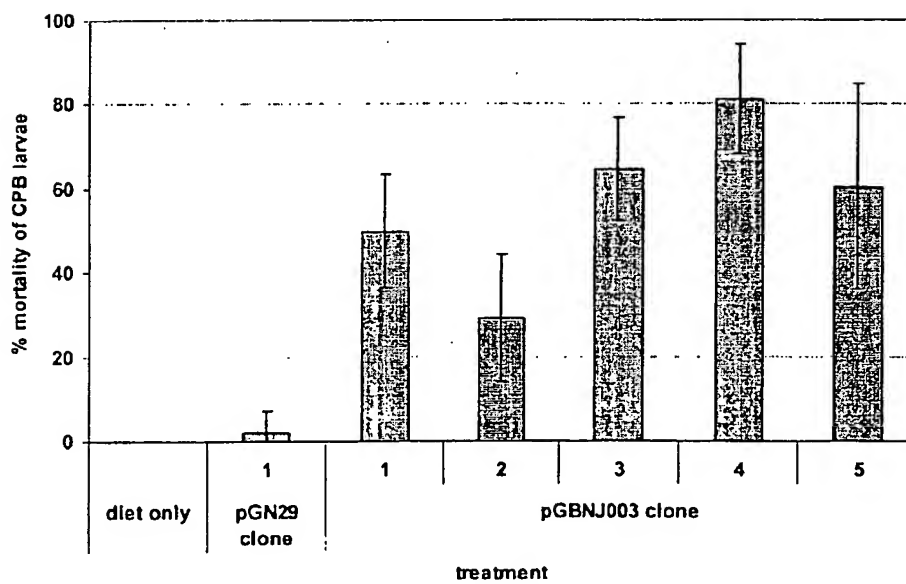
FIGURE 7-LD (a)

FIGURE 7-LD (b)
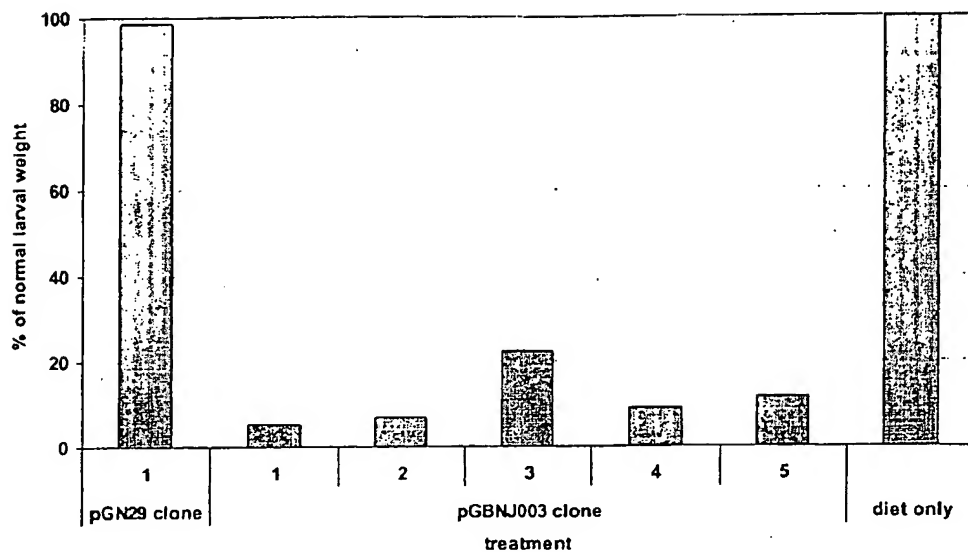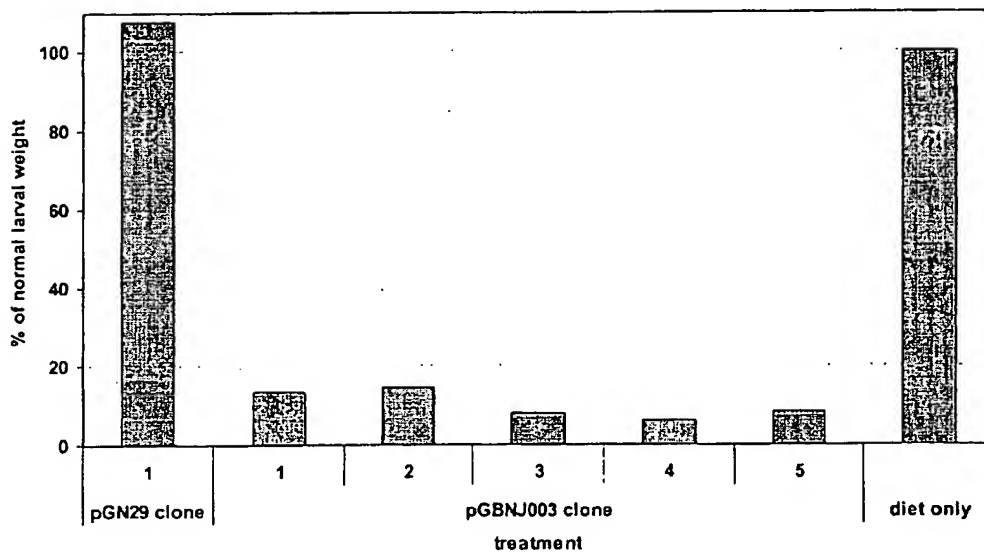
FIGURE 8-LD (a)

FIGURE 8-LD (b)
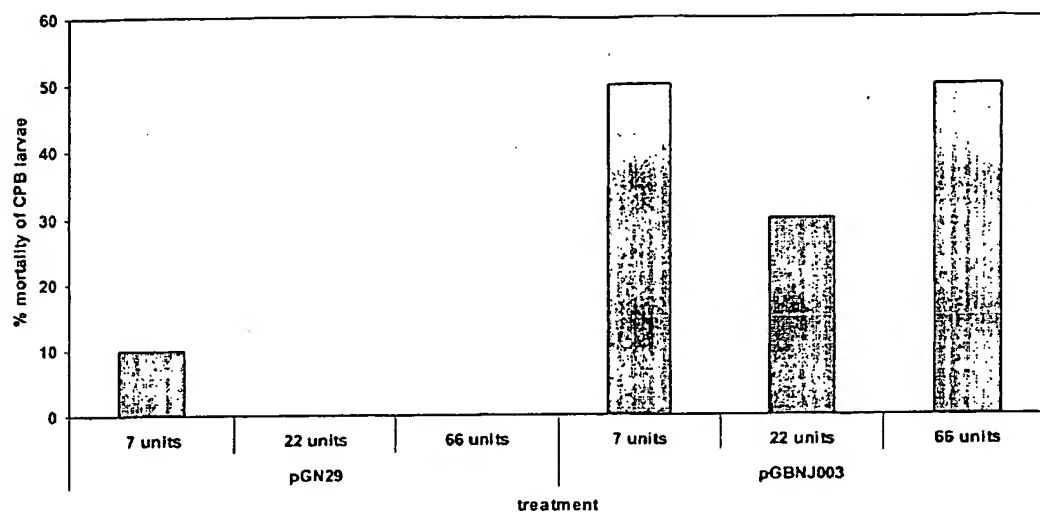
FIGURE 9-LD
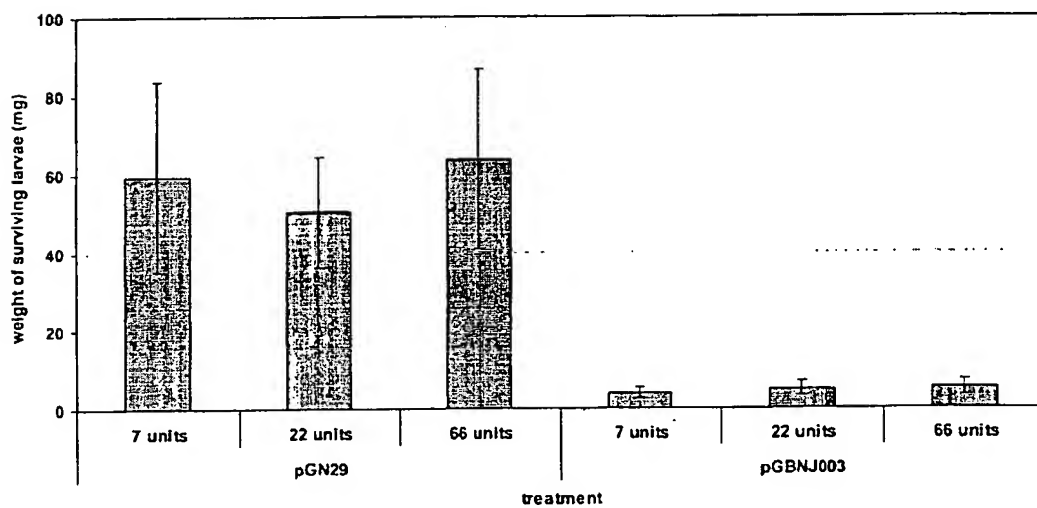
FIGURE 10-LD

FIGURE 11-LD
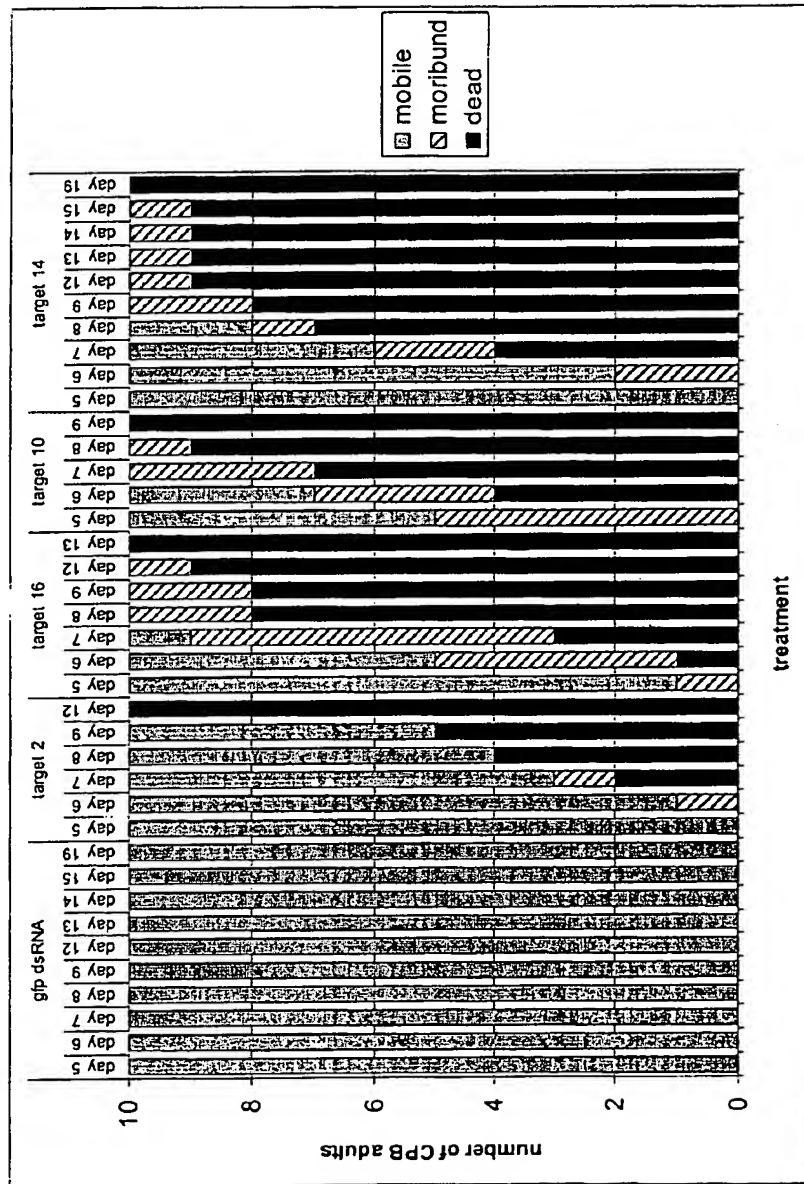
FIGURE 12-LD
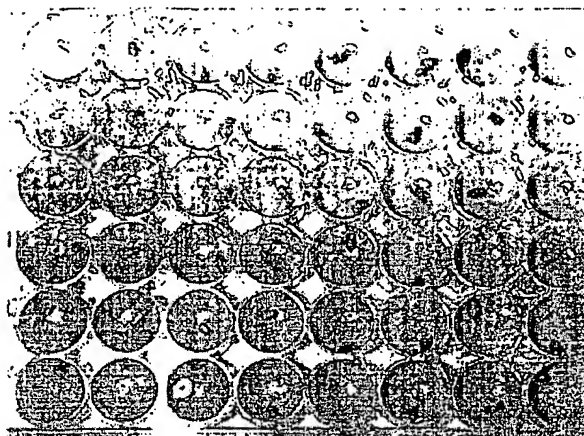
FIGURE 13-LD (a)
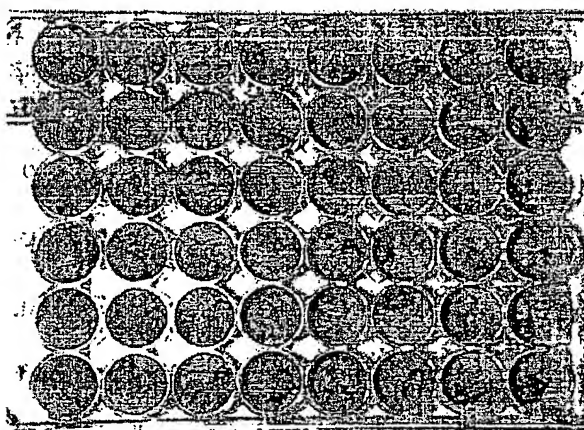
FIGURE 13-LD (b)
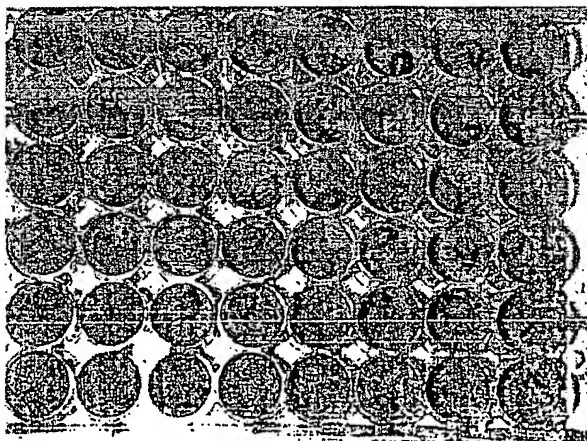
FIGURE 13-LD (c)
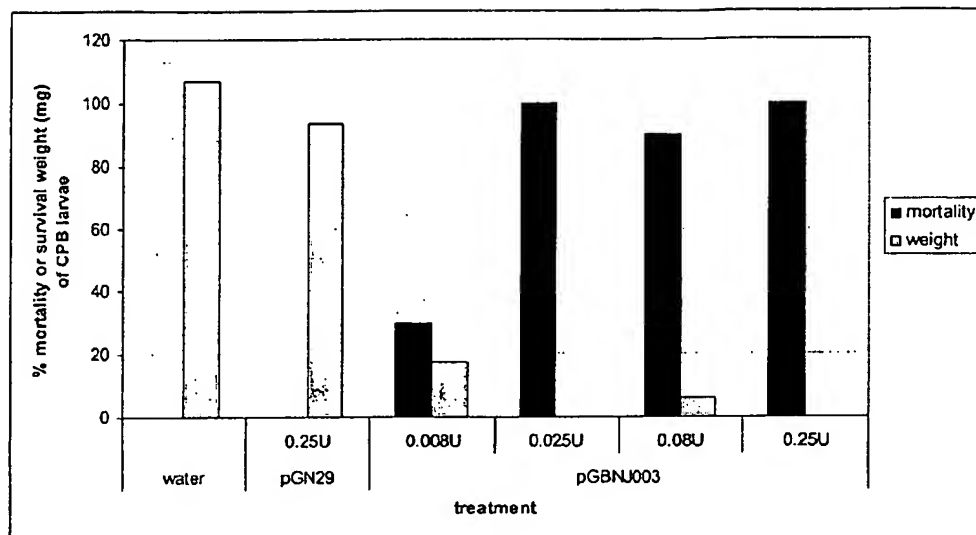
FIGURE 14-LD

FIGURE 15-LD (a)

FIGURE 15-LD (b)

FIGURE 15-LD (c)

FIGURE 15-LD (d)
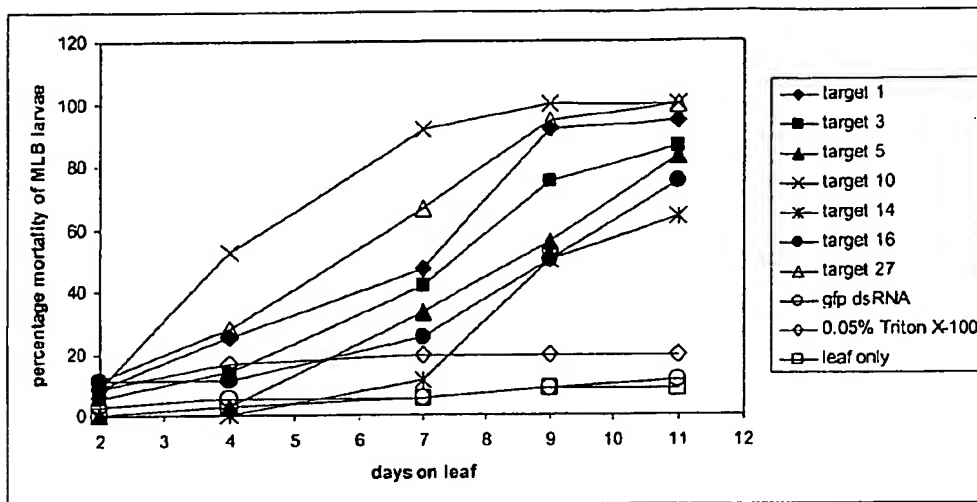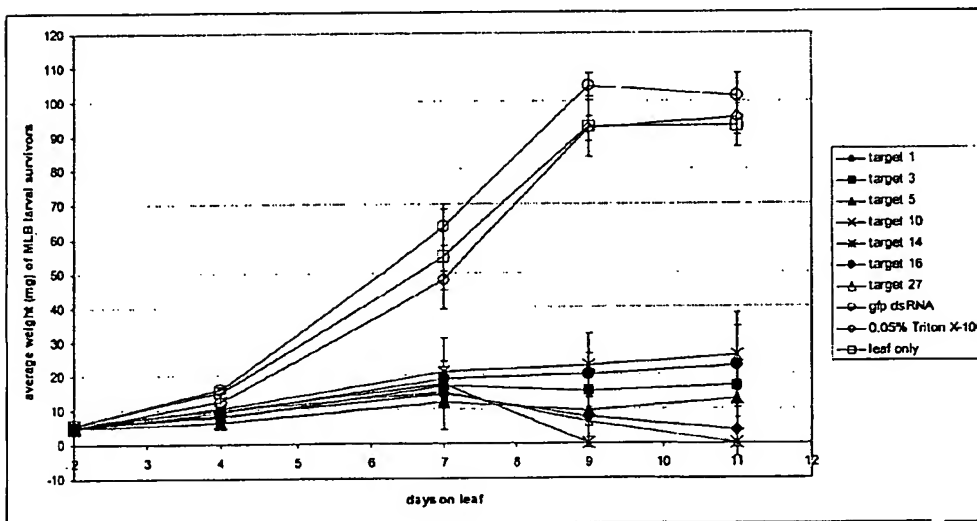
FIGURE 1-PC (a)

FIGURE 1-PC (b)
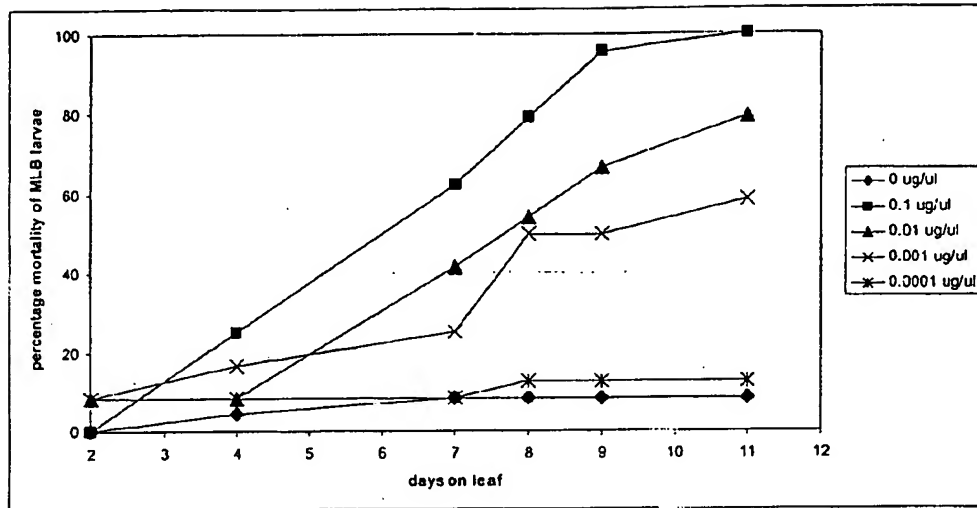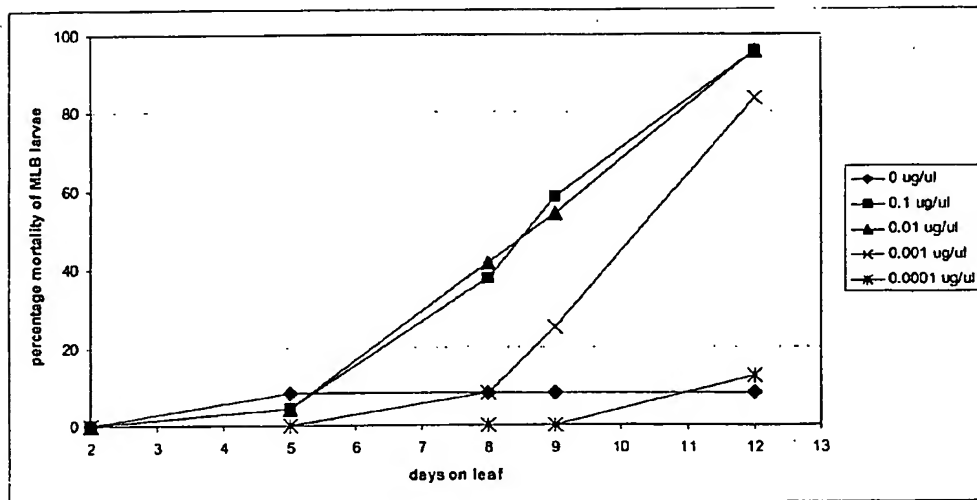
FIGURE 2-PC (a)

FIGURE 2-PC (b)
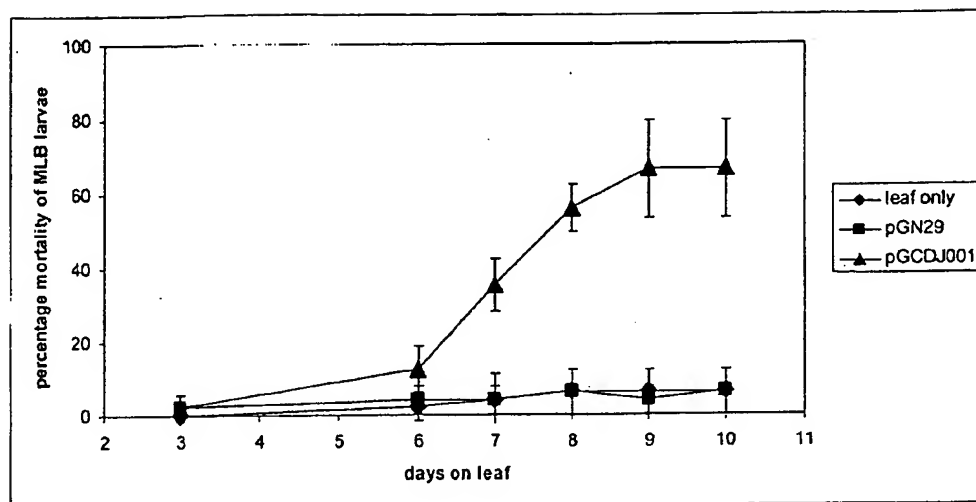
FIGURE 3-PC
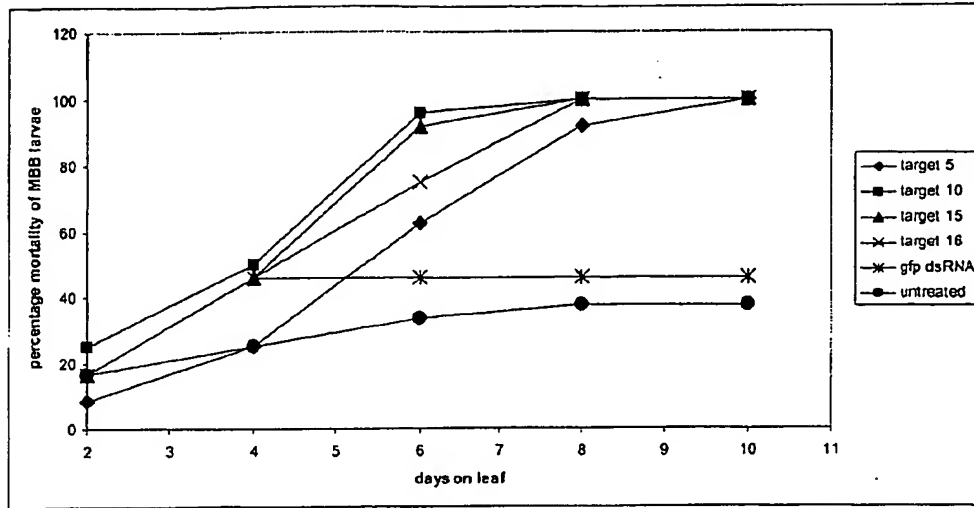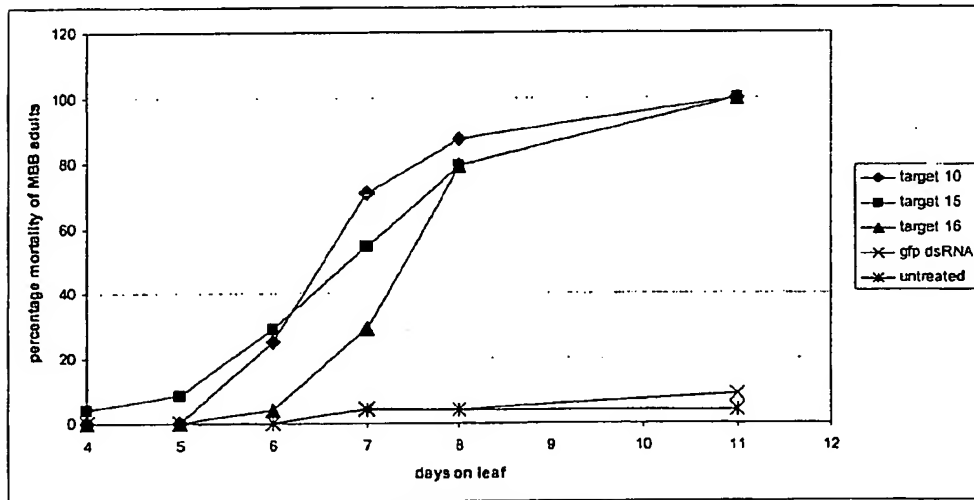
FIGURE 1-EV

FIGURE 2-EV (a)
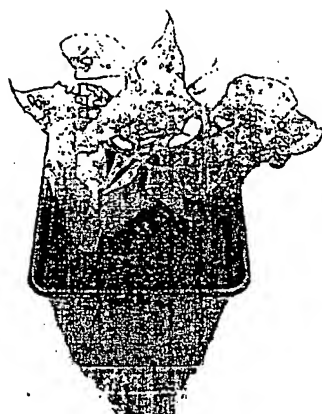
(i)

(ii)
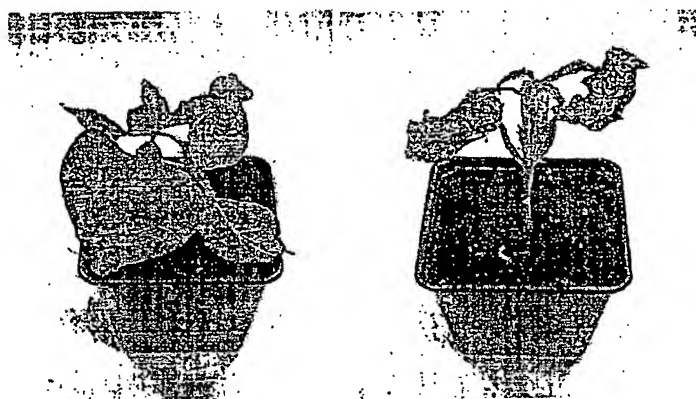
(iii)

(iv)

(v)

FIGURE 2-EV (b)
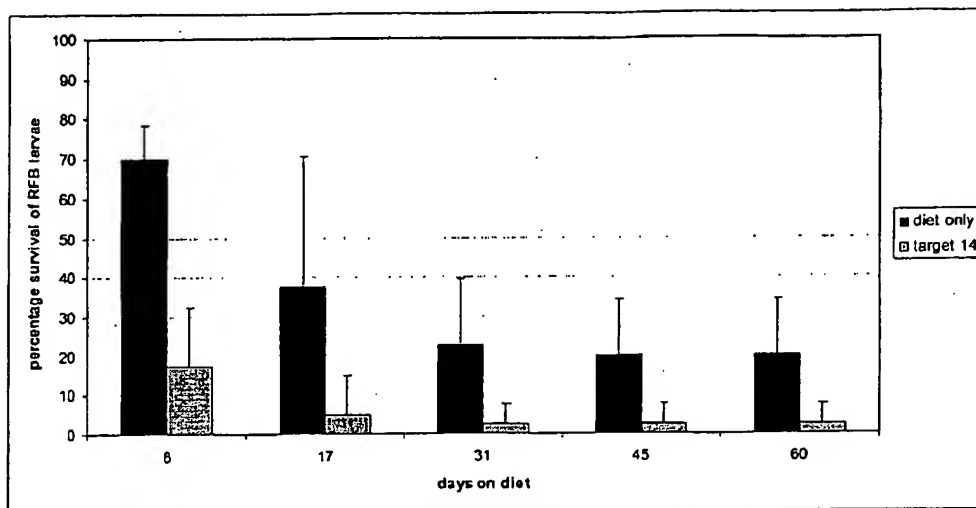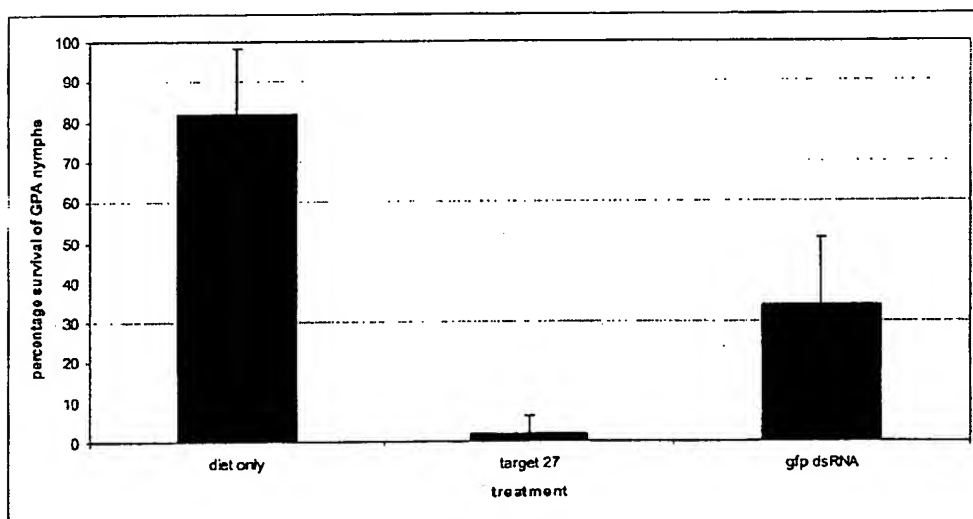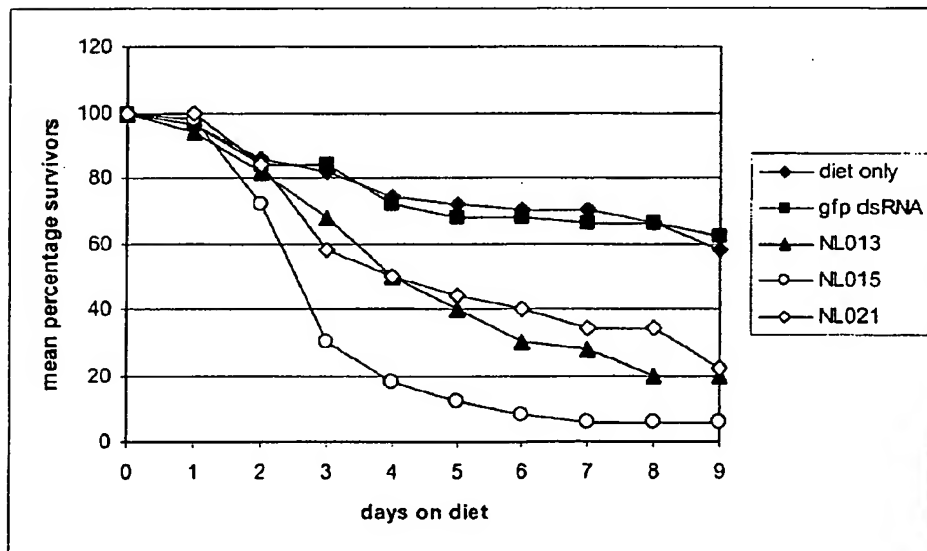
FIGURE 1-TC

FIGURE 1-MP
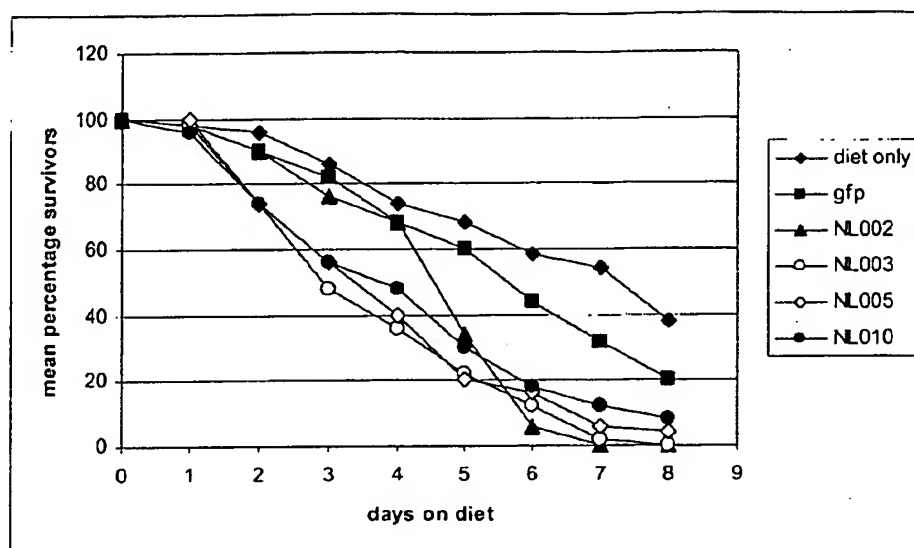
FIGURE 1-NL (a)
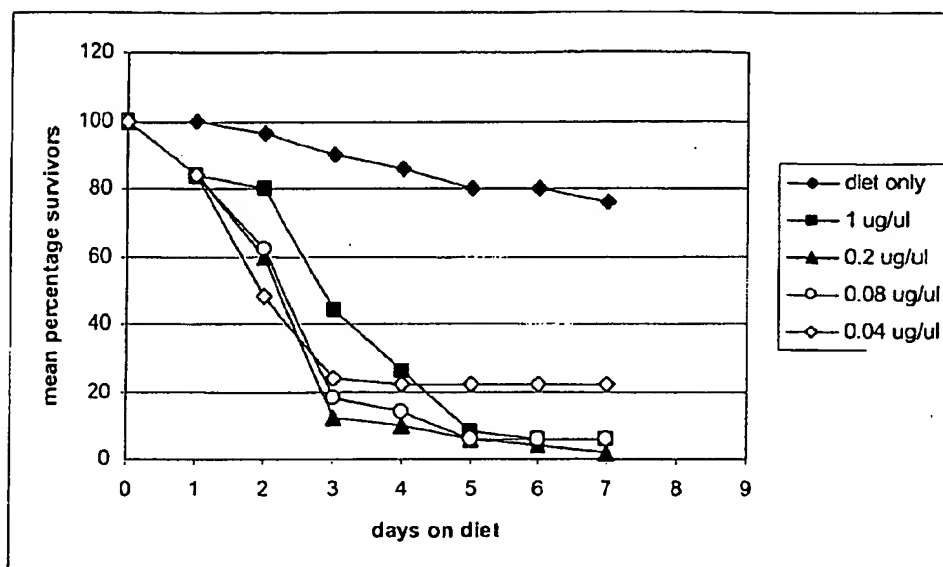

FIGURE 1-NL (b)

FIGURE 1-NL (c)

FIGURE 1-NL (d)

FIGURE 2-NL